Modelling anaerobic degradation of complex wastewater. II: parameter estimation and validation using slaughterhouse effluent

D.J. Batstone a, J. Keller a,*, R.B. Newell a, M. Newland b

a Advanced Wastewater Management Centre, The University of Queensland, St Lucia 4072, Australia
b ESI Ltd, P.O. Box 1495, Osborne Park 6916, Australia

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Abstract

This is the second part of a two-part paper developing and validating a structural model to describe the high rate anaerobic digestion of complex wastewater. A full-scale, two-stage hybrid upflow anaerobic reactor treating pig slaughterhouse effluent is assessed. Parameters and hydraulics are proposed for this system and validated. Characterisation of the system indicated that influent was a combination of equal parts (in terms of COD) particulate fat, particulate protein, and soluble protein. Reactor hydraulics were close to completely stirred tank reactor (CSTR) hydraulics, as indicated by a residence time distribution (RTD) study. The Monday morning abattoir start-up was identified as a key disturbance suitable for parameter estimation. A stepwise parameter estimation procedure was used as proposed in the previous paper. An experimental data set without recycle was used for parameter estimation. The model with these parameters performed well on independent data sets with and without recycle. The model identified several anomalies in the experimental data that may be unique to reactors treating complex wastewater.

Keywords: Abattoir; Complex; Fat; Hydrolysis; Parameter; Pig; Protein; LCFA; Simulation; Slaughterhouse; Wastewater

1. Introduction

This paper applies the model and parameter estimation philosophy presented in the first part of the investigation (Batstone et al., 2000) to a full-scale high rate system treating complex wastewater. Nomenclature for this paper is also shown in Batstone et al. (2000). A preliminary account of the parameter estimation and validation results was presented at the IAWQ Eighth International Conference on Anaerobic Digestion (Sendai, Japan); reported in Batstone et al. (1997).

The high solid and fat levels consistent with complex (protein based) wastewater require methods to alleviate biomass wash-out. These include baffles and filter media. The system examined here is a hybrid reactor. That is, the base is a traditional up-flow anaerobic sludge blanket (UASB) reactor while the upper half of the reactor is filled with coarse packing which acts as growth and solids-retention media.

2. Methods

The experimental study had two main objectives. To provide results that reflect dynamic and steady state behaviour of the system and produce experimental results easily converted to appropriate model inputs and outputs.

2.1. System

The system modelled here is a two-stage, high-rate anaerobic treatment plant in Spearwood, Western Australia (ESI, Perth, Australia) with a 1200 m³/day (12 t COD/day design load). This plant treats wastewater from a pig slaughterhouse. When the data were collected, the plant had been operating for 14 months at 50–70% of design load. The system removed 95–99% soluble COD and 70–85% total COD. Most effluent COD was anaerobic biomass.

Screened effluent from the slaughterhouse is pumped to the first reactor (acidification/equalisation) where the residence time is 12–50 h depending on tank level. The methanogenic reactor, fed by a distribution manifold, has a liquid residence time of currently 40–50 h. Each
tank is 6 m high and 18 m in diameter. A flow diagram is shown in Batstone et al. (1997).

The control system logs several variables including equalisation tank pH and level, reactor feed, effluent and reactor gas flow-rates.

2.2. Sampling protocol

The abattoir did not operate on weekends. This caused a dynamic step in influent concentration and flow on Monday mornings. Thus each data set included this step change.

Experimental runs were differentiated by a high (24 h) or low (12 h) equalisation (acidification reactor) hydraulic retention time (HRT) and with or without a 20% recycle. Influent and reactor feed samples were taken to generate 8 composites of 3 samples each during one equalisation HRT period. Effluent concentrations were measured from samples taken every 6 h for 5 days. All samples were collected using ISCO 3700 auto-samplers.

2.3. Measurement of particulate and soluble fats, proteins, and carbohydrates

The model inputs required that the influent waste be split into particulate and soluble fats, proteins and carbohydrates (units of c-mole/m³). Filtered and unfiltered samples were analysed for nitrogen, ammonia and oil and grease (O&G). Their theoretical chemical oxygen demand (COD) contributions were then calculated and the remainder evaluated as the theoretical carbohydrate concentration in the wastewater (Fig. 1).

