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Rafael Munoz Tamayo, Seppo Ahvenjärvi, Ali Reza Bayat, Ilma Tapio

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R. Muñoz-Tamayo [a], S. Ahvenjärvi [b], A. R. Bayat [b], I. Tapio [c]

[a] Université Paris-Saclay, INRAE, AgroParisTech, UMR Modélisation Systémique Appliquée aux Ruminants, 91120, Palaiseau, France
[b] Animal Nutrition, Production Systems, Natural Resources Institute Finland (Luke), Jokioinen, Finland
[c] Genomics and Breeding, Production Systems, Natural Resources Institute Finland (Luke), Jokioinen, Finland

Dynamic mathematical models have been developed to enhance understanding of rumen function. These models include Molly[1], the Dijkstra model[2], Karoline[3] and their extensions. Model evaluations showed that there is still room to enhance their accuracy for predicting volatile fatty acids concentration and methane production. Previously, Muñoz-Tamayo et al. (2016) developed an alternative model of rumen fermentation under *in vitro* conditions aimed at better representing the rumen microbiota and hydrogen dynamics. In the present work, we extended the previous model to account for *in vivo* conditions. We performed an experiment with four Nordic-Red dairy cows equipped with rumen fistulas to provide dynamic data to support model construction. The experiment determined animal daily patterns of feed intake, rumen fermentation and enteric methane production. Feed intake and methane emissions were measured in respiration chambers during two days after an adaptation period. Rumen liquid was collected every three hours for determination of volatile fatty acids concentration. In the model, the rumen microbiota is represented by three functional groups namely sugar-, amino acids- and hydrogen-utilisers. The feed is expressed in three pools as neutral detergent fiber, non-structural carbohydrates and proteins. The model consists of 18 compartments described by ordinary differential equations. The model performance was satisfactory as evaluated by the coefficient of variation of the root mean squared error, which was 9% for acetate, 11% for butyrate, 13% for propionate and 21% for methane. Our model has the potential to be used as virtual platform to simulate the dynamics of rumen fermentation and methane production.

References
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