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Development of a comprehensive model and evaluation of kinetic coefficients for treating slaughterhouse wastewater in a single stage anaerobic bioreactor

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A simplified method for determination of the kinetic coefficient for an anaerobic bioreactor has been developed in this present research. Kinetic coefficient, viz. specific substrate utilization rate (k), half-saturation constant (K_s), yield coefficient (Y) and endogenous decay rate (K_d) have been calculated using Monod kinetics for all three phases of anaerobic digestion. The single-stage anaerobic bioreactor was run under the semi-continuous mode of operation with varying Sludge Retention Time (SRT) and initial substrate concentrations (as soluble COD). The detailed experimental procedure of determination of kinetic coefficients from the experimental data set of semi-continuous studies for three different phases has been presented sequentially. The values of the kinetic coefficient are comparable with the earlier kinetics studies. The proposed method is found to be easy, accurate and fast for determination of the kinetic coefficient of individual phases of anaerobic treatment.

Keywords: Anaerobic digestion, anaerobic bioreactor, slaughterhouse wastewater, kinetic coefficients, consecutive reactions.

Introduction

The development of process kinetics plays a crucial role in designing of any biological treatment units. In order to develop a better process design and optimizing the biological reactor mathematical modelling is extremely necessary[1]. There are various types of the mathematical model, already developed for anaerobic digestion in the various time frames. The first simplest model was developed by Lawrence and McCarty 1970 using the Monod's equation stating that the consumption of substrate was associated with the growth of microorganisms[2]. A few authors considered methanogenesis as the constraining step or the change of fatty acids into biogas or the hydrolysis of suspended solids. According to the Bhatia *et al.* (1985) the development of methanogenesis is independent of cell growth process[3]. Karhadkar *et al.* (1990) proposed the model considering the process inhibition and obtained the kinetics from the performance evaluation of anaerobic bioreactor[4]. Even though reasonable numbers of steady-state models have been developed to exhibit the nature of anaerobic bioreactors, the kinetics models including the equations for the consumption of different characteristics of the substrate is required[5–7].

The ADM-1 model introduced by the International Water Association (IWA) is a structured but highly complex model which describes 7 groups of bacteria and archaea (included in a total of 32 dynamic state concentration variables) catalyzing 19 biochemical kinetic processes coupled to 105 kinetic and stoichiometric parameters. The set of Differential Equations (DE) of the ADM-1 for the calculation of the variables include 10 DE to model the evolution concentration of soluble matter in the liquid phase and two DE to model inorganic carbon and inorganic nitrogen levels in the liquid phase[8]. There is a considerable amount of modifications performed in the ADM-1 model to enhance its accuracy, which makes ADM-1 model more complicated due to the addition and modifications of DE. As per the modified ADM-1 model, the Contois kinetics was used to describe the hydrolysis reaction, where more than 30 number of DE were used. Furthermore, ADM-1 requires a large number of input parameters due to the complex model structure associated with a variety of kinetic and stoichiometric expressions[9]. Theoretically, there is no guarantee that all parameters influencing

the output can be estimated with significant reliability. Due to a large number of parameters in the model, it is quite reasonable that the parameters can be fine-tuned to fit the data perfectly[10].

Although many research works have already been documented in previous literature regarding the treatability study of slaughterhouse wastewater using the anaerobic bioreactor, very limited research was done in the area of determining the kinetic coefficients. However, the kinetic coefficients have a significant role in the rational engineering design of an anaerobic bioreactor. In most cases, the kinetic coefficients were determined in a single phase which is mainly the rate-limiting step in the anaerobic digestion process. No single methodology was derived for determining the kinetic coefficients individually for all the phases. The main reason is the complexity of earlier mathematical models in the anaerobic digestion process, which are generally difficult to be solved. Therefore, to fulfil the above-stated research gaps a simplified mathematical model was developed for single stage anaerobic bioreactor with minimum complexity level. Subsequently based on that simplified mathematical model the present study demonstrates step by step methods for determining the kinetic coefficients from the graphical approach based on Monod's growth kinetics. Determination of the kinetic coefficients such as K_s, k, Y, k_d in each anaerobic step has been possible by the proposed method.

