

Mathematical model of the bacteria-nutrient dynamics

Simeon Chioma Inyama
Department of Mathematics and Computer Science
Federal University of Technology,
Owerri, Imo State, Nigeria
e-mail-Scinyama2003@yahoo.com

Abstract

In this paper we developed a Mathematical Model of bacteria-nutrient dynamics which results in a system of first order ordinary differential equations. The analysis of the model was done using dynamical systems. It was found out that the product of the maximum nutrient uptake per cel; and the number of cells produced per unit of nutrient uptake is a constant ($VY = In 2$). It is also shown that there is a linear relationship between the concentration of the limiting nutrients and number of bacteria with a negative slope. It is finally shown that after a long time, the number of bacterial will be a constant and will depend on the initial concentration of the nutrient and the initial number of bacterial.

Keywords: Spatial patterns, hysteretic dependence bacterial, supper saturation, threshold.

1.0 Introduction

Regular patterns of organisms occur frequently in a variety of biological settings, and they are caused by a variety of mechanisms. There are two main different mechanisms for pattern formation. The first describes the patterned growth of bacteria in response to diffusing nutrient. The bacteria do not move; instead, they act as a living record of past events that have been favourable or unfavourable to their growth.

The key ingredients are the nutrient, which promotes growth, and acid, which inhibits growth. When the process is complete, there is no detectable patter structure for either the nutrient or the acid; only the differing cell population numbers at various points indicate the way in which nutrient and acid approach their uniform distributions. The second illustrates a reverse mechanism. This shows how a population's genetic structure can adapt to a pattern structure of the environment that influences genetic fitness. In this case, the population adapts to a patterned profile of fitness coefficients [4].

Bacteria can grow in spatial patterns in response to diffusion of a needed nutrient. This describes an immobile bacterial population distribution on a Petri dish. The diffusing nutrient is taken up by growing cells, and acid is produced as a by-product of cell growth. [5]. A novel feature of the model is that the cell's growth has a hysteretic dependence on the amount of nutrient and acid present. It is known that hysteretic kinetics can lead to spatial patters in chemical systems, such as *liesegang rings* formed by precipitating colloids. In that case, the hysteresis is described by Ostwald's theory of super-saturation. Other hysteretic systems that lead to patterns arise in electrophysiology and epidemiology: [3].

Some major work have been done on the mathematical model of bacteria-nutrients dynamics. Hoppensteadt, F.C. [4] presented the crystal test model involving the bacterial population size $B(r,t)$, histidine diffusion and uptake, $H(r,t)$ and buffer concentration $G(r,t)$. He observed that when growing, cells will continue to grow even as PH decreases until a higher, more favourable PH threshold is reached.

Tyson, R. et.al [8] modeled the dynamics of the bacteria-nutrient and chemoattractant and this gave rise to non-linear partial differential equation system. They presented a simple and intuitively revealing analysis of the patterns generated by their model. They observed that patterns arose from disturbances to a spatially uniform solution state. A linear analysis gave rise to a second order ordinary differential equation for the amplitude of each model present in the initial disturbance.

Marcello Vichi [7] said “Nutrient dynamics are mostly connected to carbon dynamics, except for the direct can behave as remineralization or as competitors with the phytoplankton taking up inorganic nutrient directly from the water:

Marcellor Vichi [7] modeled nutrient and carbon dynamics which resulted in a partial differential equation. He analysed the model using dynamical systems.

Kraigsley, A. et.al. [6] studied the dynamics of motile bacteria in nutrients. They looked at the analogy between spreading motile bacteria and other self-propagating fronts with respect to the dynamical properties of such fonts. Initial experiments they conducted using the E coli bacterium indeed showed behaviour analogous to reaction-diffusion system.

Most microbiological studies focuses on individual bacterium and counting the behaviour of individuals [6]. In this study, we apply thermodynamics laws and study aggregate behaviour of a large number of individuals. The test case we choose to focus on for this study is the very common and widely studied *Escherichia coli* bacterium, a motile bacterium that (like many others) swims using it’s *tentacles* or *flagella* in it’s nutrient media while frequently changing direction to seek regions of higher nutrient concentration. Specifically the bacterium has two modes of behaviour “run” mode in which it’s flagella rotate to propel it in a more or less straight line and “thumble” model where the flagella cause it change orientation with little net motion [1].

Using this knowledge of the behaviour of bacteria in nutrients we now formulate the model of the bacteria-nutrient dynamics since “pattern formation in microbiological systems is well know” [2], but reaction-diffusion theory (model) has not sufficiently been used to quantify and predict such patters.

2.0 The model

Let us first present the symbols we are going to use in this model.

$B(t)$ = number of bacterial at time t .

$N(t)$ = concentration of the limiting nutrient in a growing chamber at time t .

t = time and is chosen to correspond to the cell’s doubling time when sufficient nutrient is present

V = maximum nutrient uptake per cell

K = Michaelis or saturation constant, which is the value of N at which uptake is half it’s maximum rate.

Y = the yield, that is, the number of cell’s produced per unit of nutrient taken up

We observed that

(1) The rate of change in the number of bacteria is a product of the yield, Y , the number of bacteria and the total nutrient uptake.

