KINETIC APPROACH TO MICROBIAL GROWTH AND SUBSTRATE CONSUMPTION PROCESSES IN WASTEWATER TREATMENT BY PUF FLUIDIZED BED BIOREACTOR

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The substrate consumption and microbial growth processes in a PUF (polyurethane foam particles) fluidized bed bioreactor, were formulated by introducing microbial transport between support particle and water phase and the biological predator-prey symbiosis. In formulation, assumptions used were 1) two types of bacteria—motile and floc-forming bacteria—should inhabit simultaneously, 2) two species of protozoa-free-swimming and stalked protozoa—should coexist, 3) bacteria should grow subject to the Monod equation, but flocculation and deflocculation are influenced by protozoa mass concentrations, 4) free-swimming and stalked protozoa should grow preying on motile bacteria subject to the Monod equation, but the rates are subordinately influenced by substrate concentration. In consequence, the processes were shown to be expressed by a substrate mass balance and eight microbial mass balance equations. The numerical results to these equations were shown to explain well the actual valuations with time passage in TOC and retained and suspended microbial concentrations.

Introduction

In this decade, several types of fluidized-bed bioreactors have been applied to wastewater treatment, since the organic substrate, even highly loaded, can be removed effectively by microbes retained in particles in high density (Atkinson et al., 1979, Takahashi, 1994). Particularly, the bioreactor using relatively large support particles, like polyurethane foam (PUF), is of interest because it has advantages of easiness in separating particles from the water phase and of self-performability in controlling the biofilm thickness (Toyoda et al., 1993, Tsuno et al., 1993, Xing et al., 1991). It is thus desired to put this PUF bioreactor to practical use from the viewpoints of downsizing the facility and of saving energy. In our previous experimental investigations on dialysis wastewater treatment, we found that the substrate consumption and microbial growth processes exhibit specific time courses in TOC and microbial concentrations, caused by predator-prey symbiosis (Toyoda et al., 1994, Toyoda et al., 1995).

The substrate consumption and microbial growth processes in a PUF bioreactor, particularly in the early stages, have not yet been investigated theoretically; the specific variations as stated above have never been explained. In designing and/or operating the reactor under optimum conditions, it is very important to develop mathematical and computational approaches to simulating such processes. In this paper, the substrate consumption and the retained and suspended microbial growth processes in a PUF bioreactor are formulated and are shown to be expressed by a substrate mass balance and eight microbial mass balance equations. In formulating, the microbial transport between support particle and water phase, and biological symbiosis and predation between bacteria and protozoa are taken into account, and new models for growth rates of bacteria and protozoa are proposed. The numerical results computed for three hypothetical cases are compared with the experimental data, and validities of the respective microbial growth models and interrelations among substrate consumption and individual microbe growth processes are discussed.

1. Kinetics of Microbial Growth Process

A schematic drawing of the fluidized-bed bioreactor is shown in Fig. 1. Polyurethane particles with specific surface area a are loaded in the reactor of capacity V at a packing ratio of 1-c, the particles being fluidized uniformly in the water phase. Suppose that wastewater of concentration C₀ is fed into the bioreactor at a volume flow rate Q. Oxygen required for microbial growth is supplied by aerating from the center at the lower part of the reactor.

1.1 Basic equations

To formulate the substrate consumption and microbial growth processes, we made the following six assumptions: 1) bacteria inhabiting in PUF particles and those in the water phase are classified into two types of

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bacteria, namely motile and floc-forming bacteria, 2) they should grow subject to the Monod equation and decay in proportion to their concentration, 3) two species of protozoa, namely free-swimming and stalked protozoa, can inhabit at the same time; 4) motile bacteria are preyed on by both species of protozoa, meanwhile the floc-forming bacteria are never preyed on by protozoa (small flocks that may be preyed on are classified as motile bacteria), 5) motile bacteria are flocculated by the viscid substances secreted by the protozoa whereas floc-forming bacteria are deflocculated when the viscid substances are in shortage-flocculation and deflocculation should depend on the mass concentrations of protozoa; 6) the growth rate of protozoa is expressed by the Monod equation depending on the bacteria concentrations. The growth rate is also subordinatively influenced by substrate concentrations.