Materials and methods

Determination of LCFA through the spectrophotometric method:

To measure the different concentration of the LCFA (long chain fatty acids) (C_8 to C_{18}) the UHPLC was used. The system was equipped with the C_{18} column with a length of 30 cm and an internal diameter of 5 mm. The wavelength was set as 210 nm with the injection volume of 50 μL and the total retention time was set as the 10 min. The mobile phase used was 20 mM of NaH_2PO_4 in HPLC grade water with a pH of 2.2. To measure the LCFA, the standard solution of all the fatty acids lying between caprylic acid (C8) and oleic acid (C18) was used for preparing the calibration curve. The correlation coefficient (R^2) of these two calibration curves was obtained in the range of 0.90–0.99. The LCFA of a collected sample was considered as the sum of all the fatty acids as calculated from their respective calibration curve.

Determination of the SCFA by spectrophotometric method:

The SCFA (short chain fatty acids) concentration was considered as the volatile fatty acids (VFA) up to valeric acid level. The VFA was measured in terms of acetic acid. The VFA was estimated as per the method proposed by Chatterjee *et al.*[11].

Mathematical modelling for the anaerobic digestion process:

In-depth information on process kinetics and mathematical modelling were very essential for predicting the behaviour of the anaerobic bioreactor system and optimizing the performance in large-scale applications[12]. Therefore, in the present study, a simplified mathematical model for anaerobic digestion process in single stage anaerobic bioreactor system has been developed using Monod's rate kinetic expressions for hydrolysis, acidogenesis and methanogenesis phases at steady state condition. The model includes different microbial consortium i.e. hydrolytic, acidogenic and methanogenic bacteria acting simultaneously for biological conversion of organic matter[13,14]. Considering the consecutive steps of the anaerobic digestion process, the general kinetic expression can be written in accordance with Monod's growth approach as given below:

(i) Hydrolysis:

$$\frac{dS_H}{dt} = -\frac{K_H S_H X_H}{K_{S_H} + S_H} \qquad (1)$$

where,

K_H = Maximum specific rate of hydrolysis $(\text{day})^{-1}$

S_H = Hydrolyzable substrate concentration (mg COD/L)

X_H = Concentration of hydrolytic microorganisms (mg/L)

K_{S_H} = Half velocity constant for hydrolysis (mg COD/L)

At $t = 0$, $S_H = S_{H_0}$

(ii) Acidogenesis:

$$\frac{dS_{LCFA}}{dt} = \frac{K_H S_H X_H}{K_{S_H} + S_H} - \frac{K_A S_{LCFA} X_A}{K_{S_A} + S_{LCFA}} \qquad (2)$$

where,

K_A = Maximum specific rate of acidogenesis (day)$^{-1}$

S_{LCFA} = Concentration of LCFA (mg COD/L)

X_A = Concentration of acidogenic microorganism (mg/L)

K_{S_A} = Half velocity constant for acidogenesis (mg COD/L)

At $t = 0$, $S_{LCFA} = 0$

(iii) Methanogenesis:

$$\frac{dS_{SCFA}}{dt} = \frac{K_A S_{LCFA} X_A}{K_{S_A} + S_{LCFA}} - \frac{K_M S_{SCFA} X_M}{K_{S_M} + S_{SCFA}} \quad (3)$$

where,

K_M = Maximum specific rate of methanogenesis (day)$^{-1}$

S_{SCFA} = Concentration of SCFA (mg COD/L)

X_M = Concentration of methanogenesis microorganism (mg/L)

K_{S_A} = Half velocity constant for methanogenesis (mg COD/L)

At $t = 0$, $S_{SCFA} = 0$

Therefore,

Methane concentration (S_M)

$$S_M = S_{H0} - S_H - S_{SCFA} - S_{LCFA} \quad (4)$$

Solution procedure:

Development of kinetic coefficients for hydrolysis, acidogenesis and methanogenesis phases:

In order to determine the concentration of S_H, S_{LCFA}, S_{SCFA}, S_M the kinetic coefficients and biomass such as (K_H, K_{SH}, and X_H), (K_A, K_{SA}, and X_A) and (K_M, K_{SM}, and X_M) need to be known. Out of all these parameters (K_H, K_{SH}), (K_A, K_{SA}) and (K_M, K_{SM}) can be determined from different sets of experimental data of the semi-continuous study.

