

MATHEMATICAL MODELLING OF MICROBIAL GROWTH IN FOOD – PARAMETERS OPTIMIZATION

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ABSTRACT

Bacterial growth models are commonly used for the prediction of microbial safety and the shelf life of perishable foods. Growth is affected by several environmental factors such as temperature, acidity level and salt concentration. In this study a mathematical model to predict microbial growth in milk was developed and analyzed. Five different sets of data of microbial growth in dairy products were taken from combase and a model was prepared. And the results showed a good fit. In addition, the model provides maximum growth rate and the duration of the lag phase which may provide useful information about microbial growth. The fitting process was conducted using the computer software Origin 6.0.

KEYWORDS: Growth, Microbial and New Empirical Equation

INTRODUCTION

The predictability of bacterial growth is of major interest due to the influence of bacteria on food safety and health. The evolution of microorganisms in food products can spoil the products or even cause pathogenic effects. Foods are ecosystems composed of the environment and the organisms that live in it. In general, the growth of a homogeneous microbial population can be described by a curve with three phases if the death phase is excluded: a lag phase (adaptation period of microbial cells to their new environment) followed by an exponential growth phase (multiplication of cells exponentially) and finally a stationary phase (reaching to the maximum population density) (Isabelle et al., 2006). The need to ensure microbiological safety and quality of foods has increased the use of predictive microbiology, which is a powerful tool for predicting microorganism's growth rate under ambient conditions, and thereby determining its effective life under different conditions of time, storage temperature, pH, etc, during manufacture and distribution. One of the most frequently used mathematical models is that of Gompertz, which describes the microorganism response under different combinations of factors. This model permits the estimation of parameters, such as lag phase duration (LPD), specific growth rate (μ) and maximum p. Gompertz model [originally proposed by Gompertz (1825)] and its modified versions (Zwietering et al., 1990; Smith and Schaffner, 2004) were widely used to describe the sigmoid growth curves. The Baranyi and Roberts model (1994), which was derived from the logistic function, is also one of the widely used models, to describe isothermal and non-isothermal growth curves of microorganisms today. There are also some other, recently proposed, growth models (Van Impe et al., 2005; Poschet et al., 2005). While, all the mentioned models whether in their original or modified forms can be used, to fit isothermal growth data, none of them can be considered as unique. Moreover, "as many sigmoid growth curves can be described by mathematical expressions having only three adjustable parameters, the fit of above models (since, they have at least four adjustable parameters; depending on how you define the terms) should not come as a surprise" (Corradini and Peleg, 2005). The aim of this study was, to introduce a new empirical equation with

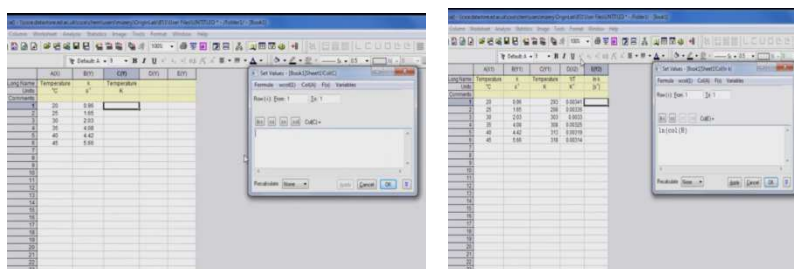
clearly interpretable parameters to be used to describe isothermal microbial growth.

MATERIALS AND METHODS

Mathematical modeling was used on focusing heat transfer and fluid dynamics but using the same mathematical modeling I will be focusing on microbial growth on food materials. For this data of 5 different microorganisms were taken from a database called Combase, using the Id codes.

- Zaika_98: *Shigella flexneri*
- Buchanan_91a: *Listeria monocytogenes*
- STU-BA: *Bacillus cereus*
- AFSCE: *Pseudomonas*
- FSA-CCFRA: *Yersinia enterocolitica*

Using the data from combase the fitting process was performed using the computer software Origin 6.0. The fitted parameters were used to determine the maximum growth rate, μ_{\max} , of each microorganism.

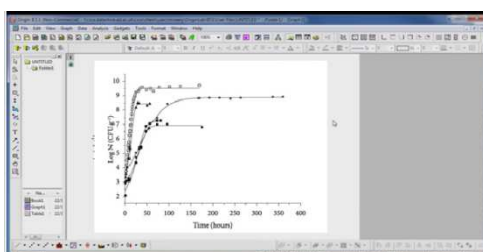


The calculations comprised the following steps:

- Experimental fit of the data from combase using the software Origin 6.0-curve-fitting.
- Fitted parameters are used to calculate μ_{\max} .
- Plotting the acceleration growth curve using the fitted parameters.

RESULTS AND DISCUSSIONS

Five microorganisms shows the determination coefficient to be higher than 0.99. That indicates a good fit.



microbes	N0	NF	m	u
Listeria	2.772	6.96	5.491	0.021
psedomonas	3.14	9.51	2.288	0.075
yersinia	3.769	8.86	3.549	0.012
sheigella	2.943	8.46	4.064	0.059
bacillus	2.311	7.27	3.934	0.028

Fitted mathematical model describing microbial growth curves in food product, A sharp presence of lag phase for some microorganisms were barely seen from the curve, However *Pseudomonas* and *Shigella flexneri* showed higher μ_{\max} values and the results showed good agreement between theory and experiment. In addition to other models found in

the literature, the model developed in this study estimates the biological parameters such as the lag phase duration, exponential phase duration, and the maximum specific growth rate. In the present study, it was proposed the use of a new parameter related to the amount of time it takes a population to increase to a given amount, which may be useful to the food industry.

REFERENCES

1. Gompertz B (1825). On the nature of the function expressive of the law of human mortality, and a new mode of determining the value of live contingencies. *Phil. Trans. Royal Soc. London* 115: 513-583.
2. Zwietering MH, Jongenburger I, Rombouts FM, Van'tRiet K (1990). Modeling of the bacterial growth curve. *Appl. Environ. Microbiol.* 56: 1875-1881.
3. Corradini MG, Peleg M (2005). Estimating non-isothermal bacterial growth in food
4. Poschet F, Vereecken KM, Geeraerd AH, Nicolai BM, Van Impe JF (2005). Analysis of a novel class of predictive microbial growth models and application to coculture growth. *Int. J. Food Microbiol.* 100: 107- 124.
5. Smith S, Schaffner DW (2004). Evaluation of the predictive model for *Clostridium perfringens* growth during cooling. *J. Food Prot.* 67: 1133- 1137.
6. Baranyi J, Roberts TA (1994). A dynamic approach to predicting bacterial growth in food. *Int. J. Food Microbiol.* 23: 277-294.
7. Van Impe JF, Poschet F, Geeraerd AH, Vereecken KM (2005). Towards a novel class of predictive microbial growth models. *Int. J. Food Microbiol.* 100: 97-105
8. Isabelle L, André L (2006). Quantitative prediction of microbial behaviour during food processing using an integrated modelling approach: a review. *Int. J. Ref.* 29: 968-984.

