Prediction of Milk Protein Concentration from Elements of the Metabolizable Protein System

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ABSTRACT

Elements of the metabolizable protein system in the United Kingdom were examined for their suitability as potential predictors of milk protein concentration. Models were based on data from 163 cows offered five forage mixtures for ad libitum intake plus concentrates at 3, 6, or 9 kg/d of dry matter. The models were then tested on a separate data set of 100 cows offered seven forage mixtures for ad libitum intake plus concentrates at 6 kg/d of dry matter. To minimize problems with collinearity, variables were arranged hierarchically; successive elements were components of variables at higher element levels. Variables from different element levels were not used in the same models. Models were constructed using ridge regression to minimize problems with collinearity.

The fit and precision of prediction were generally poor because these models did not take into account animal variables. Models using undegradable dietary protein performed slightly better than did those using digestible undegraded protein. The use of slowly degradable protein and quickly degradable protein rather than rumen-degradable protein generally resulted in improvements in prediction. Models using neutral detergent fiber and quickly fermented carbohydrate were better than those using total carbohydrate. We concluded that there was little to be gained from using the elements of the metabolizable protein system considered here for the prediction of milk protein concentration.
(**Key words**: milk protein, metabolizable protein, models)

Abbreviation key: **DUP** = digestible undegraded protein, **MP** = metabolizable protein, **MSPE** = mean square prediction error, **QFC** = quickly fermentable carbohydrate, **UDP** = undegradable dietary protein, **WSC** = water-soluble carbohydrate.

INTRODUCTION

Milk producers in the United Kingdom are generally paid according to production of milk fat and protein as well as total volume. The importance of protein in payment schedules is likely to increase as the demand for milk fat continues to decline. Therefore, it is important for producers to be able to predict the effect of changing nutritional inputs on milk protein concentration. Relatively few predictive models for milk protein concentration have been reported in the literature (4, 6, 12, 15). Of those reports, only the results of Rook et al. (12) relate to conditions in the United Kingdom. The percentage of variation in milk protein concentration accounted for by the models of Rook et al. (12) was disappointingly small. Rook et al. (12) used a set of feed descriptors that was then in common use, including only total nitrogen and silage ammonia nitrogen to describe the nitrogenous components of the feed. Since then, the metabolizable protein (**MP**) system (1, 3) has been introduced. This system incorporates a considerably more detailed description of the feeds.

Because of the increased importance of milk protein concentration and the availability of better feed descriptors, the prediction of milk protein concentration needs to be reexamined. This study was designed to examine the usefulness of elements of the MP system. Particular attention was paid to the inherent collinearity among some of these elements, which might result in models with poor predictive power. These concerns were addressed by adopting a hierarchical order of the feed descriptors such that no descriptor was used in the same model as its components.

TABLE 1. Variables used in analyses.

Variable	Estimation data		Test data	
	$\overline{X}$	SE	$\overline{X}$	SE
CP, g/kg of DM	175	8.1	184	7.2
Rumen-degradable protein, g/kg of DM	108	8.5	95	8.7
Undegradable dietary protein, g/kg of DM	67	6.7	89	8.3
Quickly degradable protein, g/kg of DM	63	7.6	55	7.2
Slowly degradable protein, g/kg of DM	45	4.0	40	1.9
Digestible undegraded protein, g/kg of DM	38	4.2	34	3.0
Total carbohydrate, g/kg of DM	690	11.2	606	29.1
Neutral detergent fiber, g/kg of DM	352	43.8	430	24.2
Quickly fermented carbohydrate, g/kg of DM	193	21.5	176	21.5
Starch, g/kg of DM	124	21.5	118	23.4
Water-soluble carbohydrate, g/kg of DM	68	25.5	58	17.8
Milk production, kg/d	24.4	0.41	25.5	0.40
Milk fat concentration, g/kg	39.7	0.56	41.4	0.52
Milk protein concentration, g/kg	31.3	0.21	31.1	0.24
Milk lactose concentration, g/kg	46.8	0.01	45.3	0.02

MATERIALS AND METHODS

Estimation Data

Data used to construct the models were from an experiment carried out at the Centre for Dairy Research (Reading, England) (8). Individual weekly records were available for 163 multiparous Holstein-Friesian cows at wk 4 to 20 of lactation. Cows were offered grass silage or one of four forage mixtures plus concentrate at 3, 6, or 9 kg/d of DM. The forage mixtures were grass silage plus brewers grains (2:1; DM basis), grass silage plus fodder beet (2:1; DM basis), grass silage plus maize silage (2:1; DM basis), or grass silage plus maize silage (1:3; DM basis). Concentrates were formulated such that the whole diet supplied a constant ratio of digestible undegraded protein (DUP) to effective RDP of 280 g/kg when offered at 6 kg/d of DM. Eighteen variables were considered to be potential predictors of milk protein concentration; details of these variables are shown in Table 1. Dry matter content of all concentrate feeds was determined by drying at 105°C overnight; for forages, the toluene method (2) was used. Ash content was determined at 550°C for 16 h in a muffle furnace. Crude protein was calculated as N × 6.25 by the Kjeldahl method (2). Water-soluble car-

