Colony formation in bacterial colony has been studied theoretically through a continuum model that considers chemotaxis. This model has been obtained explicitly by numerical results. There-
is absorbed into the medium. Thus, the effect of lubrication fluid is represented through the diffusion [12, 14].

iii) The chemotactic signal can be also a field produced directly or indirectly by the bacterial cells.

We consider the diffusion coefficient in a density-dependent form \( D(u) = M(u/\sigma)^p \), where \( M > 0 \) is diffusion constant, \( \sigma = \lim_{t \to \infty} u(x, t) \) is equilibrium density and \( p > 0 \). This represents the crowding-avoidance movement of individuals [10, 12, 20]. The growth with limited nutrient supply of bacteria is modeled as the generalized logistic law \( R(u) = \alpha u [1 - (u/\sigma)^p] \), where \( \alpha > 0 \) is rate constant [20]. The chemotactic drift velocity can be expressed as \( \vec{v}(s) = \zeta(s) \chi(s)s_x \), where \( \chi(s)s_x \) acts as the gradient sensed by the bacterium (with \( \chi(s) \) having the units of 1 over the chemical concentration) [12]. \( \zeta(s) \) is the bacterial response to the sensed gradient and it has the same units as a diffusion coefficient [12]. Therefore, we assume that \( \zeta(s) = \gamma D(u) = \gamma M(u/\sigma)^p \), where \( \gamma \) is a constant, positive for attractive chemotaxis and negative for repulsive chemotaxis [12]. Here, we are interested in a special case where the gradient sensed by the bacterium is nearly uniform and \( \chi(s)s_x \) is treated as a constant [14]. By substituting \( D(u) \), \( R(u) \) and \( \vec{v}(s) \) into Eq. (2) with the transformations \( t^* = at, x^* = (ma/M)^{1/2}x, u^* = u/\sigma \) and \( \kappa = (1/2)\gamma (mM/\alpha)^{1/2} \chi(s)s_x \), we obtain the dimensionless equation

\[
u_t = (u^m)_xx - 2\kappa (u^m)_x + u - u^m, \tag{2}\]

where \( m = p + 1 > 1 \) and the asterisk is dropped. So far, the solution of Eq. (2) has well understood as the traveling wave [14, 21, 22]. However, the exact or explicit solution in space-time coordinates has been unknown.

As studied in our previous work, without chemotaxis, Eq. (2) can be mapped to a purely diffusion process, which the exact solution can be obtained [23]. We then extend the similar technique to analyze Eq. (2). We rewrite Eq. (2) as \((m - 1)u = \frac{1}{\omega^2} \left( \frac{\omega^2}{\omega^2} + 1 \right) \left( \frac{\partial^2}{\partial y^2} - \omega^2 \right) u^m \), where \( y = x/\omega \) and \( \omega = \kappa \pm \sqrt{\kappa^2 + 1} \), and then it can be evaluated to \( e^{l - \omega^2}e^{-i\omega t}u = \omega^{-2}e^{-y\partial/\partial y}(e^{\omega^2}e^{-\omega^2}u^m) \). By introducing the transformations

\[
\begin{align*}
u(y, t) &= e^{\frac{\omega y}{l}} \Phi(y, t) \tag{3} \\
\tau(t) &= e^{(m-1)t} - 1 \tag{4} \\
\phi(y) &= e^{\frac{(m-1)\omega^2}{l}}y, \tag{5}
\end{align*}
\]

we obtain the reduced form of Eq. (2)

\[
\Phi_\tau = k|\phi^{\prime} (\Phi^m) |\phi^{\prime}, \tag{6}
\]

where \( k = \frac{1}{\omega^2 (m-1)} \frac{(m+\omega^2)}{m} \) and \( l = \frac{(\omega^2+2m+\omega^2)}{m+\omega^2} \).

Eq. (6) is known as the anomalous diffusion equation, whose solution is assumed to be the scaling function

\[
\Phi(\phi, \tau) = \frac{1}{T(\tau)} F \left( \frac{\phi}{T(\tau)} \right) = \frac{F(\theta)}{T(\tau)}, \tag{7}
\]

where \( \theta(\phi, \tau) = \phi/T(\tau) \).

By performing the calculations similar to Ref. [23], we obtain

\[
\Phi = \left\{ \frac{1}{(\tau + a)^{m+\omega^2}} \left[ b + \theta - \frac{(m-1)\omega^2}{m+\omega^2} \right] \right\}^{\frac{1}{m-1}}, \tag{7}
\]

where \( a > 0 \) and \( b \) are constant. After substituting Eq. (7) into Eq. (3), we obtain the initial density profile:

\[
u(u)(x, t) = \frac{u(0)(x)}{a^{1/p}} \left\{ 1 + b \left( e^{p\omega x/\alpha^2} \right)^{(1/p) + 1/p} \right\}^{1/p}.
\]

We consider the initial density that satisfies the following properties: \( u_0(x) = 0 \) for \( x \geq x_0 \) and \( \lim_{x \to -\infty} u_0(x) = \rho \), where \( \rho \) is initial density amplitude and \( x_0 \) is initial front position [23]. According to these conditions, we have \( a = \rho^{-p} \) and \( b = -\rho^{-p}\omega/\rho(p+1) \). Now the exact solution to Eq. (2) is given by

\[
u(x, t) = \frac{\rho e^{l}}{[p\rho(e^{pt} - 1) + 1]^2} \times \left\{ 1 - \left[ \frac{e^{p\omega x(x-x_0)} \left( p\rho(e^{pt} - 1) + 1 \right)^{1/p}}{[p\rho(e^{pt} - 1) + 1]^2} \right]^{1/p} \right\}.
\]

Since the solution Eq. (3) has two forms, depending on the value of \( \omega \), we define \( u_+(x, t) \) and \( u_-(x, t) \) as the solutions corresponding to \( \omega_+ = \kappa + \sqrt{\kappa^2 + 1} \) and \( \omega_- = \kappa - \sqrt{\kappa^2 + 1} \), respectively. As proved in our previous work [23], the linear combination of these two solutions \( w(x, t) = u_+(x, t) + u_-(x, t) \) is a solution of Eq. (2). By using an approximation \( (u_+ + u_-)^p \approx u_+^p + u_-^p \), we obtain

\[
w(x, t) = 2^{-p} \left[ u_+^p(x, t) + u_-^p(x, t) \right]^{1/p}, \tag{9}
\]

where \( (2)^{-1/p} \) is normalized factor. We note that in the case of no chemotaxis \( \kappa = 0 \), thus \( \omega = \pm 1 \), these results recover our previous work [23].

