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## Evaluation of the National Research Council (2001) dairy model and derivation of new prediction equations. 2. Rumen degradable and undegradable protein<sup>1</sup>

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### ABSTRACT

This work evaluated the National Research Council (NRC) dairy model (2001) predictions of rumen undegradable (RUP) and degradable (RDP) protein compared with measured postruminal non-ammonia, nonmicrobial (NANMN) and microbial N flows. Models were evaluated using the root mean squared prediction error (RMSPE) as a percent of the observed mean, mean and slope biases as percentages of mean squared prediction error (MSPE), and concordance correlation coefficient (CCC). The NRC (2001) over-estimated NANMN by 18% and under-estimated microbial N by 14%. Both responses had large mean biases (19% and 20% of MSPE, respectively), and NANMN had a slope bias (22% of MSPE). The NRC NANMN estimate had high RMSPE (46% of observed mean) and low CCC (0.37); updating feed library A, B, and C protein fractions and degradation rate ( $K_d$ ) estimates with newer literature only marginally improved fit. The re-fit NRC models for NANMN and microbial N had CCC of 0.89

and 0.94, respectively. When compared with a prediction of NANMN as a static mean fraction of N intake, the re-derived NRC approach did not have improved fit. A protein system of intermediate complexity was derived in an attempt to estimate NANMN with improved fit compared with the static mean NANMN model. In this system, postruminal appearance of A, B, and C protein fractions were predicted in a feed-type specific manner rather than from estimated passage and degradation rates. In a comparison to independent data achieved through cross-validation, the new protein system improved RMSPE (34 vs. 36% of observed mean) and CCC (0.42 vs. 0.30) compared with the static mean NANMN model. When the NRC microbial N equation was re-derived, the RDP term dropped from the model. Consequently, 2 new microbial protein equations were formulated, both used a saturating (increasing at a decreasing rate) form: one saturated with respect to TDN and the other saturated over increasing intakes of rumen degraded starch and NDF. Both equations expressed maximal microbial N production as a linear function of RDP intake. The function relating microbial N to intake of rumen degradable carbohydrate improved RMSPE (24 vs. 28% of the observed mean) and CCC (0.63 vs 0.30) compared with the re-derived NRC model. The newly derived equations showed modest improvements in model fit and improved capacity to account for known biological effects; however, substantial variability in NANMN and microbial N estimates remained unexplained.

**Key words:** National Research Council (2001) dairy model, duodenal flow, model evaluation

### INTRODUCTION

Predicting microbial protein and flow of RUP from the rumen is of key importance in designing dairy cattle diets because these flows make up the majority of MP

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supply and affect the composition of AA absorbed from the digestive tract. Accurate and precise estimates of these variables should allow more precise matching of MP (or AA) supply and requirements, thus improving animal efficiency and reducing N excretion. Several systems to predict microbial protein and RUP flow have been derived (NRC, 2001; Fox et al., 2004; Huhtanen and Hristov, 2009). Although a series of evaluations of predicted postruminal microbial N flows (Bateman et al., 2001; Yu et al., 2003; Tedeschi et al., 2015) and RUP percentages of CP (Seo et al., 2006; Broderick et al., 2010) have been undertaken, few have explicitly addressed errors in predicting equation inputs and how those errors contribute to estimates of protein flow.

One challenge in constructing and evaluating nutrient requirement models is the source data. There are often multiple methods of measuring fluxes in the animal, and even application of a common method can vary across laboratories. This variation in method and application of method may affect measurement accuracy and precision (Nocek, 1988; Broderick and Merchen, 1992; Owens and Hanson, 1992). Incomplete nutrient input data are often reported in the literature (Angel et al., 2015; McNamara et al., 2016), necessitating use of tabular values to represent the missing dietary nutrients (White et al., 2017). Substituting missing data with mean book values does not account for the source of variation and may also result in mean bias in inputs. Systematic deviations in both input and output data will result in biased model equations, and failure to consider input variation may inhibit opportunities to evaluate underlying system behavior. The potential for data-related errors is greater for measurements that are more complicated to make using methods that are not standardized. Examples are microbial N and non-ammonia, non-microbial N (NANMN) flows from the rumen because they compound errors from sampling, different flow marker approaches, and different microbial markers. The risk is even greater for NANMN because it is calculated by difference from total N flow and microbial N flow. As such, a re-evaluation of the intermediate steps in the calculation of MP supply is warranted to better understand the source of errors within the model. In a companion paper (White et al., 2017), the digestibility predictions within the NRC (2001) lactating dairy cow model were evaluated, and new equations were derived to estimate digestibility with minimal mean and slope bias. At present, the degree to which imprecise and inaccurate estimates of nutrient digestibility resulted in misrepresented estimates of microbial N and NANMN is unknown.

The objectives of this work were to evaluate predicted ruminal outflows of microbial N and NANMN provided by the NRC (2001) dairy model against a lit-

erature data set and, when necessary, to derive and test new equation forms. We hypothesized that (1) ruminal outflow estimates would have poor accuracy when compared with measured data, and (2) accuracy would be improved by re-deriving coefficients used in the current equation forms.

## MATERIALS AND METHODS

This study used a 5-part methodology that will be described in order. First, data were collected from the literature and any missing input data were simulated. The NRC (2001) model predictions were evaluated against literature NANMN and microbial N measurements. The NRC (2001) model was then evaluated using a library of revised and updated A, B, and C protein fractions for feeds. The NRC (2001) models were then re-derived, and new equation forms were fitted to the data. Re-derived models were fit using both old and new A, B, and C protein fractions. The re-derived NRC (2001) model and the new equation forms were compared using Monte Carlo cross-validation (Lendasse et al., 2003). Details of each step are provided in the subsequent sections.

### Data Collection

Data were collected as described in White et al. (2017). Briefly, the collection of papers used in deriving the NRC (2001) was updated with more recent work published between the early 2000s and mid-2015. The complete data set contained usable data from 550 treatment means from 147 studies conducted on lactating or dry dairy cows. In total, 125 of those studies reported duodenal or omasal N flow measurements, leaving 525 treatments for use in estimating microbial N and 507 treatments for use in estimating NANMN. The summary statistics for major production variables are included in White et al. (2017), and a copy of the data can be downloaded from the National Animal Nutrition Program (2015) website. Summary statistics of the key variables evaluated in this study are included in Table 1.

### Evaluating and Correcting Ingredient Biases

All studies reported the inclusion rates of the ingredients used in diets; however, few studies reported the complete nutrient composition of all ingredients. When ingredient-specific data were not available, data were populated from the NRC (2001) feed tables. Library feed nutrient compositions were adjusted as described in White et al. (2017) and by Hanigan et al. (2013). For variables where dietary composition was not re-

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