

### Conclusion and implications

Including individual information such as reticulorumen capacity in the models for predicting reticulorumen  $k_p$  of particles or solutes considerably increase the accuracy and precision of the predictions. The reticulorumen  $k_p$  of particles demonstrated dependent on  $k_p$  of solutes suggesting solutes have a role in caring particles out of reticulorumen.

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## 22. A mechanistic model to predict post-ruminal flow of cobalamin

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### Introduction

In dairy cows, cobalamin ( $B_{12}$ ) supply is completely dependent on synthesis by the rumen microbiota (Strobel, 1992). The metabolic pathways in which  $B_{12}$  is used, including its co-enzyme role with methylmalonyl-CoA mutase for propionate production, are essential to fulfilling the cow's energy requirements (Strobel, 1992). Extant rumen models do not consider the synthesis and degradation of B vitamins such as  $B_{12}$  and its role in rumen function. A meta-analysis conducted by Brisson et al. (2022) highlighted key factors correlated with  $B_{12}$  apparent ruminal synthesis, which is equal to the post-ruminal flow (PRF), including DMI, total ruminal VFA concentration and dietary starch. Therefore, the objective of this work was to develop a mechanistic sub-model to describe a hypothesis of ruminal synthesis and degradation of  $B_{12}$  in lactating dairy cows.

### Material and methods

The  $B_{12}$  sub-model (Fig. 1) was developed to fit within the existing ANSJE rumen model (Dijkstra et al., 1992). The model consists of two new  $B_{12}$  pools (Cbfl, Cbso), representing the vitamin presence in both rumen fluid and rumen solids. These pools follow existing microbial growth and passage fluxes and simulate the degradation and recycling of  $B_{12}$  in the rumen through its use in propionate synthesis (Prop).

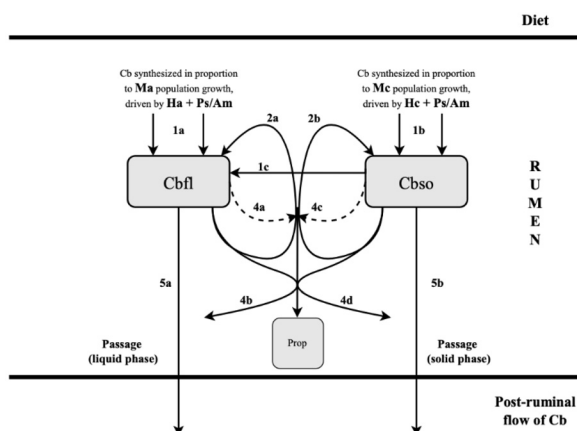


Fig. 1. Diagrammatic representation of the cobalamin (Cb) ruminal synthesis sub-model and the resulting post-ruminal flows of Cb. Boxes indicate state variables (mg), full-line arrows indicate fluxes (mg/day), and dotted lines represent the inhibition of Cb recycling with increased Cb concentration. Abbreviations used: Am, ammonia; Cb, cobalamin; Cbfl, cobalamin in rumen fluid; Cbso, cobalamin in rumen solids; Ha, hexose available to amylolytic microbes; Hc, hexose available to cellulolytic microbes; Ma, amylolytic microbial mass; Mc, cellulolytic microbial mass; Prop, propionate; Ps, rumen fluid-soluble protein. 1a/1b/1c. = Inputs into Cb pools; 2a/2b. = Recycling of Cb between Cb pools; 3 = propionate synthesis rate; 4a/4c. = Inhibition of Cb recycling with increased concentration of Cb; 4b/4d. = Catabolism of Cb after use in propionate synthesis; 5a/5b. = Cb flow out of rumen.

