Reevaluation of the breakpoint estimates for the NRC (2001) required concentrations of lysine and methionine in metabolizable protein for maximal content and yield of milk protein

C. Schwab*, N. Whitehouse¹, D. Luchini², and B. Sloan² (¹University of New Hampshire, Durham, ²Adisseo, Atlanta, GA.)

INTRODUCTION

• It was well established, before the development of NRC (2001), that some essential amino acids (EAA) were more limiting than others for lactating dairy cows, and that the profile of absorbed EAA affects their efficiency of use for milk protein synthesis. To allow NRC (2001) to be as accurate as possible in predicting the profile of absorbed AA, the model was developed to predict:
  1) content of RDP and RUP in feed CP
  2) passage of microbial CP (MCP), rumen-undegraded feed protein (RUP) and endogenous protein (EndogCP) to the small intestine, and
  3) content of essential AA (EAA) in metabolizable protein (MP)

• Increased prediction of nutrient supply was achieved by recognizing:
  1) that the RDP and RUP content of a feed is not constant and is affected by competing rates of ruminal degradation (Kd) and passage (Kp)
  2) that feedstuffs differ in RUP digestibility (50 to 100%), and
  3) that endogenous secretions contribute to AA supply

• To avoid the biases of prediction of content of EAA in duodenal protein encountered with true factorial AA submodels [e.g., CNCPS (O’Conner et al., 1993) and the AA submodel of Rulquin et al. (1998)], a multivariate regression approach was used to predict content of EAA in duodenal protein. In contrast to true factorial models, in which both the structure and the parameters are determined on theoretical grounds, the multivariate regression (semi-factorial) approach allows for some of the parameters to be determined by regression. This allows the model (i.e., equations) to adapt to the measured data, and allows for at least partial correction of the errors of the mechanistically determined variables (e.g., RUP). While this approach requires the development of an equation for each of the EAA and one for predicting flows of total EAA, it has the potential for increased accuracy of prediction. It also eliminated the need to assign "unsure" values of AA composition to predicted supplies of microbial protein and endogenous protein.

• The regression equations in NRC (2001) for predicting passage of total EAA to the small intestine and content of Lys and Met in total EAA (as two examples of EAA) of duodenal protein are:
  - Total EAA (g/d) = 30.9 + 0.863(EAA from RUP, g/d) + 0.433(MCP, g/d)
  - Lys (% of EAA in duodenal protein) = 13.66 + 0.3276(Lys, % of total EAA in RUP) - 0.07497(RUP, % of duodenal CP)
  - Met (% of total EAA in duodenal protein) = 2.90 + 0.391(Met, % of EAA in RUP) – 0.00742(RUP, % of duodenal CP)

• To ensure that the best approach had been taken, the NRC (2001) subcommittee used the same data base to evaluate the use of a semi-mechanistic approach to predict directly the “flows” of individual EAA to the duodenum. While the parameter estimates that resulted for contributions of endogCP, fractional contribution of RUP to flows from RUP, and fractional content of the EAA in MCP appeared reasonable, a comparison of the RMSPE obtained from the two sets of residual plots (“g/d” and “% of total EAA”) for each of the approaches indicated that the equations that predicted percentages directly predicted more accurately both the “percentages” of individual EAA in duodenal total EAA and the “flows” (g/d) of individual EAA.

• Thus, the model was extended to predict flows of MP-EAA and the content of EAA in MP. To accomplish this, nine equations are used that:
  1) calculate duodenal flows of each EAA from RUP supply (from each feedstuff and the AA composition of the feed),
  2) calculate flows of “digestible” EAA from RUP using the assigned digestibility coefficient of RUP for each feedstuff,
  3) calculate “percent digestibility” for each EAA from results of equations 1 and 2,
  4) discount predicted flows of each EAA from RUP by 13.7% [because the equation for predicting total EAA flows (see above) has a coefficient of 0.863 associated with it for RUP-EAA, indicating an apparent “correction of error” of the mechanistically determined RUP values],
  5) calculate flows of individual EAA from MCP plus EndogCP (total flows - adjusted supplies from RUP),
  6) calculate “adjusted” flows of each digestible EAA from RUP (discounted predicted flows x percent digestibility),
  7) multiply flows of individual EAA from MCP plus EndogCP by 0.80 (true protein of both is assumed to have a digestibility of 80%),
  8) sum the flows of digestible EAA from RUP and MCP plus EndogCP, and that
  9) calculate each digestible EAA as a percentage of MP.

