

# **Mathematical Modeling of Microbial Growth in Tilapia Sausage**

**Eddy Afrianto**

Department of Fishery, Faculty of Fishery and Marine Sciences, Universitas Padjadjaran, Indonesia  
eddy.afrianto@unpad.ac.id

**Subiyanto**

Department of Marine Science, Faculty of Fishery and Marine Sciences, Universitas Padjadjaran, Indonesia  
subiyanto@unpad.ac.id

**Pramono Sidi**

Department of Mathematics, Faculty of Sciences and Technology, Universitas Terbuka, Indonesia  
pramsidi@yahoo.co.id

**Abdul Talib Bon**

Department of Production and Operations, University Tun Hussein Onn Malaysia, Malaysia  
talibon@gmail.com

## **Abstract**

Mathematical models for predicting microbial growth in tilapia sausage were developed and analyzed. Mathematical models are formed from a coupled system of ordinary differential equations. The subject of this research is the bacteria present in tilapia, the data collection technique used in this study is a laboratory process which looks at the growth rate of the bacteria. The data analysis technique is the differential equation model approach. Based on observations, the results of the test of the growth rate of bacteria present in tilapia is clearly seen that the rate of development or growth is increasing, this shows that these bacteria have very rapid growth.

## **Keywords:**

Microbial, mathematical model, ordinary differential equations, tilapia sausage.

## **1. Introduction**

Tilapia (*Oreochromis niloticus*) is one of the most consumed fish worldwide, of which its global production reached approximately 4.200 million tons in 2016 (Pulido et al., 2019). Tilapia is a type of freshwater fish consumption. The fish was introduced from Africa, specifically eastern Africa, in 1969, and is now a popular fish in freshwater ponds in Indonesia as well as pests in every river and lake in Indonesia (Brzeski and Doyle, 1995). Tilapia is a worldwide practice that has brought beneficial economic impact to developing countries in Asia (Soto et al., 2019).

The study of microbial growth in tilapias by using equations that can predict fish age has been very useful, because they encapsulate information from a data series into a small set of parameters that can be transferred biologically. Microbial growth is a field of microbiology that has been known in the last two decades, and in the last ten years, hundreds of papers have been published with the keyword microbial growth (Akkermans and Van Impe, 2018; Baranyi and Roberts, 1994; Cárdenas et al., 2008; Giannuzzi et al., 1998; Khoshdel and Mahmoodzadeh Vaziri, 2016; López et al., 2004; McClure et al., 1994; Teleken et al., 2011; Tianyuan et al., 2019; Van Impe et al., 1992; Wade et al., 2016; Whiting and Cygnarowicz-Provost, 1992). This emphasizes the need to describe microbial responses to different environments by mathematical models. The mathematical modeling is used to represent and explain physical systems or problems in the real world and in mathematical statements, so that an understanding of real world problems is obtained more precisely. Related to natural phenomena, people often need a mathematical model to solve the problem encountered. Many mathematical problems of natural phenomena that mathematical models can be formulated in the

form of order differential equations. The main purpose of this paper is to propose and evaluate mathematical models that describe the growth of microbes in tilapia sausages.

## 2. Materials and methods

### 2.1 Model description

A number of mathematical functions have been proposed that describe the sigmoid curve and have been used to model microbial growth (Akkermans and Van Impe, 2018; Dalsenter et al., 2005; Khoshdel and Mahmoodzadeh Vaziri, 2016; López et al., 2004; Teleken et al., 2011; Wade et al., 2016). In this paper, a system equation of microbe growth by two ordinary differential equations (ODE) was employed. The system ODE as follows:

$$\frac{\partial M(t)}{\partial t} = r(M).M(t) \quad (1)$$

$$\frac{\partial r(M)}{\partial M} = -\beta M^\alpha \quad (2)$$

where  $M(t)$  represents the cell density of microbe in Tilapia and  $r(M)$  defines the specific growth rate.  $\beta$  is a positive parameter, which is assumed to depend only on environmental variables and not on microbes in tilapia. The parameter  $\alpha$  is assumed to depend only on microbes in tilapia and not on environmental variables.