The biological values to describe the initial and average concentrations of B<sub>12</sub> in rumen fluid and rumen solids were extracted from the literature (Santschi et al., 2005). Additionally, three new parameters using Michaelis-Menten kinetics which describe B<sub>12</sub> recycling, including the inhibition of B<sub>12</sub> recycling by B<sub>12</sub> concentration ( $J_{Cbfl, PrCbfl} = 1.0$  mg/L;  $J_{Cbso, PrCbso} = 10.0$  mg/L) and the theoretical maximal recycling rate of B<sub>12</sub> ( $R_{Cb, PrCb} = 0.95$  mg/d) if B<sub>12</sub> concentration was to reach zero were defined, using treatment means from an available database describing B<sub>12</sub> flows across the rumen (Brisson et al., 2022). Model parameter fitting was performed, assuming steady-state, by calculating the residual sum of squares between predicted and observed B<sub>12</sub> PRF across 34 treatment means for all parameter combinations ( $J_{Cb, CbflPr}$  and  $J_{Cb, CbsoPr} = 1.0$  to 10.0 by 0.5 mg/L;  $R_{Cb, PrCb} = 0.5$  to 1.0 by 0.05 mg/d).

### Results and discussion

With the newly fitted parameters, the B<sub>12</sub> sub-model predicts mean PRF of 11.4 mg B<sub>12</sub>/d ( $\pm 1.42$  mg/d) compared to an observed mean B<sub>12</sub> PRF of 12.0 mg B<sub>12</sub>/d ( $\pm 5.71$  mg/d). The model performance indicates fitting of predictions (rMSPE, 21.7%; CCC, 0.056) (Bibby and Toutenburg, 1977; Lin, 1989) requires further consideration to capture greater variation. This unexplained variation may be due to simplified representation of biology in the hypothesized B<sub>12</sub> sub-model, prediction errors within the base model itself, or biological variation present in the data not captured by the model.

### Conclusion and implications

The sub-model developed was used to test a hypothesis explaining B<sub>12</sub> synthesis regulation in the rumen, using current knowledge about factors involved in the regulation of B<sub>12</sub> ruminal synthesis and degradation. The current fitted model predictions of the average B<sub>12</sub> require testing on an independent database and the model performance could be improved with further research and data collection to better capture additional sources of variation. This work represents the first attempt at mechanistic modelling of duodenal B<sub>12</sub> flows in the dairy cow.

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## 23. Predicting fiber digestibility in Holstein dairy cows fed dry-hay based rations

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### Introduction

The entire Parmigiano Reggiano (PR) production chain is strictly regulated by its consortium, from animal origin to feedstuffs use. Rations are based on fresh forages and/or dry hay, while silages are not allowed. Considering that diets must contain at least 50% of forages, good quality feedstuffs are necessary to meet the energy requirements of animals and milk quality (Mordenti et al., 2017). Hence, dry matter intake needs to be improved. It could be achieved by selecting highly digestible forages with a low concentration of indigestible NDF (uNDF240), or reducing dietary particle size (Fustini et al., 2011). Fiber digestibility (FD) is one of the main topics on dairy cows' rationing. In the last few years, total-tract potentially digestible fiber digestibility (TTpdNDF240D) evaluation has been used to evaluate feed efficiency at the herd and individual cow level (Combs et al., 2013). The objective of this study was to investigate dietary factors that could play a role in predicting the TTpdNDF240D in cows fed PR diet, and compare the different proposed models in order to produce an equation for FD prediction. The scope is to provide nutritionists with a fast tool to use on-field practice.

### Material and methods

A total of 7 studies, performed at the University of Bologna Dairy-Unit, involving 53 dairy cows, 15 diets and 1364 fecal samples were examined. All the involved cows were completely adapted (14 d) to the diets. Diet and fecal analysis were assessed by the university lab. Cows' body-weight (BW) was measured twice a day by an electronic scale. DMI was individually measured in a tie-stall area. Cows were monitored during all the trials for health conditions and production. Correlations between parameters were studied by Multivariate methods. Based on previous results three different Standard Least Square Models with a factorial arrangement for dietary factors were