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EXTENDING TWO STEPS ANAEROBIC DIGESTION MODELS TO INCORPORATE SURFACE AREA EFFECT

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Abstract- The surface area is a significant factor in anaerobic digestion since bacterial growth depends on the spaces available on these surfaces. This study involves modifying the original two-step model to incorporate the influence of interior extended surface areas on digestion dynamics. In addition, initial substrate concentration effects on the anaerobic digestion performance also study. Cow dung was used as a substrate for digesters operating under mesophilic conditions. Four household batch anaerobic digesters augmented by four circular horizontal extended surfaces of width 0, 2, 4 and 6 cm were prepared. Particle swarm optimization coding (MATLAB 2018a) was used to estimate the model parameters according to measured data for each individual digester. The modeling results are safisticated parameter predictions and understanding of parameters' role in anaerobic digestion for each digester. It was found that digester performance is directly proportional to extended internal surface area. In addition, an acceptable agreement was observed between experimental and numerical data; the maximum mean absolute percent error was less than 16.3 %.

Keywords: Anaerobic Digestion, Batch Digester, Extended Surfaces, Cow Dung, Modified AM2.

1. INTRODUCTION

Recently, the energy from natural sources, like petroleum, coal and natural gas, is increased due to higher consumption in residual building, industrials, power generation etc. However, using these sources is expensive and leads to population, health hazards and increasing global warning due to natural resources degradation and burning of fossil fuels. Hence, renewable energies, like solar, biomass, wind and geothermal, are alternatives to fossil fuels.

Biogas is one type of renewable energy and the relative substitute for fossil fuels. It is the result of an anaerobic digestion (AD) process that turns waste volumes such as animal, industrial, and agricultural wastes. etc., into biogas which contains (55-75 % of CH4 and 25-40 % of CO_2) in the absence of oxygen by using anaerobic bacteria. AD processes are environmentally friendly and include hydrolysis, acidogenesis process, acetogenesis process, and methanogenesis process [1]. Biologically, the organic substrate in the above steps is consumed and converted by bacteria, so bacteria's growth and decay are responsible for the metabolism. As a result, the bacteria activity and growth increased on the surfaces.

AD modeling is essential for monitoring and controlling process performance, investigating the sensitivity of process behavior to operational parameters, and determining the feasibility of using new substrates with varying characteristics, biodegradability, and working conditions. There are many computational models related to these events in the literature; however, they are sometimes highly complicated and inappropriate for management.

Zhou, et al. [2] implemented and calibrated a modified anaerobic digestion model No. 1 (ADM1) using a laboratory biodigester with a supplied mixture of cow dung (CD) of 30% and corn maize silage of 70 %. Rodriguez, et al. [3] used Romero model in the fit and analysis of experimental results of biogas production and organic matter consumption of batch anaerobic digestion for municipal solid waste at mesophilic (35 °C) and thermophilic (55 °C) conditions. Yuan, et al. [4] presented stoichiometric coefficients calculation for amino acid acidogenesis during the blue algae AD to facilitate the ADM1 application based on Monte Carlo simulation. Mattei, et al.

[5] present a mathematical model to simulate a sulfate-reduction biofilm's biological, chemical and physical processes under dynamic conditions. Budiyono, et al. [6] studied anaerobic treatment of two kinds of substrates compositions (vinasse and rumen) and (vinasse, rumen and urea) with variation initial pH 6, 7 and 8 for each substrate in the batch anaerobic digester at room temperature by using modified Gompertz model and first-order kinetic model. Gen, et al. [7] proposed a blending strategy based on a linear programming optimization method for maximizing COD conversion into methane for multiple substrates anaerobic co-

digestion to enhance biogas production. Fedailaine, et al. mathematical model to simulate anaerobic digestion. Arzate, et al. [9] proposed the AMOCO two-step model to fit the experimental data from pilot-scale biogas digester using maize silage as substrate under mesophilic conditions. Bona, et al. [10] formulated a linear fractional transformation model utilizing a symbolic tool designed for linear models and adapted for nonlinear ones.The model used generated data from ADM1 model and experimental data of laboratory semi-batch anaerobic digestion using cheese whey. Bravo, et al. [11] presented an assessment of the AD optimization model based on the global sensitivity analysis application, parameters uncertainty estimation and multi-start optimization procedure in batch test.

