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Food waste as substrate to obtain two different enriched microbiomes for model development

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Abstract: Anaerobic microbial processes allow treatment and simultaneous valorisation of food waste (FW). The metabolic network formed by reactor microbiomes can be steered towards product selectivity by altering the operational parameters. In this research two enriched microbiomes are cultivated by altering operational conditions, one to select for anaerobic digestion (AD) to produce methane and the other for acidogenic fermentation (AF) to produce volatile fatty acids (VFA). Experimental results with enriched cultures are compared with AD model simulations in order to: 1) estimate kinetic parameters, 2) test predictions capabilities and 3) future scenario evaluation.

Keywords: Anaerobic microbiome; fermentation; food waste

Introduction

The global amount of FW is estimated around 1.3 billion tonnes year⁻¹, with a carbon footprint of 3.3 GT CO₂ equivalents due to disposal [1]. Some generation of FW is inevitable, even when food processing is optimized, so an optimal treatment method to promote valorisation needs to be developed. Anaerobic digestion is a well-established process in wastewater treatment (WWT), which is also currently used to process organics from FW and produce biogas. Hence, GHG emissions related to landfill disposal of FW are circumvented while the high biodegradability of FW makes it a preferred renewable feedstock for energy production. Recent research is focussing on similar bioreactor processes that valorise organic wastes by producing high value biochemicals such as VFA or bioenergy as biohydrogen [2].

A mechanistic understanding of microbial ecology is required to drive fermentation towards selective production of such compounds. Laboratory experiments can identify the required reactor conditions such as temperature, pH, substrate, feeding pattern, or organic loading [3]. In parallel, mathematical models can enhance understanding and predict microbial behaviour and fermentation outcomes [4]. Current biological WWT technologies make extensive use of mathematical models for AD that have continuously been improved, adapted and expanded over the last few decades based on numerous sets of process data [5]. This project aims to compare experimental results of acidogenic fermentation with an enriched microbiome with traditional AD models. Under altered operating conditions the microbiome composition diversifies and thus changes the metabolic network available in the system, which in turn impacts the metabolite profile, kinetics and product outcomes.

Material and Methods

Two 1 L lab-scale semi-continuous reactors were set to enrich microbiomes. They were fed with FW and inoculated with sludge from an anaerobic digester processing FW which was sourced from GENeco (Bristol, UK). One lab-scale reactor was operated to select for methanogenesis (AD) by setting a food-to-microbial biomass ratio (F/M) of 0.8 and pH of 7.2 ± 0.2. The other was to favour acidogenic fermentation (AF) by organic overloading (F/M>1)

and adjusting pH to 6 ± 0.2 [6]. Batch tests were performed to determine kinetic parameters, biochemical methane potential (BMP), and VFA production, by respectively digesting (F/M=0.5) or fermenting (F/M=5) FW with different microbiomes: two full scale AD and two enriched cultures. Experimental results are evaluated against the Benchmark Simulation Model No. 2 version of the Anaerobic Digestion Model No. 1, in Matlab / Simulink [5].

Results and Conclusions

The AD reactor produced around $1 \text{ L biogas d}^{-1}$ (30% CO_2 , 70% CH_4) during the first 2 weeks of operation. Organic overloading at Day 18, caused by fluctuation in FW, resulted in acidification of AD, reduced total biogas production to below 0.25 L d^{-1} (CH_4 content falling to <10%) and accumulation of VFA (Figure 1). Re-inoculating the AD reactor at Day 53 and re-establishing the F/M ratio restored CH_4 production. The AF reactor produced less biogas (about 0.5 L d^{-1}) with nearly no CH_4 content, but 25% H_2 . Accumulation of VFA occurred up to a total of $11.1 \text{ g}_{\text{COD}} \text{ L}^{-1}$, $3.6 \text{ g}_{\text{COD}} \text{ L}^{-1}$ and $10.6 \text{ g}_{\text{COD}} \text{ L}^{-1}$ respectively of acetic, propionic and butyric acid. The AF reactor does not reduce solids, whereas AD does. There was a maximum volatile solids (VS) of $88 \pm 3 \text{ g}_{\text{VS}} \text{ L}^{-1}$ in AF and $20.4 \pm 0.5 \text{ g}_{\text{VS}} \text{ L}^{-1}$ in AD. Operational conditions allowed selection of either CH_4 or VFA production, and deviation from the set reactor conditions alters the working of the microbiome as seen in the AD reactor.

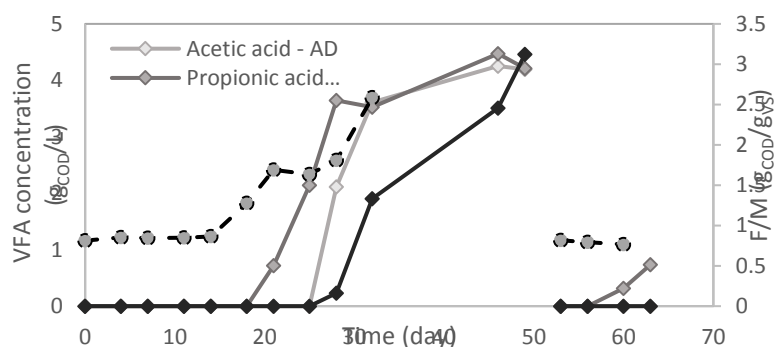


Figure 1 Volatile fatty acid accumulation in AD reactor caused by organic overloading (F/M > 1).

By comparing experimental data with predicted values from AD models appropriate changes in the model structures i.e. inclusion of intermediates, are evaluated.

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