To calculate the O&G contribution to COD, a sample of fat from the factory fat separation unit was weighed and analysed. The COD contribution and C:N ratio of 1:7 for proteins used was taken from Henze et al. (1995).

Samples were filtered using a 0.45 μm cellulose acetate membrane filter. Standard Methods (APHA, 1992) was used for O&G analysis while TN, ammonia and COD were analysed using Merck colorimetric tests 14,773, 14,559, and 14,541, respectively (Merck, Melbourne, Australia).

2.4. Analysis of volatile fatty acids (VFA)

VFA analysis was by a Perkin-Elmer Autosystem Gas Chromatograph (GC) with J&W DB-FFAP Megabore column. Samples were prepared by diluting to 90% with 10% w/v phosphoric acid and placing in 1 ml GC vials.

2.5. On-line measurements

Reactor feed and effluent flows were measured by Danfoss DN100 flow-meters, the gas flow-rate by a Panametrics GP68, equalisation tank level by a Hawk LP30 ultrasonic level transmitter and equalisation tank pH by a Yokogawa PH200G retractable pH probe. All on-line measurements were recorded each minute via an Allen-Bradley 5/03 PLC and logged on a 486 DX2-66 PC interface with WinSpirs MMI (Rockwell Software). These values were averaged into 1.5 or 3 h values for model inputs and outputs.

2.6. Hydraulic retention time distribution study

Rhodamine WT (8 g) was injected into the reactor feed. This was sufficient for an average concentration of 5 μg/l of dye in the reactor. Samples were taken in glass containers every 40 min and combined to 2 h composites over a duration of 72 h. The samples were analysed using a Hitachi F-2000 fluorescence spectrophotometer with an excitation wavelength of 558 nm and emission wavelength of 581 nm.

3. Plant analysis

3.1. Reactor hydraulics

An HRT distribution study on a reactor without gas generation showed plug flow dynamics (data not shown). However, gas production increases reactor mixing and the extent of this needed to be evaluated. The residence time distribution measured was compared with a two-tank hydraulic model. The optimal model was found with a tank volume ratio of 1:15 (i.e., one tank 15 times the volume of the other, Fig. 2). Plant flow data was used as input to the model.

The results deviate from CSTR behaviour mainly in the first 8 h. Therefore, the short-term behaviour of the system may have significant deviations from a CSTR model. To investigate this further, reaction dynamics of the optimal two and one-tank CSTR models were compared using the fully validated dynamic model seen

![O&G (mg/l) COD (mg/l) N (mg/l)](image)

Fig. 1. Theoretical conversions for particulate and soluble fats and nitrogen to COD were used to evaluate their COD contributions.
later in this paper. A feed concentration of 200 c-mole/m³ soluble protein and flowrate of 30 m³/h was used. Limited solids re-circulation within the two-tank model allowed for increased biomass in the first reactor.

The results of these simulations using hydraulic and concentration step increases indicated no significant difference between predictions (based on errors in organic acid measurement). Therefore, CSTR hydraulics are adequate for simulation under most conditions except during low gas and liquid flows (e.g., start-up).

3.2. Influent matrix

Initial experimental work indicated influent flow consisted mainly of fat and protein of which 45% was soluble. However, improvements in fat separation in the pre-treatment plant meant soluble fat dropped significantly during the main sampling period (Table 1).

Carbohydrates were found only during very low load periods. The main sampling period showed approximately even contributions to COD from particulate protein, soluble protein and particulate fat.

The volume average particle size was consistently in the range 0.02–0.03 mm. This did not increase appreciably during cleaning or other factory activities. Therefore, a detailed description of the effect of solids size on hydrolysis was not necessary.

3.3. Reactor feed matrix

It was immediately evident from all the experimental data sets that the reactor feed soluble COD could be attributed completely to organic acids (Table 2). These results combined with a carbon balance indicated the process appears largely hydrolysis-limited for particulate degradation while degradation of soluble protein is rapid.

4. Parameter estimation

The first part of this study outlined an approach to parameter estimation. This section applies that approach. The parameter set can be grouped into three broad groups (Table 3). While there are many parameters, most of these are directly applicable from previous studies.