Determination of Y and K_d:

The concentration of hydrolytic, acidogenic and methanogenic microorganism may be considered as a variable fraction of the total amount of biomass present under the steady-state condition those can be theoretically estimated as,

$$X_H = \frac{Y_H.(S_{H0} - S_H)}{(1 + k_{dH}.\theta_C)}.\left(\frac{\theta_C}{\theta_H}\right) \quad (5)$$

$$X_A = \frac{Y_A.S_{LCFA}}{(1 + k_{dA}.\theta_C)}.\left(\frac{\theta_C}{\theta_A}\right) \quad (6)$$

[At $t = 0$, $S_{LCFA} = 0$ and at $t = \theta$, $S_{LCFA} = S_{LCFA}$]

$$\text{And, } X_M = \frac{Y_M.S_{SCFA}}{(1 + k_{dM}.\theta_C)}.\left(\frac{\theta_C}{\theta_M}\right) \quad (7)$$

[At $t = 0$, $S_{SCFA} = 0$ and at $t = 0$, $S_{SCFA} = S_{SCFA}$]

where,

Y_H, Y_A, Y_M = yield coefficients for hydrolysis, acidogenesis and methanogenesis respectively.

θ_H, θ_A, θ_M = Hydraulic Retention Time (HRT) for hydrolysis, acidogenesis and methanogenesis respectively = θ, as they co-exist with each other in the same bioreactor.

K_{dH}, k_{dA}, k_{dM} = endogenous decay coefficients for hydrolytic, acidogenic, and methanogenic microorganisms respectively. θ_C = solid retention time (SRT), which should be the same for all types of microorganisms, as they co-exist with each other in the same bioreactor.

Therefore, the growth kinetics of hydrolytic, acidogenic and methanogenic microorganisms can be expressed as under, which are nothing but the modifications of eqs. (5), (6) and (7).

$$\frac{1}{\theta_C} = \frac{Y_H(S_{H0} - S_H)}{\theta X_H} - k_{dH} \quad (8)$$

$$\frac{1}{\theta_C} = \frac{Y_A.S_{LCFA}}{\theta X_A} - k_{dA} \quad (9)$$

$$\frac{1}{\theta_C} = \frac{Y_M.S_{SCFA}}{\theta X_M} - k_{dM} \quad (10)$$

If the steady-state biomass concentration in the bioreactor is measured as X, the values of X_H, X_A, and X_M can be rationally estimated as follows.

$$X_H = \frac{\dfrac{Y_H.(S_{H0} - S_H)}{(1 + k_{dH}.\theta_C)}}{\dfrac{Y_H.(S_{H0} - S_H)}{(1 + k_{dH}.\theta_C)} + \dfrac{Y_A S_{LCFA}}{(1 + k_{dA}.\theta_C)} + \dfrac{Y_M.S_{SCFA}}{(1 + k_{dM}.\theta_C)}}.X \quad (11)$$

$X_A =$

$$\frac{\dfrac{Y_A S_{LCFA}}{(1+k_{dA}.\theta_C)}}{\dfrac{Y_H.(S_{H0}-S_H)}{(1+k_{dH}.\theta_C)}+\dfrac{Y_A S_{LCFA}}{(1+k_{dA}.\theta_C)}+\dfrac{Y_M.S_{SCFA}}{(1+k_{dM}.\theta_C)}}.X \quad (12)$$

$X_M =$

$$\frac{\dfrac{Y_M S_{SCFA}}{(1+k_{dM}.\theta_C)}}{\dfrac{Y_H.(S_{H0}-S_H)}{(1+k_{dH}.\theta_C)}+\dfrac{Y_A S_{LCFA}}{(1+k_{dA}.\theta_C)}+\dfrac{Y_M.S_{SCFA}}{(1+k_{dM}.\theta_C)}}.X \quad (13)$$