### 2.2 Experimental data

In this study, to determine the number of microbes in tilapia fish the total plate count (TPC) method was used. TPC method can be used to count cells that are still alive, determine the type of microbes that grow in the media and can be used to determine the type of microbial colony (Van Nevel et al., 2017). The data of microbe density of tilapia sausage is presented in Table 1.

Table 1. Data of microbe density in Tilapia

Time (day)	Cell Density of Microbe (CFU)
1	1.40 x10 <sup>4</sup>
4	5.90 x10 <sup>4</sup>
7	9.10 x10 <sup>4</sup>
9	1.10 x10 <sup>5</sup>
10	2.30 x10 <sup>5</sup>
11	4.40 x10 <sup>6</sup>
12	5.80 x10 <sup>6</sup>
13	8.00 x10 <sup>6</sup>
14	8.00 x10 <sup>6</sup>
15	1.50 x10 <sup>7</sup>

## 3. Results and Discussion

The experimental results were used to build mathematical model is presented in Table 1. Based on this table, a graph can be made of the relationship between  $\log M$  with the time of microbial growth in tilapia fish sausages. The graph is shown in Figure 1.

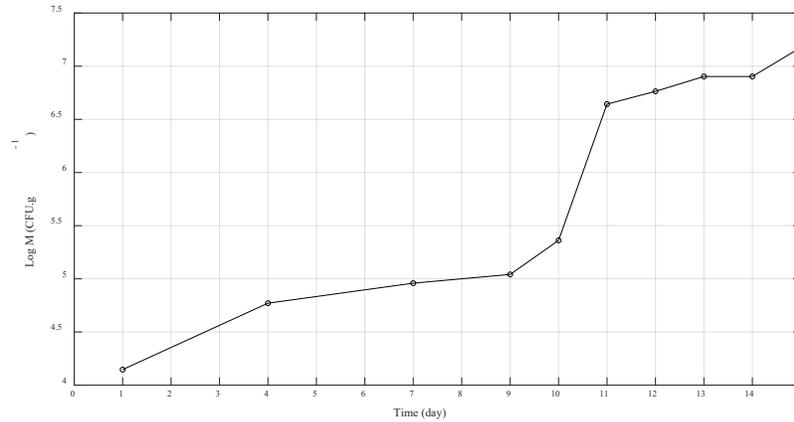


Figure 1. Microbial growth in tilapia sausage with log  $M$  unit.

Based on Figure 1, it can be seen that on days 1 to 9 is a lag phase of microbes where microbes do not occur significant growth. Then, starting on day 9 there was a significant microbial growth until saturation occurred. In this paper, a mathematical model of microbial growth in tilapia sausages will be made starting from a significant growth phase to saturation. In this paper,  $r(M)$  is the specific growth rate, and generally depends on the microbial population at time  $t$ . So that,  $r(M)$  in equation 2 is assumed linear at time  $t$ .

$$r(M) = a - bM(t) \quad (3)$$

Substitute equation 3 to equation 1, it can be produced:

$$\frac{\partial M(t)}{\partial t} = \{a - bM(t)\} \cdot M(t) \quad (4)$$

The maximum amount of microbial growth when  $\frac{\partial M(t)}{\partial t} = 0$ , these conditions will be fulfilled when  $M = 0$  and

$M = \frac{a}{b}$ . In order to find the solution of equation 4, integration can be done from the equation.

$$\int \frac{\partial M(t)}{\{a - bM(t)\} \cdot M(t)} = \int \partial t \quad (5)$$

In order to solve equation 5, the left part of the equation can be modified as follows:

$$\begin{aligned} \frac{1}{\{a - bM(t)\} \cdot M(t)} &= \frac{A}{M(t)} + \frac{B}{a - bM(t)} \\ &= \frac{Aa - AbM(t) - BM(t)}{\{a - bM(t)\} \cdot M(t)} \end{aligned} \quad (6)$$