bohydrate (WSC) was determined by the method of Smith et al. (13). Neutral detergent fiber was determined by the method of Van Soest and Wine (17). Starch was determined by the method of MacRae and Armstrong (7). Quickly fermentable carbohydrate (QFC) was calculated as the sum of starch and WSC. Total carbohydrate was calculated as the sum of QFC plus NDF. Protein fractions were calculated from book values (1) for the individual components of the forage mixtures and concentrates. Details of milk production and composition are also given in Table 1. Milk composition was analyzed using a Milkoscan analyzer (model 133b; Foss Electric, Hillerød, Denmark).

Test Data

A second set of data from the Centre for Dairy Research was used to test the models. These data were individual weekly records for 100 multiparous cows at wk 4 to 20 of lactation (9). The cows were offered grass silage or one of six forage mixtures plus concentrate at 6 kg/d of DM. The forage mixtures were the same as those used for the estimation data set plus two additional treatments: grass silage plus fermented whole-crop wheat (2:1; DM basis) and grass silage plus whole-crop wheat treated with urea (2:1; DM basis). The concentrate was formulated such that the supply of dietary CP was equalized for all diets. Details of the variables recorded in this data set are shown in Table 1. All variables were determined or calculated similar to the estimation data.

Statistical Analyses

Simple correlations between milk protein concentration and predictor variables were calculated. For more complex regression models, a major potential problem was the presence of collinearity between the predictor variables that caused unstable estimates of regression coefficients and poor prediction for the independent data sets. Two strategies were adopted to avoid this problem. First, the predictor variables were arranged in hierarchical order such that variables at one element level were components of variables at the next higher element level (Figure 1). Variables in different element levels were not used in the same model to avoid inherent collinearity. In addition, all models were constructed using ridge regression (5). The estimators of the regression coefficients produced by this method are biased but tend to have a smaller mean square error than ordinary least squares estimates and thus yield more accurate prediction for independent data sets. The technique has been exemplified by Rook et al. (11).
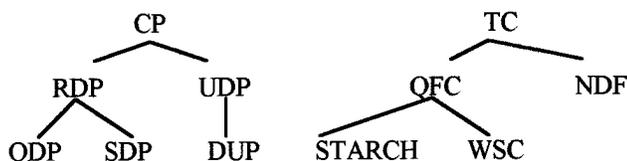
Figure 1. Hierarchical arrangement of variables used in model construction. TC = Total carbohydrate, UDP = undegradable dietary protein, QFC = quickly fermentable carbohydrate, QDP = quickly degradable protein, SDP = slowly degradable protein, DUP = digestible undegraded protein, and WSC = water-soluble carbohydrate.

TABLE 2. Simple correlations between milk protein concentration and potential predictor variables.

Variable[1]	Correlation[2]
CP	0.34
RDP	0.11
UDP	0.26
QDP	−0.08
SDP	0.38
DUP	0.26
TC	−0.29
NDF	−0.19
QFC	0.35
Starch	0.22
WSC	0.11

[1]UDP = Undegradable dietary protein, QDP = quickly degradable protein, SDP = slowly degradable protein, DUP = digestible undegraded protein, TC = total carbohydrate, QFC = quickly fermentable carbohydrate, and WSC = water-soluble carbohydrate.

[2]All correlations were significant ($P < 0.001$).

Actual and predicted milk protein concentrations in the test data were compared using the mean square prediction error (**MSPE**):

$$MSPE = (\overline{A} - \overline{P})^2 + S_p^2 (1 - b)^2 + (1 - r^2) S_A^2$$

where $\overline{A}$ and $\overline{P}$ = mean actual and predicted values, respectively; S_A^2 S_p^2 variances of the actual and predicted values, respectively; b = slope of the regression of actual values on predicted values; and r = correlation between actual and predicted values. The three components of MSPE are mean bias, the deviation of the slope of the regression of A on P from 1, and the random variation about this line. Mean bias generally reflects differences between estimation and test data, and line bias indicates problems with the functional form of the models. The proportional contribution of these components to MSPE is reported. The square root of MSPE is the mean prediction error, which is reported as a proportion of the mean actual value.

RESULTS

Simple correlations between milk protein concentration and potential predictor variables are shown in Table 2. Of the nitrogenous components, only slowly degradable protein was better correlated with milk protein concentration than was CP. The QFC was more correlated with milk protein concentration than was total carbohydrate, although its constituents, starch and WSC, were not as closely correlated.

Fit and prediction statistics for ridge regression models are shown in Table 3. Differences in fit among the models were small. Models using undegraded dietary protein (**UDP**) fitted slightly better than models using DUP. Models using NDF and QFC were better than those using total carbohydrate, but there was no further advantage from using starch and WSC. Models using DUP consistently predicted more

poorly than did those using UDP, but neither performed as well as models using CP, except when starch and WSC were included. The use of slowly degradable protein and quickly degradable protein rather than RDP generally resulted in small improvements in prediction. The effect on prediction of using starch and WSC rather than QFC was inconsistent.

