

Growth inhibitory model of *Cronobacter sakazakii*.

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Introduction

C. sakazakii belongs to Enterobacteriaceae, mainly parasitic in the intestine of humans and animals [1]. When humans and animals infected by *C. sakazakii* can cause a series of diseases, such as neonatal meningitis, necrotizing colitis, bacteremia [2,3]. Medical studies have shown that antibiotics can be used to treat diseases, but it may cause some side effects. The lowest mortality rate for such diseases is 40%, the highest can reach 80% [4]. In 1961, the United States for the first time found meningitis by the infection of *Enterobacter sakazakii* [5]. After that, Belgium, Greece and other countries occurred in the case of *C. sakazakii* [6]. By using mathematical methods to describe the relationship between changes in the number of bacteria and external environmental factors under different environmental conditions is now conventional and effective.

The concept of predictive microbiology was first proposed by Scott in 1937, and Ross proposed "microbial prediction techniques" in the 1980s. In 1983, a microbiologist used computers to predict the shelf life of food, established a database of spoilage growth. Predicting the microbial model and the corresponding model parameters will enable the growth state of the microorganisms to be displayed in mathematical models and corresponding parameter forms [7]. And provide some guidance for the processing of food, storage and key control in the process of circulation [8,9]. As the research on microbes continues to increase, the prediction model of microbes is also increased accordingly. There are new and better data simulation models, and some early development of the data model. At present, the microbial prediction model can be divided into three categories, primary, secondary and tertiary model.

Primary Model

The primary model is a description of the relationship between the number and duration of growth of microorganisms under different external conditions. The growth curve of microbes generally includes three parts, lag phase, logarithmic phase, stationary phase, and the decline phase is not manifested in the data model.

Three primary growth models were used to describe *C. sakazakii* growth curves, which were the Huang model, Baranyi model and Gompertz model [10-13].

$$Y(t) = Y_0 + Y_{\max} - \ln \left\{ e^{Y_0} + \left[e^{Y_{\max}} - e^{Y_0} \right] e^{-\mu_{\max} B(t)} \right\} \quad (1)$$

$$B(t) = t + \frac{1}{\alpha} \ln \frac{1 + e^{-\alpha(t-\lambda)}}{1 + e^{\alpha\lambda}} \quad (2)$$

$$Y(t) = Y_0 + \mu_{\max} F(t) - \ln \left[1 + \frac{e^{\mu_{\max} A(t)} - 1}{e^{Y_{\max} - Y_0}} \right] \quad (3)$$

$$A(t) = t + \frac{1}{\mu_{\max}} \ln \left(e^{-\mu_{\max} t} + e^{-h_0} - e^{-\mu_{\max} t - h_0} \right) \quad (4)$$

$$Y(t) = y_0 + (y_{\max} - y_0) * \exp \left[-\exp \left[\frac{\mu_{\max}^e}{y_{\max} - y_0} (\lambda - t) + 1 \right] \right] \quad (5)$$

In equations 1-5, Y(t) represents the natural logarithm of bacterial counts (Ln CFU/g) at time t; Y0 is the initial bacterial counts (Ln CFU/g); Ymax is the bacterial counts (Ln CFU/g) at the stationary phase; μ_{\max} is the specific growth rate (h⁻¹); λ is the lag phase duration (h). h0 reflects the physiological state of the microorganism. The parameter α (=4) is a coefficient used to define the transition from the lag phase to exponential growth curve [14].

Prospective

Food additives are often used in food processing to inhibit the growth of microorganisms. Traditional antimicrobial chemicals such as potassium sorbet have good antimicrobial utility, but they possess potential side effects, and their use is also limited. Scientists are increasingly accepting natural antibacterial agents as an alternative to the processing and production of food [15]. With the development of science, the level of medical progress, more and more antibiotics and drugs in the course of treatment has been widely used, leading to increased resistance to bacteria, seriously affecting the human and animal health [16]. Natural antibacterial agents are considered to be effective and safe antibacterial agents, with both nutritional value and other effects. Therefore, the search for antimicrobial substances from natural product is one of the hotspots of current international research. Predictive microbiology provides strong theoretical support for food production, processing, hazard analysis, and safety control [17-21]. The use of microbiology, mathematics, statistics, combined with computer software to build the model.

Author Contributions

All authors have given approval to the final version of the manuscript.

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