Janke, et al. [12] studied optimization of the sugarcane filter cake AD with an emphasis on volatile fatty acid (VFA) generation and Cumulative CH4 production fit to a two-step dual-pool model to offer an early assessment of AD. Zareei and Khodaei [13] designed an adaptive neuro-fuzzy interference method for identifying and improving AD biogas generation of maize straw with cow manure under various carbon to nitrogen ratios, total solid and stirring intensity for full-scale batch digester under mesophilic conditions. Momoh and Ouki [14] developed fractal-like kinetic model to study the effect of particle size of rice husk on hydrolysis and biogas production of anaerobic co-digestion with cow manure mixture into batch reactor at ambient conditions. Arzate, et al. [15] performed the modified AMOCO model (AM2) to simulate biogas formulation using maize silage as a dynamic feedstock supply. Because the model is appropriate for the extremely slow responses that happen with anaerobic microbes supplied in a real-time dynamic system, optimization employs a sophisticated as well as nonlinear model.

Rathaur, et al. [1] improved the biogas production quantity and quality from parthenium hysterophorus, Paper trash, canteen waste, and their combination treated with catalyst (silica gel, poultry litter, and cow urine) and effective inoculum (slurry of gobar gas) under mesophilic temperature (37 oC) for batch digester. First-order kinetic model describes the bio-methane production from all wastes and their mixtures. Ivanovs, et al. [16] designed a model that considers the specific features of fish waste as substrate. The model included two ways of anaerobic digestion processes: chemical reactions and microorganisms growth kinetics in the system. Zhang, et al. [17] used cone model, transfer function model and first-order kinetic to evaluate the reactor performance and explore the kinetics of anaerobic digestion biogas production when added nano zero-valent iron and Fe_3O_4 nanoparticles were to anaerobic digestion reactor under mesophilic conditions.

Pati, et al. [18] used food waste as a substrate mixed with different ratios of CD as inoculum, and these were given as feedstock to anaerobic digester to deliver biogas. Technique response surface methodology modeled the process behavior at different conditions. Nong, et al. [19] employed a modified Gompertz model to estimate rate of maximum biogas production and potential of biogas yield [8] built a biomass mass balance-based of swine manure and CD in batch anaerobic digestion. Rajput, et al. [20] studied the influence of sunflower meal and wheat straw co-digestion blinds thermally pretreated at (120, 140, 160 and 180 oC) on biogas production experimentally. It was validated with three different nonlinear kinetic models. Alfa, et al.

[21] determined the optimum mixture percentage of cow dung and horse dung for enhanced biogas production was carried out in five identical 25L cylindrical digesters under ambient temperature of 33 oC. The modified Gompertz model predicted the relevant kinetic variables of the digestion process. Elagroudy, et al. [22] optimized four different models: modified Gompertz, logistic function, reaction curve and exponential rise under seven different microwave sludge pretreatment intensities of biogas generation. Noonari, et al. [23] investigated the impact of pretreatment on isolated fungal strains of Aspergillus (niger, terrerus and sojae) for methane production through rice straw in a 30:70 ratio with buffalo dung experimentally and fitted with the Gompertz model. Gonzalez, et al. [24] applied for first order, Gompertz and cone models to evaluate kinetic parameters on the methane produced from four biomasses (microalgae, sorghum, corn stabble, rapeseed oil) in AD carried out in batch reactor. Rahmani, et al. [25] used modified Gompertz, first order, transference and logistic models to ensure co-digestion synergic effects and determine the optimal inoculum-to-substrate ratio. Su, et al. [26] developed a model to predict dynamic biogas production in passive solar-assisted biogas digester. It combines soil heat transmission and feeding with a biogas AD kinetic model.

The objective of this work is to develop and modify the original AMOCO two-step model (AM2) to corporate the effect of horizontal extended surfaces area added to the interior of anaerobic batch digesters on biogas production. Measurements of pH, CH4 flow rate, and CO2 flow rate were fit into particle swarm optimization coding (MATLAB 2018a) to optimize model parameters.