Therefore, the values of X_H, X_A, and X_M depend on Y_H, Y_A, and Y_M as well as k_{dH}, k_{dA}, and k_{dM}, whereas the determination of all such parameters needs the values of X_H, X_A, and X_M. Considering this fact, a set of trial values of Y_H, Y_A, and Y_M as well as k_{dH}, k_{dA}, and k_{dM} can be assumed to find out X_H, X_A, and X_M using eqs. (11), (12) and (13). Then, as per eq. (8), the values of $1/\theta_c$ can be plotted with respect to $(S_{H0}-S_H)/\theta X_H$ to determine Y_H and k_{dH} from the slope and intercept respectively of the said graph. Similarly, as per eq. (9), the values of $1/\theta_C$ can be plotted with respect to $S_{LCFA}/\theta X_A$ to determine Y_A and k_{dA} from the slope and intercept respectively of the said graph. Finally, as per eq. (10), the values of $1/\theta_C$ can be plotted with respect to $S_{LCFA}/\theta X_M$ to determine Y_M and k_{dM} from the slope and intercept respectively of the said graph. All such values of Y_H, Y_A, and Y_M as well as k_{dH}, k_{dA} and k_{dM} must be checked with their values, assumed earlier. If those are not matching, the latest determined values of Y_H, Y_A, and Y_M as well as k_{dH}, k_{dA}, and k_{dM} need to be considered as their next trial values. The process will continue in an iterative manner until the final values of Y_H, Y_A, and Y_M as well as k_{dH}, k_{dA}, and k_{dM} become equal to their immediately previous assumed values.

The kinetic coefficients such as (K_H, K_{SH}), (K_A, K_{SA}) and (K_M, K_{SM}) can be determined in general using the following techniques:

From hydrolysis eq. (1),

$$\frac{dS_H}{dt} = -\frac{K_H S_H X_H}{K_{SH}+S_H}$$

$$\text{or, } \frac{\theta X_H}{S_{H0}-S_H)} = \left(\frac{K_{SH}}{K_H}\right)\left(\frac{1}{S_H}\right)\left(\frac{1}{K_H}\right) \quad (14)$$

Now, from different sets of experimental data of the semi-continuous study, the $\theta X_H/(S_{H0}-S_H)$ values can be plotted with respect to $(1/S_H)$ to determine K_{SH} and K_H.

From acidogenesis eq. (2),

$$\frac{dS_{LCFA}}{dt} = \frac{K_H S_H X_H}{K_{SH}+S_H} - \frac{K_A S_{LCFA} X_A}{K_{SA}+S_{LCFA}}$$

$$\text{or, } \frac{K_A S_{LCFA} X_A}{K_{SA}+S_{LCFA}} = -\frac{S_{LCFA}}{\theta} + \frac{K_H S_H X_H}{K_{SH}+S_H} = A \text{ (say)}$$

Therefore,

$$\frac{K_{SA}+S_{LCFA}}{K_A S_{LCFA}} = \frac{X_A}{A}$$

$$\text{or, } \frac{K_{SA}}{K_A}\left(\frac{1}{S_{LCFA}}\right) + \frac{1}{K_A} = \frac{X_A}{A} \quad (15)$$

Now, from different sets of experimental data of the semi-continuous study, the X_A/A values can be plotted with respect to $(1/S_{LCFA})$ to determine K_{SA} and K_A.

From methanogenesis eq. (3),

$$\frac{dS_{SCFA}}{dt} = \frac{K_A S_{LCFA} X_A}{K_{SA}+S_{LCFA}} - \frac{K_M S_{SCFA} X_M}{K_{SM}+S_{SCFA}}$$

$$\text{or, } \frac{K_M S_{SCFA} X_M}{K_{SM}+S_{SCFA}} = -\frac{S_{SCFA}}{\theta} + \frac{K_A S_{LCFA} X_A}{K_{SA}+S_{LCFA}} = B \text{ (say)}$$

$$\text{Therefore, } \frac{K_{SM}+S_{SCFA}}{K_M S_{SCFA}} = \frac{X_M}{B}$$

$$\text{or, } \frac{K_{SM}}{K_M}\left(\frac{1}{S_{SCFA}}\right) + \frac{1}{K_M} = \frac{X_M}{B} \quad (16)$$