• Because Lys and Met are typically the two most limiting AA for lactating dairy cows (NRC, 2001), and that balancing for the most limiting AA in MP is the first step to balancing diets for AA, NRC (2001) presents dose-response plots showing changes in milk protein content and yield to predicted concentrations of Met and Lys in MP. The “indirect” dose-response approach of Rulquin et al. (1993) was used. An important feature of the approach is that requirement values are estimated using the same model as that used to predict concentrations of EAA in MP.
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INTRODUCTION (cont.)

• The breakpoint estimates for the required concentrations of Lys and Met in MP for maximal content of milk protein were 7.24 and 2.38%, respectively; corresponding values for maximal yield of milk protein were 7.08 and 2.35%.

OBJECTIVES

Because the AA submodel (AA equations) had to be developed before the final version of the NRC model was available, a beta version of the model was used to predict the concentrations of Lys and Met in MP in the studies that were used in developing the dose-response plots. The objective of this study was to generate new dose-response plots, using the final version of the model to predict concentrations of Lys and Met in MP.

APPROACH

All steps were repeated as stated in NRC (2001). Generating the dose-response plots involves 5 steps: 1) predicting concentrations of Lys and Met in MP for control and treatment groups in experiments in which postruminal supplies of Lys, Met, or both were increased and production responses were measured, 2) identifying “fixed” concentrations of Lys and Met in MP that are intermediate to the lowest and highest values in the greatest number of Lys and Met experiments, 3) calculating, by linear regression, a “reference production value” for each production parameter in each Lys experiment that corresponded to the “fixed” level of Lys in MP and in each Met experiment that corresponded to the “fixed” level of Met in MP, 4) calculating “production responses” (plus and minus values) for control and treatment groups relative to the “reference production values”, and 5) regressing the production responses on the predicted concentrations of Lys and Met in MP.
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<table>
<thead>
<tr>
<th>Digestible Lys, % MP</th>
<th>Milk protein content responses, g/100 g</th>
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</thead>
<tbody>
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<td></td>
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</table>

Regression analysis for Lys was limited to data where Met was 1.95 % or greater of MP. For the linear part of the model $y = -0.712 + 0.106x$ and for the plateau $y = -0.712 + 0.106 \times 7.24$.
The reference value used to determine the relative response was 6.67. (n=41)

<table>
<thead>
<tr>
<th>Digestible Lys, % MP</th>
<th>Milk protein yield responses, (g/d)</th>
</tr>
</thead>
<tbody>
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<td></td>
<td></td>
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</tbody>
</table>

Regression analysis for Lys was limited to data where Met was 2.07 % or greater of MP. For the linear part of the model $y = -0.818 + 0.125x$ and for the plateau $y = -0.818 + 0.125 \times 6.80$.
The reference value used to determine the relative response was 6.70. (n=41)

Lysine Published Plots

Lysine Revised Plots
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**Methionine Published Plots**

Regression analysis for Met was limited to data where Lys was 6.50 % or greater of MP. For the linear part of the model \( y = -0.496 + 0.238x \) and for the plateau \( y = -0.496 + 0.238 \times 2.38 \).
The reference value used to determine the relative response was 2.06. (n=48)

**Methionine Revised Plots**

Regression analysis for Met was limited to data where Lys was 6.16 % or greater of MP. For the linear part of the model \( y = -0.560 + 0.271x \) and for the plateau \( y = -0.560 + 0.271 \times 2.29 \).
The reference value used to determine the relative response was 2.06. (n=48)
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Table 1: Breakpoint estimates for required concentrations of Lys and Met in MP for maximal content and yield of milk protein for the beta and published NRC (2001) models.