2. METHODOLOGY

2.1. Experimental Set-Up

Biomethanation from CD substrate during AD processes was conducted in four household batch cylindrical digesters D1, D2, D3 and D4. These digesters fabricated from PVC plastic with 13 L capacity have dimensions of 29 cm height * 24 cm diameter each. The lid is sealed to prevent air leakage. The effecting working volume for each batch digester is 10 L (5 kg Total Solids) at 22 cm height. Three holes are provided on the top of each digester. The first hole is used to collect biogas into the gas storage, the second is for temperature sensor wire, and the last is for substrate feeding. In addition, a hole drain with 0.5-inch diameter at 11 cm height is provided on the side of each digester. The gas collector is fabricated from PVC plastic with a volume of 4 L, formed from an inverted cylinder into another water cylinder where the inverted cylinder floating indicates biogas production quantity. In addition, each digester was provided with two valves after the biogas hole for control

and evacuation. Figures 1 illustrates the photograph for the household anaerobic digesters set-up.

Digester (D1) has no extended surfaces, while digesters D2, D3 and D4 contain four circular horizontal extended surfaces with a thickness of 2.5 mm and width of 2, 4 and 6 cm, respectively. The spacing between extended surfaces is 5 cm, as shown in Figure 2. The RASI 700 gas data analyzer was used to determine the percentage of biogas components such as CH4 and CO2 concentrations generated by the AD system. The Data logger multi-channel instrument model AT 4508 was used to measure the anaerobic digester's temperature. Eco testr pH2 digital meter used for monitoring the value of pH for the CD in each digester every day.

Figure 1. Bbatch anaerobic digesters set-up

Figure 2. Arrangement of horizontal extended surfaces in the digesters

2.2. Model Assumption and Description

In anaerobic digestion, two important steps biological model [9] to produce biogas: the initial step is acetogenic bacteria X_1 consumed substrate S_1 to volatile fatty acids (VFA), carbon dioxide and hydrogen with microbial growth equation:

$$k_1 S_1 \xrightarrow{r_1} X_1 + k_2 S_2 + k_4 CO_2$$

In the second step, methanogens bacteria X_2 degraded the VFA S_2 and generate carbon dioxide and methane with microbial growth equation:

$$k_3 S_2 \xrightarrow{r_{21}} X_2 + k_5 CO_2 + k_6 CH_4$$

Acidogenic bacteria and methanogenic bacteria are involved in the two biological processes listed below [9]:

The acidogenesis reaction rate of substrate (r_1)

$$r_1 = \mu_1 X_1 \tag{1}$$

The methanogenesis reaction rate of (VFA) r_2

$$r_2 = \mu_2 X_2 \tag{2}$$

where, μ_1 and μ_2 are specific growth rates of acidogenic and methanogenic biomass, respectively.

2.3. Modified AMOCO Model (AM2)

The original AMOCO model [27] based on material, organic matter, and biogas mass balance was modified and applied to describe CD substrates' AD for batch anaerobic digesters. The ordinary differential equations of bacteria X_1 and X_2 modified to involve the terms kd_1 and kd_2 of the rate of bacteria decay X_1 and X_2, respectively, as illustrated in Equations (3) and (4). As seen in algebraic Equations (9) and (10) of acidogenic and methanogenic bacteria growth rates μ_1 and μ_2 for bacteria X_1 and X_2, respectively modified to contain k_{sur} surface area coefficient to represent interior surface area of the digester. The mass balance model includes six ordinary differential equations:

$$\frac{dX_1}{dt} = \left[\mu_1 - kd_1\right] X_1 \tag{3}$$

$$\frac{dX_2}{dt} = \left[\mu_2 - kd_2\right] X_2 \tag{4}$$

$$\frac{dS_1}{dt} = -k_1 \mu_1 X_1 \tag{5}$$

$$\frac{dS_2}{dt} = k_2 \mu_1 X_1 - k_3 \mu_2 X_2 \tag{6}$$

$$\frac{dZ}{dt} = 0 \tag{7}$$

$$\frac{dC}{dt} = -qc + k_4 \mu_1 X_1 + k_5 \mu_2 X_2 \tag{8}$$

where, C is the concentration of inorganic carbon (mmol C/L) and Z is the alkalinity (mmol C/L). The kinetics of acidogenic and methanogenic bacteria growth, X_1 and X_2, respectively.

$$\mu_1 = k_{sur} \mu_{1\max} \frac{S_1}{S_1 + k_{S1}} \tag{9}$$

$$\mu_2 = k_{sur} \mu_{2\max} \frac{S_2}{S_2 + k_{S2} + \frac{S_2^2}{k_{I2}}} \tag{10}$$

where, k_{S1} and k_{S2} are half-saturation constant (g/L) and (mmol/L), respectively and k_{I2} is inhibition constant (mmol/L). Calculating methane and carbon dioxide flow rates production, qc and qm, respectively.