4.1. Biological parameters

All biological parameters for carbohydrate degrading organic acid oxidising and methanogenic groups can be taken from Romli (1994) as substrate and bacteria types should not have changed (Table 4). This leaves protein-degrading and LCFA-degrading parameters.

Because degradation pathways of proteins have changed, and because hydrolysis of proteins appears to be rate limiting, kinetic parameters from Ramsay (1997) were used. Stoichiometric yields will have changed significantly and need to be estimated by steady-state or dynamic data. The exception is ammonia yield, which was initially estimated from Henze et al. (1995) and modified during dynamic-parameter estimation.

Degradations of fats and lipids also seem to be limited by hydrolysis. Kinetic parameters for LCFA are taken from Novak and Carlson (1970) for palmitic acid. Hydrogen and pH inhibition is assumed the same as butyric acid bacteria as this group also utilises β-oxidation.
4.2. Enzymatic parameters

While there are data in the biochemical literature on the hydrolysis of specific organics, they are largely not applicable as they describe specific particulate material. Parameters describing the hydrolysis of cellulose are probably directly applicable for the hydrolysis of complex carbohydrates (Humphrey, 1979). Because this wastewater has low solids levels, it is expected that enzyme concentrations may never approach limiting levels and may therefore not be significant. A sensitivity analysis of soluble nitrogen in the reactor feed to hydrolysis parameters indicated that within a factor of 10 (original values taken from hydrolysis of cellulose), and are linearly correlated. Therefore the enzyme concentration is not limiting at these levels and can be eliminated. Enzyme yield and substrate-limiting-concentrations were taken from that of cellulose.

Table 3
Parameter set

<table>
<thead>
<tr>
<th>Parameter set used by each biological group</th>
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</thead>
<tbody>
<tr>
<td>Biological parameters</td>
</tr>
<tr>
<td>$k_m$ Maximum specific growth rate</td>
</tr>
<tr>
<td>$K_c$ Half velocity rate constant</td>
</tr>
<tr>
<td>$Y$ Bacterial yield</td>
</tr>
<tr>
<td>$b$ First-order biomass death rate constant</td>
</tr>
<tr>
<td>pH$_{UL}$ Upper limit where pH inhibition first occurs</td>
</tr>
<tr>
<td>pH$_{LL}$ Lower level at which pH inhibition is total</td>
</tr>
</tbody>
</table>

1. One parameter set is used for each biological group (in this case there are 10 biological groups; therefore 60 parameters describe biological activity)
2. c-mole S and c-mole P refers to substrate and bacterial concentrations respectively in units of moles carbon

**Parameters specific to a biological group**

$\text{pr}_\text{stoich}_i$ Stoichiometric yield of production $i$ from protein | c-mole P c-mole S$^{-2}$ |

1. There are eight products from the degradation of protein
2. c-mole S and c-mole P refers to substrate and product concentrations

**Enzymatic parameters**

**Parameters describing enzymatic hydrolysis of particulates**

$K_Q$ Combined reaction and adsorption rate coefficient | (c-mole Q/m$^3$)$^{1/3}$ h$^{-1}$ |
$z$ Enzyme saturation constant | c-mole E m$^{-3}$ |
$Y_E$ Enzyme yield | c-mole E c-mole B$^{-1}$ |
$K_{E,S}$ Product related enzyme production inhibition coefficient | c-mole S m$^{-3}$ |

1. There are eight products from the degradation of protein
2. C-mole Q and c-mole E refers particulate substrate and enzyme concentrations, respectively

**Physicochemical parameters**

**Physicochemical parameters describing overall system**

$k_w$ Ionisation constant for water | K$^{-1}$ |
$I_{H_2O}$ Vapour pressure of water | Bar |
$R$ Ideal gas law constant | m$^3$mole$^{-1}$ K$^{-1}$ |
$H$ Henry’s law constant for carbon-dioxide | c-mole S/m$^3$ bar$^{-1}$ |
$\tau_{bact}$ Residence time of bacteria in reactor | h |
$\tau_{sols}$ Residence time of solids in reactor | h |
$D$ Reactor diameter | m |
$max\_liq\_vol$ Maximum liquid volume | m$^3$ |
$min\_gas\_vol$ Minimum gas volume | m$^3$ |