![FIG. 1. (Color online) The spatiotemporal evolution of the bacterial density profile \( u(x, t) \) (Eq. 5) in the case of \( p = 2 \) with initial conditions \( \rho = 0.2 \) and \( x_0 = 1 \). The solid lines represent \( u_+(x, t) \) and the dashed lines represent \( u_-(x, t) \).](image-url)
in Fig. (1). The density profiles start from the initial state \( w_0(x) \) then grow and expand to the unoccupied region. At sufficient large time scale, the density profiles reach the saturated value at 1. After that, they seem to propagate with unchanged shape; \( u_+(x,t) \) is propagating to the right whereas \( u_-(x,t) \) is propagating to the left. The roles of chemotaxis on the regulation of pattern formation in the system is reflected by parameter \( \kappa \). Since \( \kappa < \sqrt{k^2 + 1} \), \( u_+ \) is always positive whereas \( u_- \) is always negative. This causes the tails of \( u_+ \) decay as \( x \to \infty \) and the tails of \( u_- \) decay as \( x \to -\infty \). In the former case, the interface is sharper because \( |\omega_+| > |\omega_-| \). Due to the influence of chemotaxis, the distribution of density profile is biased toward to the right thus the front of \( u_+ \) is moving faster than of \( u_- \). The spatiotemporal evolution of the combined density profiles \( w(x,t) \) is also illustrated in Fig. (2). The densities \( w(x,t) \) form the pulse-like profiles that grow and expand with asymmetric shape. It behaves like \( u_+(x,t) \) for \( x > x_0 \) and like \( u_-(x,t) \) for \( x < -x_0 \). Due to the bias force from chemotaxis, the peak of \( w(x,t) \) is moving toward to the right.

From Eq. (8), we calculate the front position \( r(t) \), that the density falls to zero \( u(r,t) = 0 \) as \( r(t) = x_0 + \omega t \). The plot of relative front position \( \omega t - x_0 \) is shown in Fig. (3). The relative front position of \( u_+(x,t) \) is slow varying when compared with of \( u_-(x,t) \). At sufficient large time, that \( e^{pt} \gg 1 \) and \( \rho_p e^{pt} \gg 1 \) thus \( t' \approx -\ln \rho \), the relative front position seems to vary linearly in time \( x_0 \sim \omega t \). It implies the constant front propagating speed. Consequently, we calculate the front speed as \( v(t) = \frac{\partial r(t)}{\partial t} = \frac{\omega t}{\rho_p e^{pt}} \). At large time scale \( t \gg t' \), the front speed trends to be constant \( c = \lim_{t \to \infty} v(t) = \omega \). At this point, it is clearly seen that the spreading speed is biased by the chemotaxis through the parameter \( \kappa \).

At the large time scale, \( t \gg t' \), the bacterial density profile Eq. (5) emerges the traveling wave form

\[
\bar{u}(x - \omega t) = \left[ 1 - \frac{pe^{-\omega t}}{\rho e^{pt}} \right]^{\frac{1}{\beta}}, \quad (10)
\]

where \( \omega \) is front speed. The front speed obtained here is comparable to the minimum value for the sharp traveling wave [14, 22]. Similarly, at the large time scale \( t \gg t' \), Eq. (9) develops to the expanding pulse-like wave

\[
\bar{w}(x - \omega_\pm t) \approx 2^{-\frac{1}{\beta}} \left[ \bar{u}_+^\omega (x - \omega_+ t) + \bar{u}_-^\omega (x - \omega_- t) \right]^{\frac{1}{\beta}}, \quad (11)
\]

with the expanding speed \( \omega_\pm \).

Finally, we found that Eq. (7) forms a scaling law at large time scale \( t \gg t' \)

\[
\Phi(\phi, \tau) \approx \frac{1}{\tau^\beta} F(\frac{\phi}{\tau^\beta}), \quad (12)
\]

where \( \beta = \frac{m+\omega^2}{m(m-1)} \). It implies that the bacterial colonies evolve as the self-similar object in the terms of transformed quantities: \( \Phi \to e^{-\omega\tau/m} e^{-t} \), \( \tau \to e^{(m-1)\tau} \), and \( \phi \to e^{(m+\omega^2)(x-x_0)/m\omega} \). Moreover, they evolve from self-similar pattern form to the traveling wave pattern form. This behavior can be classified as the intermediate asymptotics of the second type [27].

In summary, the spatiotemporal pattern formation of bacterial colony in the presence of chemotaxis has been investigated at continuum level. We have shown that the bacterial colony patterns in the case of uniform gradient sensed by bacterium are self-similar; where they are scale invariant. The scaling law of bacterial colony growth has been revealed explicitly. Moreover, we found that the bacterial colonies evolve long time scale as the sharp traveling wave where the front speed is biased to move toward to the chemical attractant.

K. Khompurungsorn acknowledges the Centre of Excellence in Mathematics (Thailand) for partial financial support.
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