$$\phi = C + S_2 - Z + KH.P_T + \frac{k_6}{k_{LA}} \mu_2 X_2 \tag{11}$$

$$Pc = \frac{\phi - \sqrt{\phi^2 - 4KH.P_T(C + S_2 - Z)}}{2KH} \tag{12}$$

$$PH = -\log 10\left[K_b \frac{C - Z + S_2}{Z - S_2}\right] \tag{13}$$

$$qc = k_{LA}\left[C + S_2 - Z - KH * Pc\right] \tag{14}$$

$$qm = k_6 \mu_2 X_2 \tag{15}$$

where, Pc and P_T are carbon dioxide CO_2 partial pressure and total pressure in the digester. k_{LA} is liquid-gas transfer constant (1/d).

2.4. Optimization of Parameters

Parameters optimization of equations for the modified AM2 model for each digester were estimated using the particle swarm method during the "fmincon" function of MATLAB software. The numerical integration for six ordinary differential equations of the modified AM2 model for each digester was solved with the "ode23" function in MATLAB software to obtain output variables. Initial parameters and variables for modified AM2 model equations were used from paper in the literature [9]. Calibration results of the modified AM2 model application for four digesters to the mono-digestion of CD are depicted in Table (1).

The fifteen parameters of the modified AM2 model equations for each digester that can affect numerical results were subjected to digester performance. Parameters of kinetic Equations (9) and (10) for the acidogengnic and methanogenic bacteria growth, such as μ_{2max}, k_{S1}, k_{S2} and k_{sur} are the most influential parameters showing variation of methane production especially k_{sur} has shown high effectiveness for methane production, especially after a few days of modeling when bacteria start to search and grow on the surfaces, but kd_1 and kd_2 exhibited inhibition parameters for biogas production. Parameters μ_{1max}, k_1, k_2, k_3, k_4 and k_5 are ineffective in biogas production. Parameter k_6 only influences methane accumulation, determined by Equation (15), since it is only affected. Other parameters as k_{I2} and k_{LA} are no effect on the methane production, but the former parameter is low effectively, and the latter is high on the CO_2 production as depicted in Equation (14).

Table 1. Calibrated parameters of the modified AM2 model for four digesters

Parameter	Unit	D1	D2	D3	D4
k_1, Coefficient of substrate degradation	---	10.8	10.8	10.8	10.8
k_2, Coefficient of VFA production	mmol/g	226.6	226.6	226.6	226.6
k_3, Coefficient of VFA consumption	mmol/g	570.6	570.6	570.6	570.6
k_4, Coefficient of CO2 production	mmol/g	34.9	34.9	34.9	34.9
k_5, Coefficient of CO2 production	mmol/g	24.8	24.8	24.8	24.8
k_6, Coefficient of CH4 production	mmol/g	1977.8	2786.2	2897.9	2998.7
kd_1, Decay rate of biomass X_1	1/d	0.0033	0.004	0.0045	0.0045
kd_2, Decay rate of biomass X_2	1/d	0.002	0.0021	0.0022	0.0023
k_{I2}, Inhibition constant	mmol/L	1578.6	1735	2000	1971.2
k_{LA}, Constant of liquid gas transport	1/d	54.8	10	20	42.1
k_{S1}, Constant of half-saturation	g/L	90	95	105	105
k_{S2}, Constant of half-saturation	mmol/L	10	13.7	10	22.3
k_{sur}, Inside surface area coefficient of the digester	---	1.6	2.4	3.6	4.8
μ_{1max}, Acidogenic bacteria's maximum growth rate	1/d	0.2	0.2	0.2	0.2
μ_{2max}, Methanogenic bacteria's maximum growth rate	1/d	2.6	2.9	3.7	4.8

3. RESULTS AND DISCUSSION

3.1. Numerical Results

The modified AM2 model was implemented to simulate the AD process for four household cylindrical batch digesters augmented from inside with various areas of four circular horizontal extended surfaces. The experiments were carried out in laboratories of the Northern Technical University, Iraq-Mosul, for 73 days in digesters D1 and D2 and 77 days in digesters D3 and D4. All digesters using CD as substrate operated under mesophilic conditions at S_1=15 kgCOD/m^3. The modified AM2 model investigated the initial variation concentration of substrate S_1 at 12, 15 and 18 kgCOD/m^3 for AD process on CH4 production flow rate.

