



Predictive capabilities of a dynamic mechanistic model of *in vitro* fermentation by rumen microbiota

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August 29 2019











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Rumen modelling: a longstanding research activity with room for improvement

Baldwin et al., 1987; Dijkstra et al., 1992; Lescoat and Sauvant, 1995; Bannink et al., 2006; Mills et al., 2014; Vetharaniam et al., 2015; van Lingen et al., 2019

Still some limitations for accurate predictions of the fermentation pattern (volatile fatty acid, CH₄) (Offner and Sauvant, 2004; Alemu et al., 2011).









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Features for improvement (Ellis et al., 2008; Janssen 2010):

- Better representation of the microbiota
- Fermentation stoichiometry
- Hydrogen dynamics
- Description of pH







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Our long-term goal: to develop a model that

- Enhances the mechanistic description of rumen fermentation
- Can be used as tool for guiding sustainable feeding strategies









Results & conclusions

Strategy: a stepwise approach









 $\frac{d}{dt}$

Results & conclusions

Strategy: a stepwise approach











Results & conclusions

Animal Feed Science and Technology 220 (2016) 1-21



Mechanistic modelling of *in vitro* fermentation and methane production by rumen microbiota



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The model in a picture: satisfactory representation of *in vitro* fermentation using rumen inocula from goats



- Complexity: 18 state variables (compartments), 30 parameters
- Structure: based on models for engineering reactors (Batstone et al., 2002) and human colonic fermentation (Muñoz-Tamayo et al., 2010)
- Implementation: Matlab, Rimplementation by Kettle et al., 2018







Objective of this work

- Evaluate the model for its ability to predict VFA and CH₄ dynamics using an independent data set (cows)
- Assess whether the hydrolysis rate constants of diet polymers determined enzymatically could be integrated into the model and provide satisfactory predictions









In vitro experimental case study: rumen inocula from two cows

- Gas production adapted from Pirondini et al., 2012; Serment et al., 2016
- Five total mixed rations (TMR) collected from different dairy farms: NDF, starch, CP
- Degradability rates determined enzymatically (Gallo et al., 2017. J Anim Sci; Gallo et al., 2018. J Agric Sci; Gallo et al., 2019. J Dairy Sci)
 - Hemicellulase from Aspergillus niger
 - Amylase from *Aspergillus oryzae*, amyloglucosidase from *Aspergillus niger*
 - Cellulase from Trichoderma viride and Viscozyme L enzymes
 - Sylanase from *Thermomyces lanuginosus*
 - Protease from *Streptomyces griseus*
- Measurements: acetate, butyrate, propionate, CH₄









Model performance: example for one in vitro fermentation



First-order hydrolysis rate: adequate predictions but VFA profile exhibits a delay pattern wrt model response

$$\frac{\mathrm{d}z_{\mathrm{ndf}}}{\mathrm{d}t} = -\frac{k_{\mathrm{hyd,ndf}}}{k_{\mathrm{ndf}}} \cdot z_{\mathrm{ndf}} \tag{1}$$

*k*_{hyd,ndf}: determined enzymatically







Model performance: example for one in vitro fermentation



Model performance using Contois kinetics: 5 fermentations









Results & conclusions

Take home message

Our model represented effectively the profile of individuals VFA and methane produced during *in vitro* rumen fermentation

Contois kinetics appears more adequate than first-order

kinetics to represent hydrolysis of diet polymers

Enzymatic determination of hydrolysis rates is a promising

approach: adaptation to Contois model required









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Perspectives for model extensions to tackle methane mitigation strategies

- Lipid metabolism, additives, modulation factors (H₂, pH)
- In vivo conditions









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Diet composition

	NDF	Crude Protein	Starch	Fatty acids
1	29.04	17.53	23.82	4.09
2	31.74	17.08	23.69	3.81
3	29.49	17.25	25.14	4.89
4	36.22	14.44	20.11	3.28
5	33.81	14.58	22.04	3.52







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