Now, from different sets of experimental data of the semi-continuous study, the X_M/B values can be plotted with respect to $(1/S_{SCFA})$ to determine K_{SM} and K_M. The biomass concentration of various groups of microorganisms should be estimated using (Y_H, k_{dH}), (Y_A, k_{dA}) and (Y_M, k_{dM}) in eq. (11), (12), and (13). To determine the individual biomass concentration X_H, X_A, X_M the values of S_H, S_{LCFA}, and S_{SCFA} can be approximately considered at their steady state condition as under.

$$S_H = \frac{K_{SH}.(1 + \theta_C.k_{dH})}{\theta_C.(Y_H.K_H - k_{dH}) - 1} \quad (17)$$

$$S_{LCFA} = \frac{K_{SA}.(1 + \theta_C.k_{dA})}{\theta_C.(Y_A.K_A - k_{dA}) - 1} \quad (18)$$

$$S_{SCFA} = \frac{K_{SM}.(1 + \theta_C.k_{dM})}{\theta_C.(Y_M.K_M - k_{dM}) - 1} \quad (19)$$

Experimental data:

All the experimental data and other related data used for obtaining the kinetics value please refer[15–18].

Results and discussion

Semi-continuous study on anaerobic bioreactor:

Semi-continuous studies were performed in laboratory scale anaerobic digester to determine the bio-kinetic coefficients by the proposed method. The slaughterhouse wastewater collected from the meat processing unit was used for the experimental study. The initial soluble COD concentration was in the range of 1730–5390 mg COD/L whereas the total biomass concentration was between 2113 and 5538 mg/L. The SRT was in the range set in the range of 35.2–49.5 days throughout the study[12,15]. The bioreactor samples were collected from the inlet and outlet and analysed for various relevant parameters such as COD, Total biomass concentration, LCFA, and SCFA concentration.

Determination of kinetic coefficients:

Steady-state kinetic model equations as mentioned earlier were used to develop bio-kinetic constants. Bio-kinetic parameters like K, K_s, Y, and K_d are measured for hydrolysis, acidogenesis, and methanogenesis phases separately. The experimental data collected from the end of each semi-continues run at different initial COD concentrations. The effluent COD (S_H'), VFA and LCFA concentration can be determined using the standard method as mentioned earlier. The hydrolysable COD concentration (S_H) can be calculated by subtracting the 1.067 times VFA (SCFA) from the effluent COD concentration (S_H'). The total biomass (X) in the bioreactor was measured as MLSS concentration. The values of X_H, X_A and X_M can be theoretically calculated using eqs. (11), (12) and (13). HRT and SRT, for hydrolysis, acidogenesis and methanogenesis have been considered the same for all types of microorganisms, as they are present in the same bioreactor.

At first, the values of Y and K_d must be determined for all the phases from different sets of experimental data of the semi-continuous study using a set of rational values of Y and K_d for hydrolysis, acidogenesis, and methanogenesis. The initial values of Y, K_d are considered as one-third of that obtained in case of determination of kinetic coefficient for treatment of slaughterhouse wastewater as reported by Loganath and Mazumder (2018). The iteration study was continued until the graphically obtained values of Y and K_d became equal to their assumed values. Thereafter, the kinetic coefficients like K and K_S can be determined from different sets of experimental data and the respective individual biomass concentration using the values of Y and K_d.

In the case of hydrolysis phase which is an important step for the anaerobic treatment process, yield coefficient (Y_H) and endogenous decay coefficient (k_{dH}) was calculated using eq. (8). The iteration process was started assuming a set of Y_H, Y_A, and Y_M as well as K_{dH}, K_{dA} and K_{dM} values as one-third of those respective values as stated above. Hence, the individual biomass concentrations (i.e. X_H, X_A, and X_M) could be calculated using eqs. (11), (12) and (13). Now, the values of $1/\theta_C$ are plotted in Y-axis with respect to $(S_{H0}–S_H)/\theta X_H$ in X-axis as shown in Fig. 2. Consequently, after several trials, Y_H and k_{dH} values have been estimated as 0.069 mg/mg and 0.006 d^{-1} respectively from the slope and intercept. In the case of acidogenesis phase, yield coefficient (Y_A) and endogenous decay coefficient (k_{dA}) were calculated using eq. (9). Accordingly, the values of $1/\theta_C$ are plotted in Y-axis with respect to $S_{LCFA}/\theta X_A$ in X-axis as shown in Fig. 4. Hence, the best fit line has been drawn which yields the values of Y_A and K_{dA} as 0.08 mg/mg and 0.005 d^{-1} respectively from the slope and intercept. Finally, in the case of methanogenesis phase, the same approach is adapted to determine the yield coefficient (Y_M) and endogenous decay coefficient (k_{dM}) from eq. (10). Therefore, the values of $1/\theta_C$ are plotted in Y-axis with respect to $S_{SCFA}/\theta X_M$ in X-axis as shown in Fig. 6. Thus, the best fit line has been drawn which yields the values of Y_M and K_{dM} as 0.09 mg/mg and 0.007 d^{-1} respectively from the slope and intercept.