Based on equation 6, we have the system equation as follows:

$$Aa = 1 \quad (7)$$

$$B - Ab = 0 \quad (8)$$

So that,  $A = \frac{1}{a}$  and  $B = \frac{b}{a}$ . Substitute these results for equation 6, so that it is obtained:

$$\frac{1}{\{a - bM(t)\} \cdot M(t)} = \frac{1}{aM(t)} + \frac{b}{a\{a - bM(t)\}} \quad (9)$$

So that equation 5 can be replaced as follows:

$$\int \frac{1}{aM(t)} \partial M(t) + \int \frac{a}{b} \frac{1}{a\{a - bM(t)\}} \partial M(t) = \int \partial t \quad (10)$$

Solve equation 10, it gets a solution as follows:

$$\frac{1}{a} \ln |M(t)| - \frac{1}{a} \ln |a - bM(t)| = t + C \quad (11)$$

In order to get the value of  $C$ , let's say the initial value of  $M(0) = M_0$ . So that,

$$C = \frac{1}{a} \ln |M_0| + \frac{1}{a} \ln |a - bM_0| \quad (12)$$

Substitute equation 12 to equation 11, it can be produce:

$$\frac{1}{a} \ln |M(t)| - \frac{1}{a} \ln |a - bM(t)| = t + \frac{1}{a} \ln |M_0| + \frac{1}{a} \ln |a - bM_0| \quad (13)$$

The two segments of equation 12 are multiplied by variable  $a$  then multiplied by  $\exp$ , it can be rearranged as follows:

$$\frac{M(t)\{a - bM_0\}}{M_0\{a - bM(t)\}} = e^{at} \quad (14)$$

Based on equation 14, it is obtained:

$$M(t) = \frac{a/b}{1 + \left[ \frac{a - bM_0}{bM_0} \right] e^{-at}} \quad (15)$$

Based on experimental data, the maximum microbial growth is  $7.2 \log \text{CFU.g}^{-1}$ , so that  $\frac{a}{b} = 7.2$ . Let's say

$z = \frac{a - bM_0}{bM_0}$ , so that equation 15 can be rearranged as follows:

$$\ln |z| - at = \ln \left| \frac{7.2 - M(t)}{M(t)} \right| \quad (16)$$

Let's say  $y = \frac{7.2 - M(t)}{M(t)}$ , equation 16 can be rearranged as follows:

$$y = -at + \ln |z| \quad (17)$$

Equation 17 shows the linear equation. In order to find the variable  $a$  and  $z$ , it can be solved by using linear regression. The variables used in this linear regression are  $y = \frac{7.2 - M(t)}{M(t)}$  and time  $t$  as show in Figure 2.

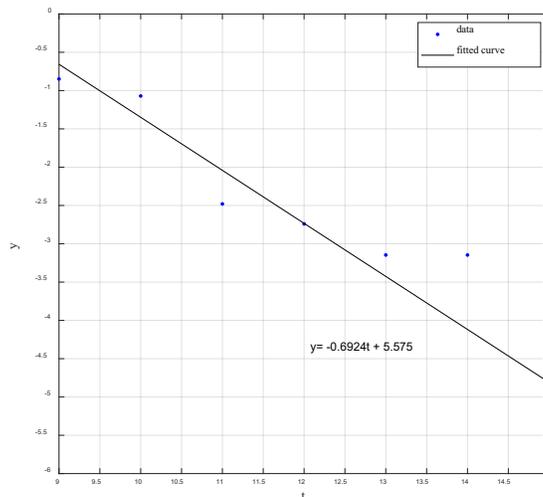


Figure 2. Linear regression between  $y = \frac{7.2 - M(t)}{M(t)}$  and time  $t$ .

Based on the results, it can be found that  $a = 0.6924$  and  $\ln |z| = 5.575$ ,  $z = 263.75$ . So that, the final mathematical model from microbial growth in Tilapia sausage after lag phase as follows:

$$M(t) = \frac{7.2}{1 + 263.75e^{-0.6924t}} \quad (18)$$

The validation of the mathematical model was performed with experimental data as shown in Figure 3. The mathematical model of microbial growth in Tilapia sausage has good agreement with experimental data. The accuracy of the model is 97.03%.