DISCUSSION

The fit and precision of prediction of the models that are presented in this study are disappointingly small. However, these models are intended primarily to illustrate the relative merits of elements of the MP system as predictors of milk protein concentration. To obtain models with sufficient predictive power for use in practice would require the inclusion of animal variables, such as previous milk production and feed (10).

Comparison of these models with those of previous research is difficult because of the different variables used and the different data sets employed. However, the simple correlation with CP (0.34) was greater than that found by Spörndly (15) (0.06), and the correlation with NDF (−0.19) was less than that in previous analyses.

These results suggest that there is an effect to be gained, although small, from the use of detailed feed analysis over and above the use of CP and total carbohydrate. However, it should be noted that most of the calculations for the protein fractions were based on published standardized values (1) for the individual feed ingredients. The direct measurement of these variables could have possibly led to better

TABLE 3. Fit and prediction statistics for ridge regression models.

Variable[2]	R[2] for Estimation data	MSPE	Proportion of MSPE[1]			MPE[3]
			Bias	Line	Random	
		(g/kg)				
TC, CP	0.12	7.98	0.08	0.23	0.69	0.091
TC, UDP, RDP	0.16	9.96	0.13	0.29	0.58	0.100
TC, DUP, RDP	0.11	164.90	0.95	0.02	0.03	0.413
TC, UDP, QDP, SDP	0.17	6.63	0.01	0.14	0.85	0.083
TC, DUP, QDP, SDP	0.16	6.66	0.00	0.18	0.82	0.083
NDF, QFC, CP	0.20	6.99	0.03	0.16	0.81	0.085
NDF, QFC, UDP, RDP	0.21	7.92	0.09	0.20	0.71	0.091
NDF, QFC, DUP, RDP	0.19	9.13	0.00	0.38	0.62	0.097
NDF, QFC, UDP, QDP, SDP	0.19	6.55	0.03	0.11	0.86	0.082
NDF, QFC, DUP, QDP, SDP	0.19	6.48	0.02	0.11	0.87	0.082
NDF, Starch, WSC, CP	0.21	8.12	0.10	0.20	0.70	0.092
NDF, Starch, WSC, UDP, RDP	0.19	6.91	0.05	0.13	0.82	0.085
NDF, Starch, WSC, DUP, RDP	0.19	7.31	0.08	0.14	0.78	0.087
NDF, Starch, WSC, UDP, QDP, SDP	0.19	6.20	0.00	0.08	0.92	0.080
NDF, Starch, WSC, DUP, QDP, SDP	0.19	8.02	0.19	0.10	0.71	0.091

[1]Mean square prediction error.

[2]TC = Total carbohydrate, UDP = undegradable dietary protein, DUP = digestible undegraded protein, QDP = quickly degradable protein, SDP = slowly degradable protein, QFC = quickly fermentable carbohydrate, and WSC = water-soluble carbohydrate.

[3]Mean prediction error.

prediction, although, in practice, the use of published values would be the norm. Models were also constructed using intakes rather than concentrations of these variables. Such values improved the prediction somewhat as might be expected (R^2 in estimation data < 0.247; mean prediction error > 0.07) (14), although in practice, intakes would not be known. The relative performance of the elements of the MP system was similar when intakes were used. Additional models in which ether extract concentration was included also improved prediction but showed a similar relative performance with respect to the protein and carbohydrate fractions and are thus not reported in detail.

For most models, the mean bias was relatively small, but the line bias was large. This result indicates that the functional form of the models was inadequate, probably because of the need to incorporate additional variables.

The better prediction obtained using UDP rather than DUP is puzzling because DUP might be expected to be more closely related to amino acid supply to the mammary gland. Digestible undegraded protein reflects the digestible UDP that has a true digestibility of 0.9 in the small intestine minus the indigestible fiber component of the diet (acid detergent-insoluble protein), which is assumed to be an indigestible fraction (1, 2) but could be degraded slightly in the ruminal compartment. The protein

components in this study were estimated values given by the Agricultural and Food Research Council (1), and only CP was measured experimentally. Therefore, there is a need to verify the models using measured protein components.

Failure to obtain improved prediction using starch and WSC rather than their sum (QFC) may indicate that both have similar effects with regard to the availability of energy for the synthesis of microbial protein. A possible explanation for the effect of starch and WSC on milk protein concentration can be related to VFA proportion. The production of propionic acid is partly influenced by starch and WSC concentration. The change in the ratio of propionic acid to acetic plus butyric acid affects plasma insulin concentration (16), which decreases milk fat secretion and perhaps supports an increase in milk protein concentration. Other feed descriptors that were not considered in this study but were considered by Smoler (14) also appear to be appropriate for the prediction of milk protein concentration.

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