**Physicochemical parameters describing individual components**

$K_{a,i}$ Gas–liquid transfer constant for carbon-dioxide | h$^{-1}$ |
$K_{s,i}$ Association–dissociation constant for acid–base pair $i$ | mole/m$^3$ |
$\sigma_{prot}$ Carbon per charged site for proteins (acids) | c-mole/mole |
$\sigma_{base}$ Carbon per charged site for proteins (bases) | c-mole/mole |
$\bar{n}_i$ Average number of carbon atoms in LCFA chain | c-mole/mole |
$\omega$ Average number of unsaturated bonds in LCFA chain | |

1. There are 13 acid–base pairs in the model
2. LCFA characteristics could be grouped with stoichiometric yield parameters as they are only used to calculate product yield
4.3. Stoichiometric parameters

All physio-chemical parameters describing the overall system except for \( s^{\text{solids}} \) and \( s^{\text{bacteria}} \) are either applicable from previous studies or are available directly from reactor dimensions and conditions.

Association/dissociation constants for all the acid-base pairs are available in the literature (Snoeyink and Jenkins, 1980). While \( \alpha^{\text{acid}} \) and \( \alpha^{\text{base}} \) will have changed there is no way of evaluating this except by analysing dynamically for amino acid compositions and, as soluble protein composition is low, it will have little effect on pH. Characteristics of the LCFA chain \( (n_c, \omega) \) were assumed the same as pig tallow; mainly consisting of palmitic and oleic acids (Austin, 1984).

The gas–liquid coefficient \( (k_L a) \), is reactor specific as it depends on area and surface properties. This needs to be estimated during dynamic parameter estimation.

5. Parameter estimation from data sets

This stage requires that the error in the model output be minimised by adjusting parameters. Most outputs are sensitive to only a small number of parameters. To simplify the parameter estimation procedure, it is necessary to optimise pairing of outputs and parameters and minimise correlation between parameters (see Batstone et al., 1997 and Figs. 3 and 4). As indicated in the previous paper, a number of parameters can be estimated by modelling only the acidification tank. A weighted model fit is used to evaluate simulation performance (Batstone et al., 1997).

5.1. Experimental data for parameter estimation

The second experimental data set was used to estimate parameters. Operating conditions used were a high equalisation tank level and no recycle. Input flow data and equalisation tank level were logged over a 160 h period (Batstone et al., 1997). Because of the long system residence time, prior concentration data was taken from weekend composites.

5.2. Estimation of parameters on equalisation tank

5.2.1. Phase 1 model implementation and initial parameter estimation

Initial parameter estimates were made from plant experience (e.g., solids retention time), from Ramsay (1997) (e.g., yields of products from protein), or similar literature data (e.g. lipid \( K_Q \) based on cellulose \( K_Q \)). Initial estimates were made of state and algebraic variables based on mass balances. A simulation over 10,000 h was done to ensure the system had reached steady state. These results were then used as the initial conditions for dynamic simulations.

5.2.2. Phase 2: soluble COD in the equalisation tank

The reactor feed soluble nitrogen and COD were used to estimate protein and fat hydrolysis, respectively. Each iteration used linear estimation to adjust \( K_Q \). The nitrogen released by hydrolysis was relatively low compared to that released from soluble protein but adequate for \( K_Q \) estimation. After this, it was necessary to compare model and experimental soluble COD to estimate \( K_Q \) for particulate fat hydrolysis. This indicated almost no hydrolysis of fat. Therefore, fat \( K_Q \) needed to be estimated from the effluent fat levels.

5.2.3. Phase 3: products from amino acid degradation

The objective here was to change the yields from protein to fit organic acid production. After this, the carbon balance was compared to estimate the carbon-dioxide yield. Inconsistencies between the carbon balance and nitrogen balance required the nitrogen yield from protein to be increased. This required several iterations between phases 2 and 3. The reactor effluent ammonia was used to check these results.

The experimental organic acids all rise significantly, which the model does not predict well in the first 24 h (Fig. 5). This is not as pronounced in the experimental results for soluble COD, which is alleviated by a rise in soluble nitrogen during this period. This may indicate that the protein kinetics were faster here than measured.