In the present work, the substrate concentration (S_1) decreased along time of digestion for all digesters due to S_1 consumed by acidogenic bacteria (X_1) and convert it to VFA concentration (S_2) as seen in figure 3, which represents the variation in substrate concentration S_1 with digestion time for four digesters. This behavior was similar to work [15]. It was noticed that the S_1 has more reduction in D4 than other digesters due to the D4 having the largest extended surface area, leading to more growth of X_1 and more consumption and degradation of S_1 .

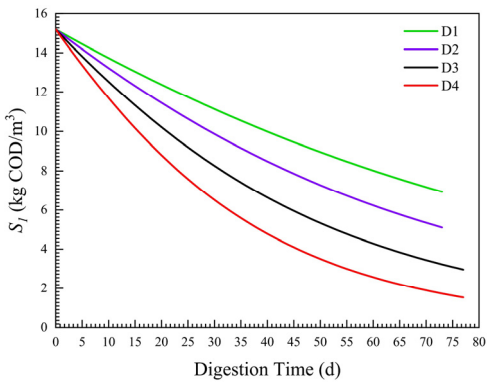


Figure 3. Variation of substrate concentration (S_1) with digestion time for four digesters.

VFAs are responsible for methanogens inhibition at higher concentrations and products of intermediate such as acetic acid, butyric acid, and propionic acid in the AD process so that increasing VFA concentration (S_2) at first days of AD process for all digesters. After that, it dropped until the AD process ceased due to degradation by methanogenic bacteria X_2 as illustrated in figure 4, which depicts the variation in VFA concentration (S_2) with digestion time for four digesters. The results are compatible with previous research [1]. It was shown that S_2 for D4 has rapidly increased to maximum value, then rapidly declined and more reduction of S_2 for D4 than other digesters. The justification back to the D4 has larger extended surface area than other digesters leads to more X_2 growth and more consumption and degradation of S_2 to generate CH_4 and CO_2.

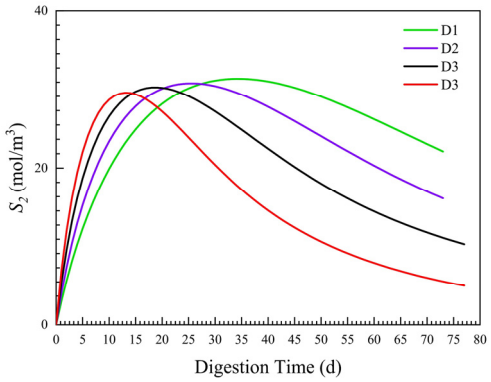


Figure 4. Variation of VFA (S_2) concentration with digestion time for four digesters

Figures 5 and 6 show variations of acidogenic X_1 and methanogenic (X_2) bacteria concentration respectively with digestion time for four digesters. It showed that behavior of (X_1) and (X_2) increased at the first days of AD process until it reached the maximum concentration value for all digesters due to bacterial growth. It started to decrease until AD process ceased due to bacterial death.

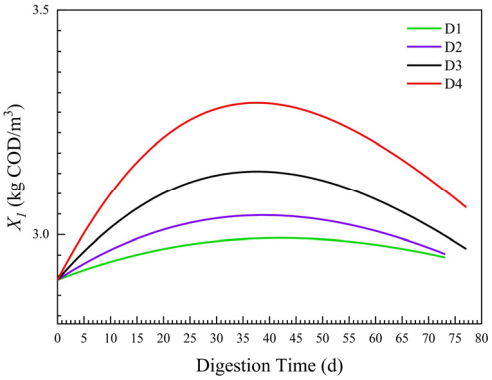


Figure 5. Variety of acidogenic bacteria concentrations (X_1) with digestion time for four digesters

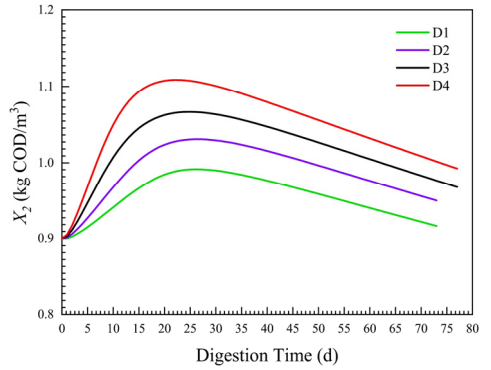


Figure 6. Variation of methanogenic bacteria concentration (X_2) with digestion time for four digesters

This behavior is similar to the previous work of [15]. The (X_1) and (X_2) values increased from the D1, which has low concentration values and without extended surface, to the D4 has high concentration values and large extended surface area because the bacteria grow on surfaces, leading to the D4 having more bacterial growth, as illustrated in Figures 5 and 6.