The specific substrate utilization rate (k_H) and half-saturation constant (K_{SH}) was calculated using eq. (14). Hence, the values $\theta X_H/(S_{H0} - S_H)$ are plotted in Y-axis with respect to $1/S_H$ in X-axis as shown in Fig. 1. As a result, K_H and K_{SH}

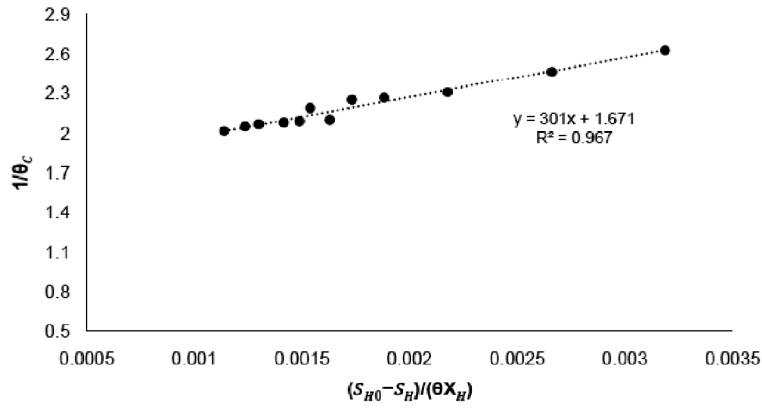

Fig. 1. Determination of K_s, k for hydrolysis phase.

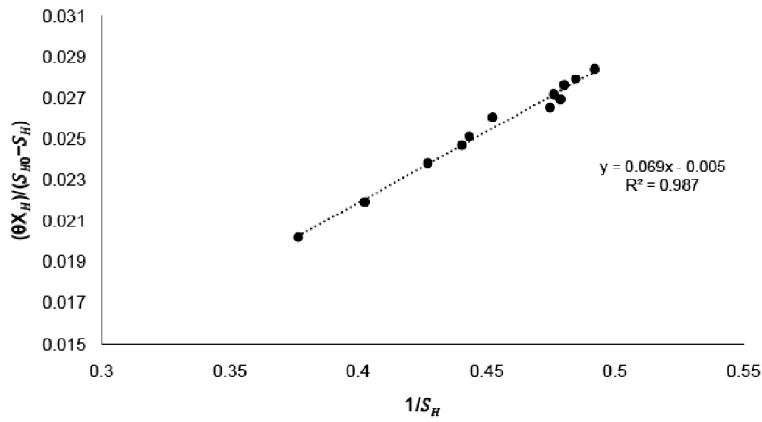

Fig. 2. Determination of y, K_d for hydrolysis phase.

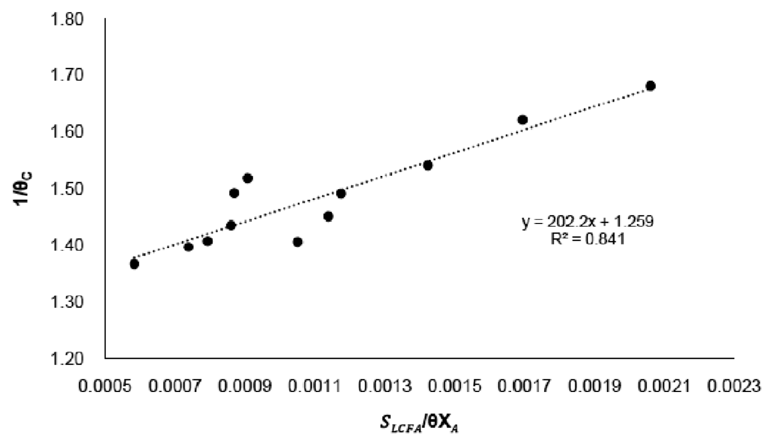

Fig. 3. Determination of K_s, k for acidogenesis phase.