<table>
<thead>
<tr>
<th>Item</th>
<th>Beta Model (published values)</th>
<th>Published Model (revised values)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Lys</td>
<td>Met</td>
</tr>
<tr>
<td>Content of milk protein</td>
<td>7.24</td>
<td>2.38</td>
</tr>
<tr>
<td>Yield of milk protein</td>
<td>7.08</td>
<td>2.35</td>
</tr>
</tbody>
</table>

Table 2: A comparison of model predicted values for the negative control diets in each experiment for the beta and published NRC (2001) models.

<table>
<thead>
<tr>
<th>Item</th>
<th>Beta Model (Lys experiments)</th>
<th>Published Model (Lys experiments)</th>
<th>Beta Model (Met experiments)</th>
<th>Published Model (Met experiments)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diet RDP, % of DM</td>
<td>9.8</td>
<td>9.4</td>
<td>9.7</td>
<td>9.6</td>
</tr>
<tr>
<td>Diet RUP, % of DM</td>
<td>5.8</td>
<td>5.6</td>
<td>5.6</td>
<td>5.6</td>
</tr>
<tr>
<td>Total diet CP, % of DM</td>
<td>15.6</td>
<td>15.0</td>
<td>15.3</td>
<td>15.2</td>
</tr>
<tr>
<td>Microbial MP, g/d</td>
<td>1016</td>
<td>998</td>
<td>1048</td>
<td>1084</td>
</tr>
<tr>
<td>Feed MP, g/d</td>
<td>933</td>
<td>957</td>
<td>1023</td>
<td>964</td>
</tr>
<tr>
<td>Endogenous MP, g/d</td>
<td>97</td>
<td>97</td>
<td>99</td>
<td>100</td>
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<tr>
<td>Total MP, g/d</td>
<td>2046</td>
<td>2052</td>
<td>2170</td>
<td>2148</td>
</tr>
<tr>
<td>Microbial MP, % of total MP</td>
<td>49.7</td>
<td>48.6</td>
<td>48.3</td>
<td>50.5</td>
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<tr>
<td>Feed MP, % of total MP</td>
<td>45.6</td>
<td>46.6</td>
<td>47.1</td>
<td>44.9</td>
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<tr>
<td>Endogenous MP, % of total MP</td>
<td>4.7</td>
<td>4.7</td>
<td>4.6</td>
<td>4.6</td>
</tr>
<tr>
<td>MP-Lys, g/d</td>
<td>126</td>
<td>125</td>
<td>149</td>
<td>149</td>
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<tr>
<td>MP-Lys, % of MP</td>
<td>6.17</td>
<td>6.11</td>
<td>6.99</td>
<td>6.94</td>
</tr>
<tr>
<td>MP-Met, g/d</td>
<td>49</td>
<td>49</td>
<td>40</td>
<td>40</td>
</tr>
<tr>
<td>MP-Met, % of MP</td>
<td>2.42</td>
<td>2.41</td>
<td>1.86</td>
<td>1.85</td>
</tr>
</tbody>
</table>
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SUMMARY AND CONCLUSIONS

Some differences were observed between “published” and “revised” breakpoint estimates for the required concentrations of Lys and Met in MP for maximal content and yield of milk protein. It is concluded from a comparison of the data generated with the two models (Table 2), along with a re-examination of feed inputs, that the primary reason for the differences are differences in feed inputs for some of the studies. There may be some minor differences between the models, as well. More data is needed to increase the accuracy of the breakpoint estimates.

IMPLICATIONS

It is suggested that the new values be used as the reference values when using the NRC (2001) model to optimize Lys and Met concentrations in MP for lactating cows.

REFERENCES