Figures 7, 8 and 9 illustrate CH_4 production flow rate (*qm*) variation with digestion time for four digesters at initial S_1 = 12, 15 and 18 kgCOD/m^3, respectively. Through first four weeks of AD process for all digesters, the *qm* was increased due to growing up of methanogenic bacteria and digestion of the acetate; after that, the *qm* was reduced until the AD ceased due to consumption of acetate and methanogenic bacterial death. This behavior was found in conformity with works [1][9][23]. It was observed that digester D4 has higher values of *qm* and lower values for digester D1 because the former has larger extended surface areas, leading to increased growth of bacteria on surfaces, more digestion of acetate, large chemical reaction areas and high methane production flow rate. Also, it was noticed that digesters D3 and D4 have a more extended period of AD process for 77 days than other digesters for 73 days. This is because the slurry exposed the larger surface area for quick methaprogen multiplication for optimal methaprogen consumption CD.

From these figures can be seen that the *qm* for four digesters increased with increasing initial S_1 due to the existence of a significant amount of microorganisms causing severe or rapid degradation of the organic feedstock methane. This behavior of the present investigation consented to previous work reported by [8].

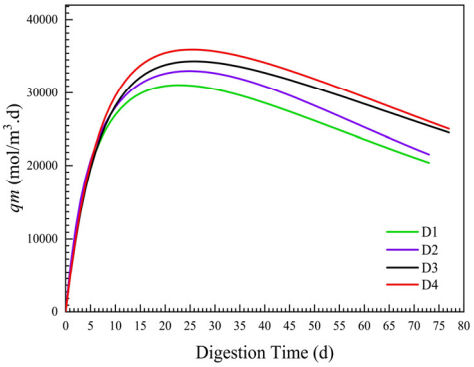


Figure 7. Variation of CH_4 production flow rate (*qm*) at S_1=12 kgCOD/m^3 with digestion time for four digesters

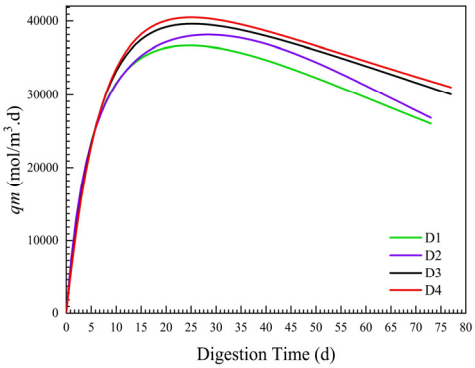


Figure 8. Variation of CH_4 production flow rate (*qm*) at S_1=15 kgCOD/m^3 with digestion time for four digesters

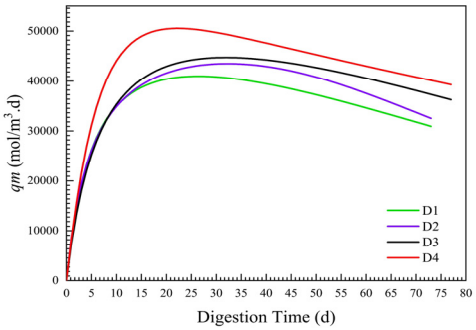


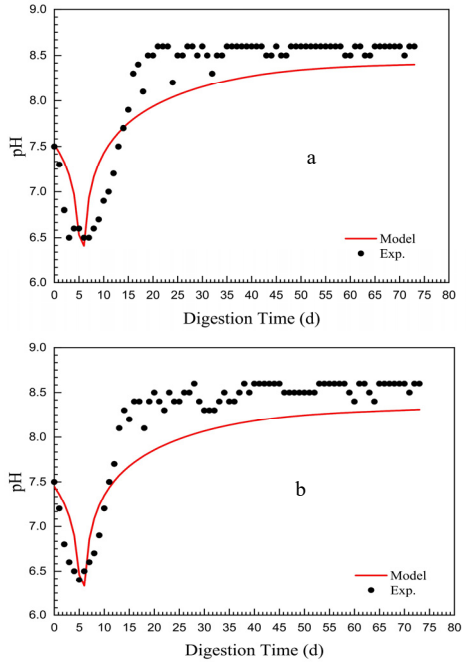
Figure 9. Variation of CH_4 production flow rate (qm) at S_1=18 kgCOD/m^3 with digestion time for four digesters