For convenience, we here express the mass concentration of the microbes retained in the particles in terms of weight per unit particle volume, mg/dm$^3$-PUF, and the concentration of the microbes suspended in the water phase in weight per water phase volume, mg/dm$^3$. Let $B_{i}$ and $B_{i}$ (i = 1, 2) be the mass concentrations of retained and suspended bacteria, respectively; the subscript i = 1 denotes the motile and i = 2 the floc-forming bacteria. Also let $P_{i}$ and $P_{i}$ (i = 1, 2) be the mass concentrations of retained and suspended protozoa, respectively; the subscript i = 1 stands for free-swimming and i = 2 for stalked protozoa. Growth processes of the motile and floc-forming bacteria can then be expressed by the following equations, for retained bacteria,

$$
(1-e)\frac{dV}{dt}B_{i}dt=(1-e)\frac{dV}{dt}[\mu B_{i} + k_{d} B_{i}]
-1-e\alpha V(k_{P_{i}}B_{i} + k_{B_{i}}B_{i})(M^{*} - B_{i} - B_{i} - P_{i} - P_{i})/M^{*}
+1-e\nu(h_{i} B_{i} - h_{i} B_{i})
$$

and for suspended bacteria,

$$
(1-e)\frac{dV}{dt}B_{i}dt=(1-e)\frac{dV}{dt}[\mu B_{i} + k_{d} B_{i}]
+1-e\alpha V(k_{P_{i}}B_{i} + k_{B_{i}}B_{i})(M^{*} - B_{i} - B_{i} - P_{i} - P_{i})/M^{*}
-1-e\nu(h_{i} B_{i} - h_{i} B_{i} - h_{i} B_{i})
$$

where $\mu_{i}$'s (i = 1, 2) are the specific growth rates, $k_{d}$'s (i = 1, 2) are the decay rate coefficients, $h_{i}$'s (i = 1, 2) are the specific flocculation rates, $h_{i}$ (i = 1, 2) are the specific deflocculation rates, $k_{s}$ is the falling-off rate coefficient, $Y_{p}$ is the yield coefficient of protozoa, and $M^{*}$ is a maximum retainable concentration of the microbes (the surface density of biofilm is assumed to be constant regardless of the microbial species).

Growth processes of free-swimming and stalked protozoa can be expressed by the following equations, for retained protozoa,

$$
(1-e)\frac{dV}{dt}P_{i}dt=(1-e)\frac{dV}{dt}[\mu P_{i} - k_{d} P_{i}]
-1-e\alpha V(k_{P_{i}}P_{i} + k_{B_{i}}P_{i} + k_{B_{i}}P_{i})(M^{*} - B_{i} - B_{i} - P_{i} - P_{i})/M^{*}
$$

and for suspended protozoa,

$$
(1-e)\frac{dV}{dt}P_{i}dt=(1-e)\frac{dV}{dt}[\mu P_{i} - k_{d} P_{i}]
+1-e\alpha V(k_{P_{i}}P_{i} + k_{B_{i}}P_{i} + k_{B_{i}}P_{i})(M^{*} - B_{i} - B_{i} - P_{i} - P_{i})/M^{*}
$$

where $\mu_{i}$'s (i = 1, 2) are the specific growth rates of the individual protozoa and $k_{d}$'s (i = 1, 2) are the decay rate coefficients.

The first terms in the right hand side of Eqs. (1) ~ (4) show the growth rates of bacteria and the second terms the rates at which bacteria are sticking to or falling-off the particles. The third terms in the right hand side of Eqs. (1), (3) show the rates at which protozoa are preying on motile bacteria. The fourth terms in Eqs. (1), (3) and the third terms in Eqs. (2), (4) show the rates of bacterial flocculation and deflocculation. The fifth term in Eq. (3) and the fourth term in Eq. (4) are the rates of effluent of the respec-
tive bacteria. The first terms in the right hand side of Eqs. (5) ~ (8) are the growth rates of protozoa and the second terms are the rates at which protozoa are sticking to or falling-off the particles. The third terms in Eqs. (7) and (8) are the rates of effluent of individual protozoa.

The substrates are consumed only by bacteria and the change in TOC concentration C can be expressed by the following equation:

\[ \text{VdCdt} = \text{QC}_0 - \text{QC} - \left(1-e^{-t}\sum B_{i} + \mu_i B_i \right) + \epsilon \left( \sum B_{i} + \mu_i B_i \right) \]

where \( Y_o \) is the yield coefficient of bacteria. In this equation, the time-derivative term should be written as, \( \epsilon \text{VdCdt} + (1-\epsilon) \left( \text{VdCdt} \right) \), which can be approximated very accurately as \( \text{VdCdt} \), since \( \epsilon = 0.98 \).