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Table 4

<table>
<thead>
<tr>
<th>Group</th>
<th>Source</th>
<th>( k_m )</th>
<th>( K_s )</th>
<th>( Y )</th>
<th>( b )</th>
<th>( pH_{UL} )</th>
<th>( pH_{UL} )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Glucose</td>
<td>1</td>
<td>5</td>
<td>40</td>
<td>( f(zn) )</td>
<td>0.00083</td>
<td>5.0</td>
<td>4.0</td>
</tr>
<tr>
<td>Protein</td>
<td>2</td>
<td>2.05</td>
<td>35</td>
<td>0.062</td>
<td>0.00083</td>
<td>7.2</td>
<td>5.2</td>
</tr>
<tr>
<td>LCFA</td>
<td>3</td>
<td>0.081</td>
<td>3.1</td>
<td>0.072</td>
<td>0.00125</td>
<td>6.0</td>
<td>4.0</td>
</tr>
<tr>
<td>Valerate</td>
<td>2</td>
<td>1.9</td>
<td>5</td>
<td>0.072</td>
<td>0.00125</td>
<td>6.0</td>
<td>4.0</td>
</tr>
<tr>
<td>Butyrate</td>
<td>1</td>
<td>4</td>
<td>7</td>
<td>0.072</td>
<td>0.00125</td>
<td>6.0</td>
<td>4.0</td>
</tr>
<tr>
<td>Lactate</td>
<td>1</td>
<td>3.8</td>
<td>1.14</td>
<td>( f(zn) )</td>
<td>0.00086</td>
<td>6.0</td>
<td>4.0</td>
</tr>
<tr>
<td>Propionate</td>
<td>1</td>
<td>0.524</td>
<td>10</td>
<td>0.064</td>
<td>0.00042</td>
<td>6.0</td>
<td>4.0</td>
</tr>
<tr>
<td>Acetate</td>
<td>1</td>
<td>0.350</td>
<td>3</td>
<td>0.048</td>
<td>0.00083</td>
<td>7.0</td>
<td>6.0</td>
</tr>
<tr>
<td>Hydrogen</td>
<td>1</td>
<td>3.6</td>
<td>0.055</td>
<td>0.03</td>
<td>0.000375</td>
<td>6.0</td>
<td>4.5</td>
</tr>
</tbody>
</table>

*Ramsey (1997), Romli (1993) and Novak and Carlson (1970), yields of glucose and lactate are dependent on zn (see previous paper, Table 2).
by Ramsay (1997). Apart from this, there is little significant change in experimental or model results.

A carbon balance indicated that the CO₂ yield was 0.19 mole CO₂/c-mole protein which is slightly higher than in Ramsay (1997) (0.157 mole CO₂/c-mole).

5.2.4. Phase 4: equalisation tank pH

The final step was to adjust buffering in the equalisation tank to match experimental and simulation pH results. This again was via linear approximation. Prediction during the sampling period was very good. Detailed results of this are presented in Batstone et al. (1997).

5.3. Estimation of remaining parameters

Phases 5–8 require estimating remaining parameters using experimental data from the methanogenic reactor. These are: solids and biomass retention time ($\tau_{\text{sols}}, \tau_{\text{bact}}$); assumed to be equal, carbon-dioxide transfer co-efficient ($k_{L,a}$) and the fat hydrolysis parameter $K_Q$. As all these variables affect gas flow, this procedure is iterative. In practice, it was found that the $k_{L,a}$ needed to be set to a value above 1 h⁻¹ to achieve the experimental CO₂ measurement of 23–25%.

From Fig. 6 it can be seen that solids retention time has less effect above 1600 h as all proteins and most fats were hydrolysed. Since the model gas flow was consistently below the experimental gas flow (see Batstone et al., 1997), a minimum residence time with near complete degradation was chosen (1000 h) as the model has a better probability of reflecting reactor behaviour under biomass limited conditions.

Additional experimental work by ESI indicated that 70–80% of fats were removed in the reactor at current loading rates. The hydrolysis kinetic parameter was modified to reflect this.

