peptides can exit the rumen with the liquid outflow.

Colombini et al. (2011) developed a method to estimate the amount of soluble protein that is released as free amino acids and the amount that is released as peptides. As a result, some proteins that are highly soluble provide more escape protein than previously assumed. This method improves the accuracy of the assessment of rumen escape amino acids and can be applied in a laboratory.

After addressing the amino acids derived from feed sources, estimates of the amino acids contributed by rumen microbes were needed. The microbial ecosystem depends on the carbohydrates fed to the animal. However, growth can be maximized only if the correct sources of nitrogen are supplied as well.

The proteins degraded in the rumen that provide peptides and ammonia are essential to the growth of the bacteria in the rumen.

In the CNCPS system, two major microbial niches in the rumen digest fiber and non-fiber carbohydrates. Fiber digestion optimization depends mainly on ammonia and the isoacids generated from the branched-chain amino acids from feed ingredients. The non-fiber bacteria are dependent on both ammonia and peptides for optimal growth.

The microbial mass that is generated in the rumen partially flows from the rumen as the particles are washed out of the rumen as well as in the liquids that leave the rumen.

Model improvement

Feed analysis methods are required to estimate the relative availability of non-protein nitrogen and peptide nitrogen to support microbial growth and to ensure that the mass exiting the rumen can be predicted with some degree of accuracy.

The research being conducted by the Forage Research Lab (Colombini et al., 2011) and The Swedish University of Agricultural Sciences (Hedqvist and Uden, 2006) is breaking new ground in that regard. The high-quality protein in bacteria provides an excellent amino acid source to the cow. Nutritionists formulating rations attempt to optimize the microbial growth in order to provide a significant amount of amino acids required by the cow on a daily basis. However, in nutritional models, it is assumed, that the amino acid profile of the microbial true protein is constant, but this is not true.

First, a varying degree of protozoal protein flows from the rumen, which has a different amino acid profile. Also, solids and liquids associated with bacteria have been shown to have different amino acid profiles. However, early researchers got over this hurdle by concluding that the differences were inconsequential and that average values could provide estimations of the profile of amino acids arising from the rumen (Bergen et al., 1968; Hvelplund, 1985; Purser and Beuchler, 1966; Harrison et al., 1973).

Since then, researchers have developed a procedure to separately predict bacterial and protozoal flow (Shabi et al., 2000). This refinement may provide further accuracy to this prediction in future models.

References


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*Dr. Charles Sniffen is with Fencrest LLC. Dr. Essi Evans is with Technical Advisory Services. Dr. Elliot Block is research fellow, animal nutrition, at Arm & Hammer Animal Nutrition. This is part 1 of two articles. The second article in the series will address how to formulate dairy diets for amino acids.*