The initial conditions for bacteria and protozoa mass concentrations are, respectively

\[ B_{oi} = B_{pi}, \quad q = r, s, i = 1, 2, \quad t = 0 \]

\[ P_{qi} = P_{pi}, \quad q = r, s, i = 1, 2, \quad t = 0 \]

In Eqs. (10), (11), particularly when \( q = r, B_{qi} = 0, P_{qi} = 0 \), the initial condition for the substrate concentration is

\[ C = C_0, \quad t = 0 \]

### 1.2 Growth rates of bacteria and protozoa

The specific growth rates \( \mu_i \)'s (\( i = 1, 2 \)) of motile and floc-forming bacteria are assumed to be expressed by the Monod equation, namely

\[ \mu_i = \mu_{i \text{max}} C / (K_i^p + C), \quad i = 1, 2 \]

where \( \mu_{i \text{max}} \)'s are the maximum specific growth rates and \( K_i^p \)'s are the saturation constants.

To the authors' knowledge, the generalized rate equation for growth of protozoa, which covers the dependency of substrate concentration, has not yet been proposed. Since the protozoa intrinsically prey upon bacteria, they are thought to grow subject to the Monod equation with bacteria concentration. Meanwhile, it is known that the stalked protozoa grow predominantly in the environment of lower organic concentration whereas the free-swimming protozoa grow predominantly in the environment of higher organic concentration (Sudo, 1977, Sudo et al., 1975). With these facts, we can express the specific growth rates of free-swimming and stalked protozoa by introducing functions \( g_i \)'s (\( i = 1, 2 \)) of organic concentration, in the following forms:

\[ \mu_i = \mu_{i \text{max}} \left( B_{qi} / \left( K_i^p + B_{qi} \right) \right) g_i \left( C ; G_i \right), \quad i = 1, 2, q = r, s \]

The functions \( g_i \)'s (\( i = 1, 2 \)) describe the rates at which the protozoa can grow depending on the organic concentration relative to Monod equation; \( g_i \) is an increasing function and \( g_{i2} \) is a decreasing function against the organic concentration, taking values between 0 and 1.

We now suppose the following two cases. One is the case where the function \( g_1 \) can be expressed by a Monod type, equation

\[ g_1 \left( C ; G_i \right) = C / (C_i + C) \]

and the other is a case where the function \( g_1 \) can be expressed by the unit step function.

\[ g_1 \left( C ; G_i \right) = U / (C - G_i) \]

where \( G_i \) is the threshold TOC concentration for inhabitation of free-swimming protozoa.

If we assume that stalked protozoa should grow in accordance with non-competitive inhibition, the function \( g_2 \) can be expressed in the following form:

\[ g_2 \left( C ; G_i \right) = G_i / (G_i + C) \]

where \( G_2 \) is the threshold TOC concentration for stalked protozoa.

### 1.3 Rates of flocculation and deflocculation

The motile bacteria are known to be flocculated by the viscid substances secreted by the protozoa (Sudo, 1977). It is thus inferred that the rate of flocculation or deflocculation should be influenced by the concentration of protozoa. We here assume that flocculation occurs in accordance with an enzyme reaction equation and the deflocculation dose in the habit of a non-competitive inhibition type of equation. The specific flocculation rates \( h_{qi} \)'s (\( q = r, s \)) are then given by

\[ h_{qi} = h_{qi \text{max}} P_{qi} / (H_{qi} + P_{qi}), \quad q = r, s \]

and the deflocculation rates \( h_{qi} \)'s (\( q = r, s \)) are

\[ h_{qi} = h_{qi \text{max}} H_{qi} / (H_{qi} + P_{qi}), \quad q = r, s \]

where \( h_{qi \text{max}} \)'s, \( h_{qi \text{max}} \)'s (\( q = r, s \)) are the maximum rates of flocculation and deflocculation, respectively and \( Hqi \)'s are the related saturation constants.