Simulations of gas flows during high load periods are close to experimental values but the model predicts much lower values during low load periods. Experi-
mental gas flows appear inconsistent with reactor load and a mass balance over the reactor indicated an accumulation of ~11% and ~25% of carbon and nitrogen, respectively, over the reactor. No accumulation occurred in the acidification reactor. This indicates that more gas was produced than could be accounted for by the incoming feed. There are several possibilities consistent with the mass balance assumptions:

Equalisation tank biomass was washed into the reactor and degraded.

The equalisation tank mixer was started 10 days prior to this experimental data set. The high gas flow during
the low load periods is due to on-going degradation of the residual solids relating from this event. Increased degradation of solids when soluble substrate is limited is well documented (Humphrey, 1979; Martinelle and Hult, 1994).

6. Validation of parameters

Model validation was done on two additional data sets, with and without recycle. Weighted fits during the parameter estimation procedure were used as in Batstone et al. (1997) to give an overall fit of 83% for the parameter estimation simulations, 88% for simulation with recycle and 74% for simulation with recycle. The lower fit for simulations with recycle was due to very low levels of organic acids measured (Table 5).

6.1. Parameter estimation without recycle

The experimental data set here was collected with no recycle and a low acidification reactor level (12 h HRT). Equalisation tank influent had the normal daily peaks while reactor influent was slowly increased from 0 to 40 m³/h during the period (Fig. 7). Soluble protein was generally higher than in the parameter estimation runs while particulate fats were slightly less. There was no soluble fat detected.

Equalisation tank VFAs are stable during the data set and while simulation of the steady-state data is good, there is little dynamic change to compare to (Table 5).

The model does not predict the equalisation tank pH well (Fig. 7), though this was outside the sampling period. During a period with no feed or internal flows within the plant, the pH rose significantly, starting immediately after stopping reactor feed. The model predicted steady pH. After this the pH dropped immediately when reactor feed flow was re-started.

During this weekend period, the tank level was low and the mixer was not operating. This means the pH probe would have been close to the surface, where CO₂ was transferring to the gas phase. This might have caused the local pH to rise. When flow and mixers were re-started, the tank was mixed again, eliminating the surface effect. This is consistent with the very rapid pH drop to the previous level. Simulation of gas flow was good.

6.2. Validation with recycle

The data set used here had a 20% recycle and a high residence time (Fig. 8). Data were not logged prior to sampling and no pre-simulation data is available but logged data were used after the sampling period despite the lack of concentration data. There were more changes to reactor feed to increase gas flow dynamics.

Equalisation tank VFAs were lower than predicted (Table 4). Prediction of gas production was very good and consistent with the higher loads. A mass balance over the system suggested that approximately 10% of the carbon accumulated in the equalisation tank and was subsequently lost from the reactor. This indicated that carbon was passing from the equalisation tank to the reactor in a form not detected by soluble COD or organic acids.

<table>
<thead>
<tr>
<th>Table 5</th>
<th>Experimental and simulation results for validation simulations (c-mole/m³)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Acetic</td>
</tr>
<tr>
<td>No recycle</td>
<td>Avg exp 16.7</td>
</tr>
<tr>
<td></td>
<td>Avg model 13.0</td>
</tr>
<tr>
<td></td>
<td>Stdev exp 1.8</td>
</tr>
<tr>
<td></td>
<td>Stdev model 0.4</td>
</tr>
<tr>
<td>20% recycle</td>
<td>Avg exp 7.4</td>
</tr>
<tr>
<td></td>
<td>Avg model 9.7</td>
</tr>
<tr>
<td></td>
<td>Stdev exp 1.5</td>
</tr>
<tr>
<td></td>
<td>Stdev model 1.1</td>
</tr>
</tbody>
</table>

Fig. 6. Contour plot of sensitivity of gas production to solids retention and CO₂, kₐ₀ (contours are % change in gas concentration).
One possible explanation is adsorption of the larger volatile fatty acids in their associated form onto the biomass surface. This is subsequently degraded in the reactor. Other elements support this:

Equalisation tank pH is low; 6.1 compared to a normal pH of 6.5–6.8. A lower pH favours adsorption as only adsorption of associated acids occurs.

The model prediction becomes worse as the organic acid order increases. Higher order organic acids adsorb onto particles more readily. Also, the association constant is greater for higher order organic acids. This means they will associate at a higher pH compared to the lower order organic acids.

