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MICROBIAL GROWTH LAG IMPLEMENTATION IN A COMPLEX BIOCONVERSION MODEL

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INTRODUCTION

Microorganisms play an important role in the anaerobic digestion (AD) of organic wastes, through which flexible renewable energy and valuable agricultural nutrients can efficiently be produced. Although numerous methods exist for the quantification and analysis of these microbial communities (Rittmann et al., 2008), the dynamic behavior of anaerobic bacteria and archaea is complex and still poorly understood. *In silico* mathematical modeling is a powerful resource and can be applied to simulate the timely changes in such microbial systems, however so far, it has mostly been successful in describing the steady-state periods of AD processes. In order to provide insights into the dynamic behavior of anaerobic microorganic communities due to changes in AD conditions, the aim of present study was therefore to focus on microbial growth lag. More specifically, a simplified anaerobic bioconversion model was first created with a time-dependent microbial growth lag implementation, in order to study the delay phenomenon in cell response to changes in environmental conditions. Further to that, the lag concept was also implemented in a scientifically proven bioconversion model and the simulated results of the model were compared to experimental data for validation.

MATERIALS AND METHODS

Initially a simplified, two-step bioconversion model was set up for the validation of the microbial growth lag concept, assuming chemostat conditions and a continuously stirred tank reactor (CSTR) configuration, with five chemical compounds and two microbial groups considered. Process stoichiometry and kinetics were adapted from Angelidaki et al. (1993). Glucose was chosen as a model substrate, and while the first step of the model involved the conversion of glucose to biomass, acetic acid, carbon dioxide (CO_2) and water via acidogenic bacterial activity, in the second step the generated acetic acid was further degraded to methane and carbon dioxide by aceticlastic methanogens. Microbial growth lag was implemented in the form of a first-order rate of change step response function, commonly known from chemical process engineering and seen in Kythreotou et al. (2014). In the second step, lag functionalities were implemented in a complex bioconversion model adapted from Angelidaki et al. (1993, 1999), and modified according to Kovalovszki et al. (2017) and Lovato et al (2017). The design of the lag implementation was identical to that of the simplified, two-step model. Simulations were run both with no lag time and a lag time of 4.47 hours, effective on aceticlastic methanogens and estimated from the simplified model implementation.

For validating the growth lag implementation in the complex model, an experimental reactor was set up and operated for a longer period, with step-wise increasing organic loading rate (OLR). For simplicity and comparability, glucose was used as the single substrate, which was fed at a rate of approximately 0.40 g-VS L^{-1} d^{-1} between days 9 to 21 and a rate of 0.93 g-VS L^{-1} d^{-1} from day 21 onwards. In order to provide the microbial community with enough nutrients, basic anaerobic medium (BAM) was also fed to the reactor, according to Angelidaki and Sanders (2004).

RESULTS AND DISCUSSION

The results of the simulations seen in Fig. 1 indicate that there is indeed a lag period in the growth of aceticlastic methanogens, as the simulation results considering the lag implementation provided much more accurate fits between experimental and simulated datasets. However, further analysis is needed to test and statistically verify the lag time coefficient, along with the response of the model when more complex substrates are involved.

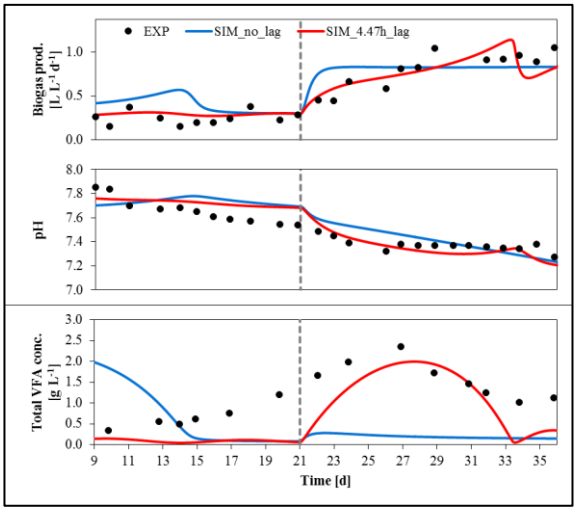

Fig. 1: Experimental and simulated methane production, pH and total volatile fatty acid (VFA) concentration in the reactor experiment. EXP are experimental points, while SIM_no_lag and SIM_4.47h_lag are simulation results with no microbial growth lag and a 4.47 hours long lag period applied to the aceticlastic methanogens, respectively. Vertical, dashed lines mark the change in OLR on day 21.

CONCLUSION

Microbial growth lag functionalities were implemented in a simplified, two-step bioconversion model, and a complex model based on similar principles. It was seen that microbial growth lag can greatly influence the overall process dynamics during AD and is an important aspect of the process that requires further, more in-depth analysis.

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