It would be more reasonable to consider that the flocculation rate dose depend on the ratio of protozoa to motile bacteria mass concentrations, because the amount of viscid substances per bacterium dose determines the rate of flocculation instead of the gross amount of viscid substances. We can then rewrite Eqs. (18), (19) in terms of \( P_{qi} / B_{qi} \) (\( q = r, s \)) as follows.

\[ h_{qi} = h_{qi \text{max}} \left( P_{qi} / B_{qi} \right) / \left( H_{qi} + \left( P_{qi} / B_{qi} \right) \right), \quad q = r, s \]


Table 1  Combinations of rate equations for case study

<table>
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<tr>
<th></th>
<th>Case I</th>
<th>Case II</th>
<th>Case III</th>
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<td>flocculation</td>
<td>Monod, Eq. (18)</td>
<td>Monod, Eq. (18)</td>
<td>Monod, Eq. (20)</td>
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<tr>
<td>deflocculation</td>
<td>non-competitive, Eq. (19)</td>
<td>non-competitive, Eq. (19)</td>
<td>non-competitive, Eq. (21)</td>
</tr>
<tr>
<td>function $g_1(C; G_1)$</td>
<td>Monod, Eq. (15)</td>
<td>unit step, Eq. (16)</td>
<td>unit step, Eq. (16)</td>
</tr>
<tr>
<td>function $g_2(C; G_2)$</td>
<td>non-competitive, Eq. (17)</td>
<td>non-competitive, Eq. (17)</td>
<td>non-competitive, Eq. (17)</td>
</tr>
</tbody>
</table>

\[ h_{q2} = h_{q2\text{max}} H_{q2} / \langle H_{q2} + [P_q / B_3] \rangle, \quad q = r, s \]  \hspace{1cm} (21)

where, $P_q = P_{q1} + P_{q2}$ ($q = r, s$)

1.4 Microbial growth models with assumed rate equations

In the foregoing section, we proposed Eq. (13) for growth rates of motile and floc-forming bacteria, Eqs. (14) ~ (17) for those of free-swimming and stalked protozoa, and Eqs. (18), (19) or Eqs. (20), (21) for flocculation and deflocculation rates. At present, however, we have no definite knowledge about which equations and what constitution of them can approach well the microbial growth processes. We therefore try to constitute these rate equations for a case study. In Table 1, three presumable cases for combination of assumed rate equations are tabulated.

Fig. 2  Time courses of effluent TOC concentrations, predicted by case I, II and III, comparison with experimental data

\[ h_{q2} = h_{q2\text{max}} H_{q2} / \langle H_{q2} + [P_q / B_3] \rangle, \quad q = r, s \]

2.  Review in Experimental Results

We first review briefly the characteristics of substrate consumption and microbial growth processes observed in our previous investigations on dialysis wastewater treatment by a PUF fluidized bed bioreactor (Toyoda et al., 1994, Toyoda et al., 1995). In Figs. 2, 3 and 4, experimental data for variations with time passage in TOC concentration and retained and suspended microbial mass concentrations are shown, respectively (Toyoda et al., 1994, Toyoda et al., 1995). The bioreactor used in experiments is a 3.35 dm$^3$ fluidized bed in which a 0.4dm$^3$ equivalent of 10mm-cubic PUF particles with 1575 pores/m$^3$ and specific area of 60 dm$^2$/dm$^3$ were loaded at a packing ratio of 0.12. The initial TOC was set at 10mg/dm$^3$. The feeding rate of wastewater is 4.2dm$^3$/day and the rate of aeration in 2 Ndm$^3$/min. The amount of seed microbes, which had been acclimated, was 268mg (= 80mg/dm$^3 \times 3.35$dm$^3$). The operating temper-
value at around twenty days experiencing a declining stage. The inhabitation characteristics of motile and flock-forming bacteria, free swimming and stalked protozoa as observed the microscopic investigation, have been described in detail elsewhere (Toyoda et al., 1994, Toyoda et al., 1995).

3. Numerical Results and Discussion

In numerical analysis, basic equations, Eqs. (1) ~ (9), were discretized with the time interval, $\Delta t = 3.6 \text{ min.}$, and were computed subject to the initial conditions Eqs. (10) ~ (12). The initial values here taken are $C_0 = 10 \text{ mg/dm}^3$, $B_0 = 30 \text{ mg/dm}^3$, $B_{x0} = 30 \text{ mg/dm}^3$, $P_0 = 10 \text{ mg/dm}^3$, and $P_{x0} = 10 \text{ mg/dm}^3$, so that the total amount corresponds to the experimental value. The relevant rate constants used in computation are shown in Table 2, wherein $\mu_b^{max}$, $H^{P}_{b_{max}}$, $K_{r_x}^p$, $G_s$, $K_{a}$, $Y_b$, and $Y_{x}$ were cited from publications (Sudo, 1977, Sudo et al., 1975), and the other constants were determined so that the numerical results would correlate with the experimental results.