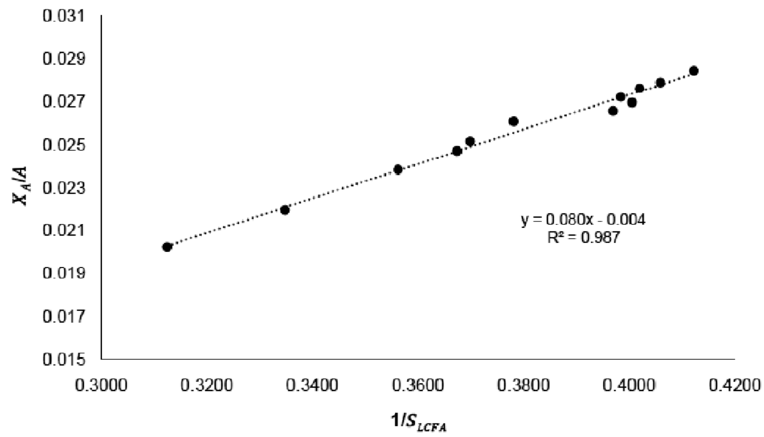

Fig. 4. Determination of y, K_d for acidogenesis phase.

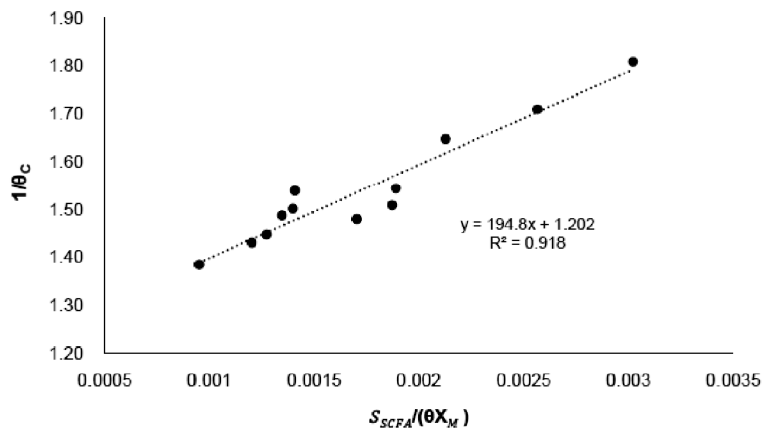

Fig. 5. Determination of K_s, k for methanogenesis phase.

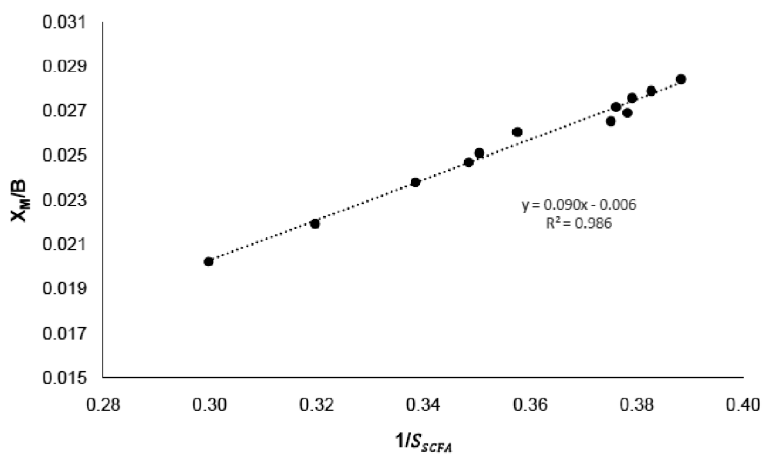

Fig. 6. Determination of y, K_d for methanogenesis phase.