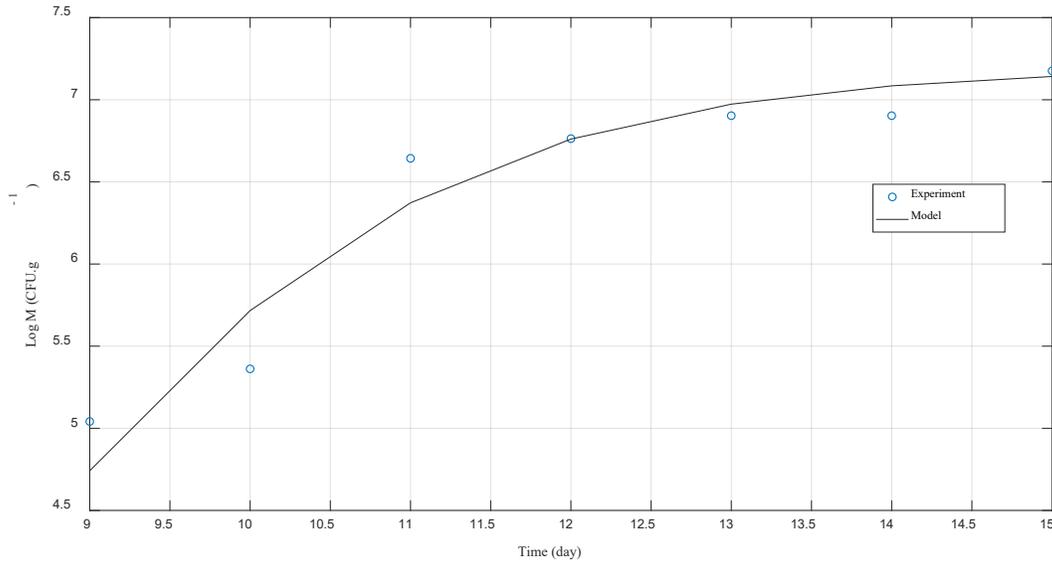


Figure 3. Microbial growth in tilapia sausage from experiment and model

#### 4. Conclusion

A mathematical model that describes microbial growth curves in Tilapia sausage was presented. A mathematical model of microbial growth in Tilapia sausage were validated with the experimental data. The error of estimation from this model is 2.97%. The results of validation showed good agreement between model and experiment. In this study, the equation developed is the equation of microbial growth after the lag phase. For further research, the development of mathematical models that involve all phases of growth of the microbial in Tilapia sausage need to be done.

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## Biographies

**Eddy Afrianto** is lecturer in the Department of Fishery, Faculty of Fishery and Marine Science, Universitas Padjadjaran. The field of post-harvest technology, with a field of fisheries microbiology.

**Subiyanto** is a lecturer in the Department of Marine Science, Faculty of Fishery and Marine Science, Universitas Padjadjaran. He received his Ph.D in School of Ocean Engineering from Universiti Malaysia Terengganu (UMT), Malaysia in 2017. His research focuses on applied mathematics, numerical analysis and computational science.

**Pramono Sidi** is a lecturer in the Department of Mathematics, Faculty of Sciences and Technology, Universitas Terbuka. The field of applied mathematics, with a field of concentration of financial mathematics and actuarial sciences.

**Abdul Talib Bon** is a professor of Production and Operations Management in the Faculty of Technology Management and Business at the Universiti Tun Hussein Onn Malaysia since 1999. He has a PhD in Computer Science, which he obtained from the Universite de La Rochelle, France in the year 2008. His doctoral thesis was on topic Process Quality Improvement on Beltline Moulding Manufacturing. He studied Business Administration in the Universiti Kebangsaan Malaysia for which he was awarded the MBA in the year 1998. He's bachelor degree and diploma in Mechanical Engineering which his obtained from the Universiti Teknologi Malaysia. He received his postgraduate certificate in Mechatronics and Robotics from Carlisle, United Kingdom in 1997. He had published more 150 International Proceedings and International Journals and 8 books. He is a member of MSORSM, IIF, IEOM, IIE, INFORMS, TAM and MIM.