The time courses of substrate concentration, i.e. TOC, computed in cases I, II and III are compared with the experimental results in Figs. 2a, 2b and 2c, respectively. As seen in Fig. 2a, the numerical results in case I explain qualitatively the presence of the first and second peaks which are found in experimental plots. The second peak predicted, however, appears about two days later than in the actual case. In addition, the appearance of the third peak cannot be predicted. In Fig. 2b, the second peak in the TOC value predicted in case II appears at around three days, about two days earlier than predicted in case I. The numerical results also show that each TOC curve shows a third small peak, at around eight days. In case III, as seen in Fig. 2c, the numerical results show that TOC has the distinct third peak at around eight days, which is not predicted in case I. In this case, the constants $H^{P}_{b_{max}}$, ($q = r, s; i = 1, 2$) are dimensionless values different from those in cases I and II, and are also given in Table 2.

The time courses of retained microbe mass concentration, $M_r = (B_{r1} + B_{r2} + P_{r1} + P_{r2})$ computed in cases I, II and

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![Table 2 Biological rate constants and related coefficient](image)

<table>
<thead>
<tr>
<th>$\mu_b^{max}$ (i = 1, 2)</th>
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<td>$K_{r_x}^p$ (i = 1, 2)</td>
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</tr>
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<td>$a^{-1}$</td>
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<tr>
<td>$Y_b$</td>
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<td>mg·TOC/dm$^3$</td>
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<tr>
<td>$h_{b_{max}}$ (r, s)</td>
<td>25000</td>
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</table>

* in Eqs. (20) ~ (21)
Fig. 5 Time courses of individual microbial concentrations, numerical in Case III, $C_0 = 308\text{mg-TOC/dm}^3$.

III are compared with the experimental results in Figs. 3a, 3b and 3c, respectively. In Fig. 3a, the numerical results in case I show that $M_i$ increases in the beginning three days to reach a maximum, decreases after that in about two days to show a minimum at around five days, and increases again to approach a steady value. In each case of influent TOC, the predicted day when the maximum occurs, however, deviates by about one day earlier, and the day when the minimum occurs deviates by about three days earlier, compared with the experimental data. The numerical results cannot predict a stagnant stage at around three days. The mass concentration $M_i$ in case II, as shown in Fig. 3b, exhibits a small maximum at around two days, and another relatively distinct maximum at around seven days. The first maximum comes from the maximum at around four days in Fig. 3a, which is shifted earlier by about two days. The decrement period after seven days predicted by the numerical results, however, is much shorter than that found in the experimental data. The numerical results in case III, as shown in Fig. 3c, are seen to correlate with the experimental data much better than those predicted in cases I and II.

The time courses of suspended microbe mass concentration, $M_i = (B_{i1} + P_{i1} + P_{i2})$ computed in cases I, II and III are compared with the experimental results in Figs. 4a, 4b and 4c, respectively. The variations with time passage in $M_i$ are found to be very similar to those of $M_i$, with the exception of the declining period just after seeding. In Fig. 4c, the numerical curve for TOC = 154mg/dm$^3$ overestimates the experimental values, whereas that for TOC = 615mg/dm$^3$ underestimates the experimental values, the numerical results in case III are seen to correlate with the experimental data much better than those predicted in cases I and II.

In relation to microbial inhabitation characteristics, it is meaningful to examine the variations with time passage in concentration of the individual bacteria and protozoa. Numerical values of $B_{i}$'s and $P_{i}$'s ($i = 1, 2$), and those of $B_{si}$'s and $P_{si}$'s ($i = 1, 2$), are shown against time passage in Figs. 5a and 5b. In these figures, influent TOC has been set at 308mg/dm$^3$. In Fig. 5a, the concentration $B_{i1}$ of motile bacteria shows two knolls with respective peaks at two and six days, with the second one being much more appreciable. After eight days, $B_{i1}$ takes a constant value as small as 10mg/dm$^3$-PUF. The concentration $B_{i2}$ of floc-forming bacteria starts to increase at around two days, shows a maximum at four days, and approaches a steady value of about 6600mg/dm$^3$-PUF, experiencing an appreciable predator-prey oscillation with a minimum at seven days. Meanwhile, the concentration $P_{i1}$ of free-swimming protozoa increases in the first two days, shows a maximum at 2.5 and 7.5 days, approaching zero thereafter as time passes by. The concentration $P_{i2}$ of stalked protozoa starts to increase at about five days, shows a maximum at seven days, and approaches a steady value of about 1600mg/dm$^3$-PUF.