3.2. Model Validation

In order to assess the calibrated parameters and modified AM2 model validation of AD, a validation investigation was conducted. The numerical results for pH, *qm* and *qc* were compared to measured values of AD process carried out in four 13 L batch digesters operated at mesophilic conditions using CD as substrate.

Measured experimental values and numerical data of the modified AM2 model for pH in four digesters with digestion time are depicted in Figure 10. It can be observed that the numerical results of pH with digestion time of AD process predicted reasonably the dynamic behavior with measured experimental data for four digesters. The mean absolute percent error (MAPE) between the numerical results and measured experimental data for pH were 3.8, 4.1, 5.3 and 5.7 % for D1, D2, D3 and D4, respectively.

Figure 11 represents the numerical results of the modified AM2 model and measured data of experiment for *qm* and *qc* for four digesters with digestion time. The MAPE between them of *qm* were 8.5, 3.6, 4.9 and 6.1 %, and the MAPE of *qc* were 12.6, 12.9, 14.7 and 16.3 % for D1, D2, D3 and D4, respectively. It can be noticed the numerical results of *qm* and *qc* with digestion time of AD process have a relatively acceptable fit to measured experimental data for four digesters.



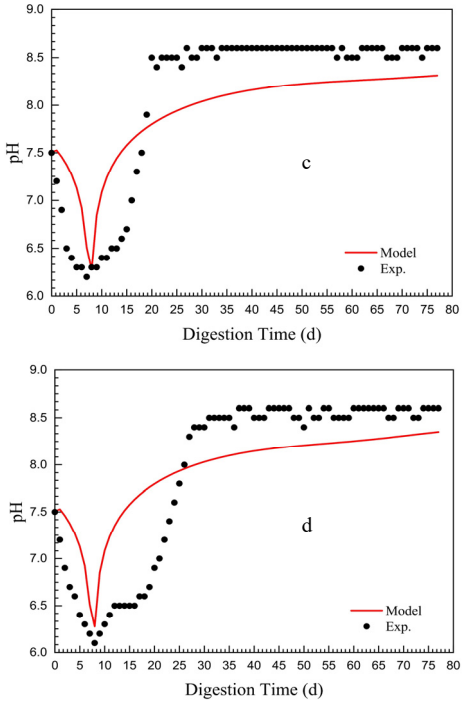
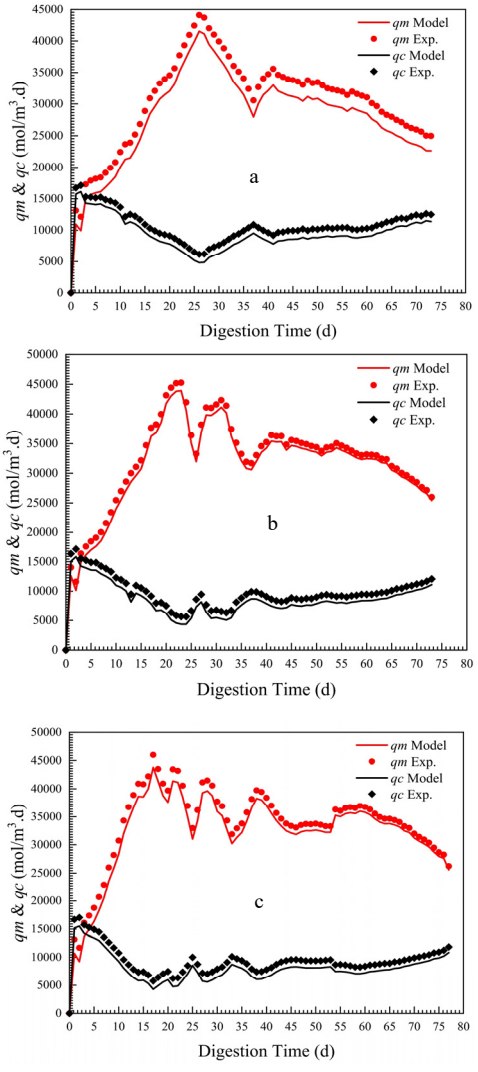