Particulate COD is higher than expected for this data set.

There is methanogenic biomass present in the equalisation tank. Methanogens are thought to be generally hydrophobic while acidogens are generally hydrophilic (Thaveesri et al., 1995). Adsorption of organic acids will occur more readily on hydrophobic surfaces.

7. Discussion

7.1. Model strengths and weaknesses

The structure of the model allows for a high level of flexibility, which is of major concern when modelling complex wastewater. Also, because major intermediates are shown, it is easier to understand the origin of specific problems or anomalies. This has been demonstrated here in two cases:

(a) Protein and fat hydrolysis were shown to be very slow. This indicates that particulate material accumulates in the reactor, perhaps causing long term overloading and solids related operational problems.

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Fig. 7. Validation without recycle: (a) influent (---), reactor feed (—), and equalisation tank level (●●●●); (b) reactor gas production experimental (○) and model (—); (c) equalisation tank pH experimental (●) and model (—).

Fig. 8. Validation with recycle: (a) influent (---), reactor feed/recycle (—), and equalisation tank level (●●●●); (b) reactor gas production experimental (○) and model (—).
(b) The reactor feed measured organic acid concentrations and soluble COD were low in the final experimental data set. Their influence on reactor outputs such as gas production was comparatively high. The model simulations indicated that they were degraded. Additional measurements such as pH and particulate COD support the conclusion that organic acids were probably adsorbing onto the surface of the biomass.

Currently, the model contains no mechanisms for description of inhibition via LCFA or sulphide. These were not included here as they were not issues in the plant under investigation but these forms of inhibition can cause problems in other reactors. However, the kinetics of LCFA inhibition is well documented (Rinzema et al., 1994; Angelidaki et al., 1997) and the provision of physicochemical effects allows for a better implementation. The effects of sulphide inhibition are more complicated but are also well documented (Speece, 1996). The modular structure of the model allows these to be implemented if required.

Currently, it is assumed that biomass and solids both have identical, fixed retention times. However, retention is likely to be subject to various inputs such as liquid upflow velocity, gas flow rates, granule size, granule shear strength, fat and lipid levels and others. To accurately reflect the response of biomass to these inputs and state variables, it is necessary to understand granulation in complex wastewaters which is still poorly understood.

7.2. Applications

There are two broad areas of application for this work: theoretical and practical.

An example of theoretical application is the prediction of intermediates not easily measurable (such as hydrogen) where large numbers of in-series reactors are used. It is thought that hydrogen is a factor in several aspects of reactor operation such as intermediate regulation and granulation.

Practical applications include on-line prediction and reactor analysis and analysis of reactor configuration and hydraulic design. The model is particularly useful for theoretical reactor behaviour for a particular protein based substrate as the equations in Ramsay (1997) can predict the intermediates for a given protein primary structure.

8. Conclusions

A hydraulic retention study indicated two CSTRs in series could model the hydraulics of the methanogenic reactor. Simulations using this hydraulic model however showed no significant differences to a single CSTR model.

The generic parameter estimation procedure outlined in the first paper was applied here. Particularly, by modelling acidogenesis and methanogenesis separately in a data set without alkalinity recycle, dynamic parameter estimation was considerably simplified.

The model was validated on independent data sets with and without recycle. The only instance of poor model performance was overprediction of acidification tank VFA concentrations during recycle. This was probably due to adsorption of associated organic acids onto the surface of methanogenic biomass. Soluble COD is used as a measure of short term methanogenic reactor load. In plants that are heavily loaded, relative adsorption should be much less.

Previous designs assumed that particulates were degraded in the acidification reactor (Newland et al., 1997). The results given here indicate that it is very difficult to degrade protein based particulate substrate and the longer solids residence times of the reactor are required. Indeed, un-degraded solids can maintain significant gas production for a long time after the reactor feed is stopped.

Unlike other studies (Angelidaki et al., 1997; McInerney, 1988), hydrolysis of fats was rate limiting rather than conversion of LCFA to acetic acid. This is probably because the fat here is in solid form, minimising emulsification and consequently lowering solid-liquid interface area.

Acknowledgements

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References