The decrease in $B_{i1}$ between 1.5 - 2.5 days is caused by the fact that the motile bacteria are preyed on by free-swimming protozoa. Appearance of the second knoll in $B_{i1}$ is caused by the symbiosis effects. $P_{i1}$ decreases at around four days so that the bacteria are hardly preyed on and defloculation is enhanced as well due to a shortage of viscid substances, which results in increasing $B_{i1}$. At around six days, $P_{i2}$ increases so that the bacteria are preyed on, which results in decreasing $B_{i1}$. The increase in $B_{i2}$, on the other hand, is caused by the fact that bacteria are flocculated under the presence of protozoa and get to be hardly preyed on by protozoa. Appearance of the second small peak in, $P_{i1}$ is caused by the third peak in TOC, of which concentration is high enough to grow free-swimming protozoa. The $P_{i1}$ decreases down to zero at steady state. This is caused by the fact that the free-swimming protozoa can not grow under the condition of fairly low substrate concentration.

Appearance of the first peak in the TOC curve, as shown in Fig. 2, is obvious, since higher TOC of influent is supplied at the start up time. The second peak in the TOC curve is attributed to the fact that the motile bacteria are preyed on by protozoa and there exist very few motile bacteria at around three days. Since the motile bacteria are preferably preyed on by protozoa, the gross amount of bacteria decreases sharply around seven days, which causes the TOC curve to show the third peak.

As seen in Fig. 5b, variations with time passage in concentration of the individual suspended microbes are found to be very similar to those of retained microbes.

Conclusion

The microbial growth and substrate consumption
processes in wastewater treatment by a PUF fluidized bed bioreactor were simulated numerically. It was shown that the actual time courses of TOC and mass concentrations of retained and suspended microbes are explained well by a substrate mass balance and the eight microbial mass balance equations, which include the effects of biological predator-prey and symbiosis with the following proposals:

1) The bacteria are classified broadly into motile and flocc-forming bacteria; they should grow subject to the Monod equation; 2) The protozoa are classified broadly into free-swimming and stalked protozoa. The specific growth rate of free-swimming protozoa is expressed by the Monod equation modified with the unit step function, Eq. (14) with Eq. (16), and that of stalked protozoa by the Monod equation, modified with the non-competitive inhibition formula, Eq. (14) with Eq. (17); 3) The rates of flocculation of motile bacteria are expressed by Eq. (20), and those of deflocculation of floc-forming bacteria by Eq. (21). In addition, interrelations among substrate consumption process and individual microbe growth processes are also made clear.

Nomenclature

- \( a \) = specific surface of support particle \([ \text{dm}^2/\text{dm}^3] \)
- \( B_{ri} \) = mass concentration of retained bacteria \([ \text{mg/ dm}^3 - \text{PUF}] \)
- \( B_{si} \) = mass concentration of suspended bacteria \([ \text{mg/dm}^3] \)
- \( C \) = substrate concentration \([ \text{mg/TOC/dm}^3] \)
- \( G_i \) = threshold concentration \([ \text{mg/TOC/dm}^3] \)
- \( h_{f1} (q, r, s) \) = rate of flocculation \([ \text{d}^{-1}] \)
- \( h_{df} (q, r, s) \) = rate of deflocculation \([ \text{d}^{-1}] \)
- \( H_{s1} (q, r, s) \) = saturation constant of flocculation \([ \text{mg/ dm}^3] \)
- \( H_{df} (q, r, s) \) = saturation constant of deflocculation \([ \text{mg/ dm}^3] \)
- \( k_{si}^b (q, b, p) \) = saturation constant \([ \text{mg/TOC/dm}^3] \)
- \( k_{ai} (q, b, p) \) = decay rate coefficient \([ \text{d}^{-1}] \)
- \( k_{r} \) = falling-off rate coefficient \([ \text{dm} \cdot \text{d}^{-1}] \)
- \( k_+ \) = sticking rate coefficient \([ \text{dm}^{-1}] \)
- \( M_r \) = mass concentration \([ \text{mg/ dm}^3 - \text{PUF}] \)
- \( M_s \) = mass concentration \([ \text{mg/dm}^3] \)
- \( M_{rc} \) = saturation concentration \([ \text{mg/ dm}^3 - \text{PUF}] \)
- \( P_{ri} \) = mass concentration of retained protozoa \([ \text{mg/dm}^3 - \text{PUF}] \)
- \( P_{si} \) = mass concentration of suspended protozoa \([ \text{mg/dm}^3] \)
- \( Q \) = volume flow rate \([ \text{dm}^3/\text{d}] \)
- \( V \) = volume of reactor \([ \text{dm}^3] \)

**Literature cited**