values are determined as 0.606 d^{-1} and 192.29 mg/L respectively. Similarly, the specific substrate utilization rate (k_A) and half-saturation constant (K_{SA}) were calculated using eq. (15). The values of X_A/A are plotted in Y-axis with respect to $1/S_{LCFA}$ in X-axis as shown in Fig. 3. As a result, k_A and K_{SA} values are estimated as 0.795 d^{-1} and 154.63 mg/L respectively. The specific substrate utilization rate (k_M) and half-saturation constant (K_{SM}) were calculated using eq. (16). The values of X_M/B are plotted in Y-axis with respect to $1/S_{SCFA}$ in X-axis as shown in Fig. 5. Thus, K_M and K_{SM} are evaluated as 0.828 d^{-1} and 157 mg/L respectively. The summary of all kinetic co-efficient values such as maximum specific substrate utilization rate (K), half velocity constant (K_s), yield coefficient (Y) and endogenous decay coefficient (K_d) for slaughterhouse wastewater treatment through three distinct anaerobic steps is presented in Table 1.

Table 1. Values of bio-kinetic coefficients for anaerobic reactor treating slaughterhouse wastewater

Kinetic coefficients	For hydrolysis	For acidogenesis	For methanogenesis
k (d^{-1})	0.606	0.795	0.828
K_s (mg/L)	192.29	154.63	157
Y (mg/mg)	0.069	0.08	0.09
k_d (d^{-1})	0.006	0.005	0.007

There is no research work accomplished so far to determine the various kinetic coefficients for hydrolysis phases in anaerobic for treatment of slaughterhouse wastewater using Monod's growth kinetic approach. Therefore, the kinetic coefficient values are not fully comparable with previously published literature. In the case of acidogenesis phase, the value of K_A is obtained as 0.798 d^{-1}, which is close to the respective value reported by Novak and Carlson (1970). It is also noticed that much lower value of K_{SA} is obtained as 154.63 mg/L in the present study, compared to the literature values[19], which is in the range of 143–3180 mg/L. In the case of methanogenesis phase, yield coefficient (Y_M) is obtained as 0.09 mg/mg, which is slightly higher than previously published works by Lawrence and McCarty (1969) treating acetate containing synthetic wastewater in laboratory scale anaerobic digester. Lawrence and McCarty (1969) reported the range of values as 0.04–0.054 mg/mg in the anaerobic digester. Biomass decay coefficients k_{dM} is obtained as 0.007 d^{-1} which is slightly lower than the range 0.01–0.037 d^{-1} reported earlier[20].

It is also noticed that the value of maximum specific substrate utilization rate (k_m) in case of methanogenic phases is 0.828 d^{-1} which is higher than that observed in the case of synthetic wastewater. Lawrence and McCarty (1969) reported the value of maximum specific substrate utilization rate as 4.8–15.6 d^{-1}, which is much higher than the respective value from the present study. However, in the case of K_{SM} value is found as 157 mg/L which is considerably lower than from earlier research investigation[20]. As a whole, it is observed that the main inconsistency occurs in K_s values in all different phases. This significant difference in K_S value for various phases possibly may have occurred due to variation in initial substrate concentration and influent wastewater condition from one experimental condition to another.

Conclusion

In the present study, an attempt was made to determine kinetic coefficients for all three stages such as hydrolysis, acidogenesis, and methanogenesis in a single stage anaerobic bioreactor. The process variables like COD, LCFA, SCFA, and MLSS are utilized to develop the kinetics of various stages of the anaerobic process so that all those can be predicted reasonably. The present method is very simple and easy to calculate the kinetic coefficients from simple straight-line equations derived out of linearization of Monod's growth kinetics using intercepts or slope of the straight-line graph. The specific substrate utilization rate (k), yield coefficient (Y) and endogenous decay rate (K_d) are partially comparable with the data available from earlier findings. However, inconsistency is observed in K_s values for all the phases. All the kinetic coefficients values like K_s, K, Y and K_d for various stages can be evaluated by the proposed technique. The complexity in the proposed model has been lowered compared to ADM-1 and modified ADM-1 models making it simple and good fit for the analysis of anaerobic digestion process. This proposed model can also be used for the optimization any anaerobic reactor treating the high strength wastewater.

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