(2) The rate of change in the concentration of limiting nutrient is a product of the number of bacterial and the negative of the nutrient uptake. This means that:

$$\begin{aligned} dB / dt &= YBN_u \\ dN / dt &= -BN_u \end{aligned} \tag{2.1}$$

where N_u is the nutrient uptake. But the Jacob-Monod model of nutrient uptake is described by:

$$N_u = \frac{VN}{K + N} \tag{2.2}$$

Putting (2.2) in (2.1) gives

$$\begin{aligned}\frac{dB}{dt} &= VY \left(\frac{N}{K+N} \right) B \\ \frac{dN}{dt} &= - \left(\frac{VN}{K+N} \right) B\end{aligned}\tag{2.3}$$

(2.3) is now the required model of bacterial-nutrient dynamics.

3.0 Analysis of the model

In this section we

- (1) Find the value of VY
- (2) Solve the model for N as a function of B
- (3) Described the dynamics of B as a function of t

3.1 The Value of VY

When sufficiently nutrient is present ($N > 1$), then

$$\frac{dB}{dt} = VYB \frac{N}{K+N} = 1 \Rightarrow \frac{dB}{B} = VYdt \Rightarrow \ln B = VYt \text{ or } B(t) = B_0 e^{VYt} \text{ where } B_0 = B(0).$$

Since the time scale corresponds to cell doubling, $B(1) = 2 B(0)$. Hence

$$\begin{aligned}e^{VY} &= 2 \\ VY &= \ln 2\end{aligned}\tag{3.1}$$

This shows that VY is a constant.

3.2 Solving N as a function of B

Divide the second equation of (2.3) with the first equation to get

$$\frac{dN}{dB} = -\frac{1}{Y}, \quad dN = -\frac{1}{Y} dB \Rightarrow N = -\frac{B}{Y}$$

Let $N(0) = N_0$, $B(0) = B_0$, then

$$N = N_0 - \frac{(B - B_0)}{Y}\tag{3.2}$$

$$\Rightarrow (N(t) = (N_0 + \frac{B_0}{Y}) - B(t))$$

$$\Rightarrow N(t) = a - bB(t)\tag{3.3}$$

where $a = N_0 + \frac{B_0}{Y}$, $b = \frac{1}{Y}$

3.3 The dynamics of B as a function of t

Put (3.2) in the first equation of (2.3) to get

$$\frac{dB}{dt} = VY \left(\frac{YN_0 + B_0 - B}{YK + YN_0 + B_0 - B} \right) = \left[\frac{(VY^2 N_0 + VYB_0 - VYB)}{(YK + YN_0 + B_0 - B)} \right] B, \text{ Therefore } \frac{dB}{dt} = \left(\frac{a - \alpha B}{b - B} \right) B$$

where $a = VY^2 N_0 + VYB_0$, $\alpha = VY$, $b = YK + YN_0 + B_0 \Rightarrow \frac{b - B}{B(a - \alpha B)} dB = dt$

Resolving this into partial fractions we have

$$\Rightarrow \left\{ \frac{b/a}{B} + \frac{(b\alpha - a)}{a - \alpha B} \right\} dB = dt \Rightarrow \frac{b}{a} \ln B - \frac{b\alpha - a}{a\alpha} \ln[a - \alpha B] = t + c \Rightarrow b/a \ln B - (b/a - 1/\alpha)$$

$$\ln(a - \alpha B) = t + c \Rightarrow \ln \left[\frac{B^{b/a}}{(a - \alpha B)^{b/a - 1/\alpha}} \right] = t + c \quad \text{or} \quad \ln \left[\frac{(a - \alpha B)^{b/a - 1/\alpha}}{(a - \alpha B)^{b/a}} \right] = -t - c$$

$$\Rightarrow \frac{(a - \alpha B)^{b/a - 1/\alpha}}{B^{b/a}} = ue^{-t}$$

As $t \rightarrow \infty$, $a - \alpha B = 0$ and by the value of a and α defined above, it means that as $t \rightarrow \infty$, $B(t) \rightarrow N_0 + B_0 / Y$ which is also a constant.

4.0 Summary and conclusion

We have been able to develop a model for the bacteria-nutrient dynamics. We found out that $VY = \ln 2$. This means that the product of maximum nutrient uptake per cell and the number of cells produced per unit of nutrient uptake is a constant. We also found out that $N(t) = a - b(B(t))$. This means that there is a linear relationship with negative slope between the concentration of limiting nutrient and number of bacteria. Which means that the yield (the number of cells produced per unit of nutrient taken up) is inversely proportional to the maximum nutrient uptake per cell. We finally found that $B(t) = N_0 + B_0 / Y$ as $t \rightarrow \infty$. This means that the number of bacteria after a long time will be a constant and will be dependent on the initial concentration of the limiting nutrient and the initial number of bacteria. These results are in agreement with the crystal test model presented by Hoppensteadt, F.C. [4]; though Hoppensteadt's crystal test model was a system of first order linear differential equation while the model presented here is a system of non-linear first order differential equation. This paper has succeeded in throwing more light on what happens when bacteria are in nutrient.

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