Figure 10. Numerical and experimental results for pH variation with digestion time for four digesters a: D1, b; D2, c: D3, d: D4



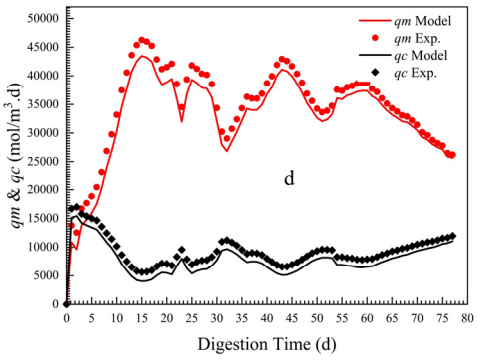


Figure 11. Numerical and experimental results for qm and qc variation with digestion time for four digesters a: D1, b: D2, c: D3, d: D4

4. CONCLUSION

AM2 model is developed and modified to investigate the effect of different horizontal extended surface areas augmented to inside batch anaerobic digester on CH_4 production. The experimental trial tests were conducted to calibrate and identify parameters under mesophilic conditions for four digesters.

The AM2 model gave good predictions and understanding of each parameter role identification in the process dynamic in each anaerobic batch digester. Parameters like μ_{2max}, k_{S1}, k_{S2} and k_{sur} had higher impact on the AD process than other parameters. Parameters kd_1 and kd_2 presented to consider inhibition effect variables in biogas products, such as bacterial death and competition.

The substrate concentration S_1 and S_2 where found to be inversely proportional to extended surface area inside digester, although bacterial concentration X_1 and X_2 where directly proportional to the surface area, and qm likewise. Initial S_1 concentration has significant effect on substrate degradation, bacterial growth and CH_4 production.

In summary, digester D4 has Superior performance as its largest interior surface area, which generally confirms the abovementioned theory of effect the surface area.

Finally, an acceptable agreement is shown between measured and simulated values for the modified AM2 model and for all process outcomes, such as pH, CH_4 and CO_2 variation with digestion time. The maximum MAPE was less than 16.3 % among all simulation results compared to measured values.

NOMENCLATURES

1. Acronyms

AD	Anaerobic Digestion
ADM1	Anaerobic Digestion Model NO.1
AM2	AMOCO model
CD	Cow Dung
Exp.	Experimental
MAPE	Mean Absolute Percent Error
VFA	Volatile fatty acids

2. Symbols / Parameters

C: Concentration of inorganic carbon (mmol C/L)
k_1 : Coefficient of material degradation
k_2: Coefficient of VFA production (mmol/g)
k_3: Coefficient of VFA consumption (mmol/g)
k_4: Coefficient of CO_2 production (mmol/g)
k_5: Coefficient of CO_2 production (mmol/g)
k_6: Coefficient of CH_4 production (mmol/g)
K_b: Affinity constant of inorganic carbon reaction (mmol/L)
kd_1: Biomass decay rate X_1 (1/d)
kd_2: Biomass decay rate X_2 (1/d)
KH: Henry-coefficient (mmol/atm L)
k_{I2}: Inhibition constant (mmol/L)
k_{LA}: Constant of liquid to gas transport (1/d)
k_{S1}: Constant of half saturation (g/L)
k_{S2}: Constant of half saturation (mmol/L)
k_{sur}: Inside surface area coefficient of the digester
P_C: CO_2 partial pressure (Atm)
P_T: Pressure inside the digester (Atm)
qc: CO_2 flow rate (mmol/L d)
qm: CH_4 flow rate (mmol/L d)
r_1: Reaction rate of acidogenesis (1/d)
r_2: Reaction rate of methanogenic (1/d)
S_1: Concentration of substrate (gCOD/L)
S_2: Concentration of VFA (mmol/L)
t: Time (d)
X_1: Acidogenic bacterium concentration (gCOD/L)
X_2: Methanogenic bacterium concentration (gCOD/L)
Z: Alkalinity (mmol/L)
μ_1: Acidogenic bacteria's growth rate (1/d)
μ_2: Methanogenic bacteria's growth rate (1/d)
μ_{1max}: Acidogenic bacteria's maximum growth rate (1/d)
μ_{2max}: Methanogenic bacteria's maximum growth rate (1/d)

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