Research Article
Establishment and Development of Computer Simulation Model on Fruit and Vegetable Microbial Fermentation Process

Yonghua Zhang
Shijiazhuang University of Economics, Shijiazhuang, China

Abstract: This study aims to develop a set of computer simulation model on fruit and vegetable microbial fermentation process. The existing data is used to model the decomposition process of the fruit and vegetable through the ordinary differential equation. The model is validated through the mathematical simulation software MATLAB and the experience shows that the method can truly reproduce the decomposition process of the fruit and vegetable under different circumstances. The research can provide an important technical means for the preservation and corrosion prevention of fruit and vegetable.

Keywords: Computer simulation model, MATLAB, microbial fermentation

INTRODUCTION

In 1857, the microbiologist L. Pasteur confirmed that the fermentation process of the alcohol. With the long-term research, he laid the foundation of microbiology, solved the major loss problem brought by the deterioration of the wine on the brewing industry in France at that time and created Pasteurization. The sterilization method is still used in the sterilization of wine, vinegar, soy, milk, fruit juice and other foods nowadays. Since the 20th century, the invention of electron microscopy and the development of the biochemistry and chemical analysis and other disciplines have promoted the microbiology to enter into the molecular level from the cellular level and sub-cellular level (Gobbetti *et al*., 2010). Especially the development of genetic engineering science in the 1970s vigorously promoted the development of food microbiology. The high-yielding microorganism fine strain for fermented food bred through the mutagenesis, cell fusion and other technologies can increase the production and change the feature of food industry. Reducing the bacterial contamination and extending the shelf life of the food have been the issues commonly concerned by the food industry (Davis, 2008). The food is nutritious and it is easily to be corrupted in the processing, transportation, storage and sales process. Generally speaking, the fruit and vegetable contain a large number of water, carbohydrate, rich vitamins and a certain amount of protein (Peilong and Yipeng, 2013). The pH of most fruits is below 4.5, while that of vegetable is 5.0-7.0. These factors determine that the bacterial effect is the most obvious among the multiple factors deciding the decomposition of fruit and vegetable. The annual decomposition of fruit and vegetable caused by the microorganism brings great economic losses for the whole world.

It is predictable that through the establishment with computer simulation model, the shelf life of fruit and vegetable under different physical and chemical conditions can provide an important means for the corrosion prevention of the food. Conducting the corrosion-prevention test through simulation technology can shorten the test cycle, save the money, timely amend or adjust the experiment situation. Moreover, it can help establish an objective standard to design and evaluate the fruit and vegetable for the processing plant. The establishment of dynamic model in the study can provide an important tool for the preservation and corrosion prevention of the food.

METHODS AND MODEL

Regression model is based on the mathematical statistics and it is obtained through the quantitative analysis according to a large number of experimental data and empirical formulas. Meanwhile, due to the experimental condition, experimental method and human factor, it is hard for the regression model to predict the growth of food microorganism in the actual production sector; However, the dynamical model is based on the dynamics, which can deal that all variables must occupy the actual possible value under all conditions of temperature, pH, water activity along with the time change in the continuous method, therefore, it can better predict the growth of microorganism in food. The paper has collected the best fitting Gompertz model and modified model in the microbial growth and established the corresponding dynamic model.

Due to the feature that the unicellular microorganism shows the exponential growth, the

logarithm time of relative cell number [$X = \ln (N/N_0)$] can obtain a S-shaped curve. The formula is (1):

$$\log N = \log N_0 + A \times \exp\{-\exp[\frac{U \times e}{A}(M-t)+1]\} \quad (1)$$

wherein, N is the biomass of the microorganism in time t, N_0 is the biomass when $t = -\infty$ (approximately equivalent to the initial number of bacteria when t = O), A is log N/N_0 when $t = +\infty$ and it is the corresponding value when N is maximum, U is growth rate (day-1) and M is the time (day) needed to reach the relatively maximum growth rate. The parameters with microbiological significance shall be replaced by the following formula (2):

$$x = a \times \exp[-\exp(b-ct)] \quad (2)$$

When $a = A; b = (\mu_m e / A) \times \lambda + 1; c = \mu_m e / A$

The modified Gompertz equation is formula (3):

$$Y = A \times \exp\{-\exp[(\mu_m e / A) \times (\lambda - t)+1]\} \quad (3)$$

wherein,
μ_m = The maximum specific growth rate
λ = The time of lag phase

Temperature is an important factor influencing the growth of microorganism, the growth temperature for the microorganism in general food is 0-40°C, Ratkowsky and others propose an empirical model according that the growth rate or the reciprocal of lag phase exists the linear relationship under the temperature condition formula (4):

$$\mu_m = b_1^2 (T - T_{\min})^2$$
$$1 / \lambda = b_1^2 (T - T_{\min})^2 \quad (4)$$

wherein,
b_1 = The coefficient ($C^{-1}/h^{0.5}$)
T = Culture temperature (°C)
$T_{\min}$ = The lowest growth temperature (°C)

pH is also an important factor influencing the growth of microorganism. Zwietering and others hold the Ratkowsky equation can be adopted:

$$\mu_m = b_2^2 (pH - pH_{\min})^2 \quad (5)$$

wherein,
b_2 = The coefficient
pH = Represents that in the environment
$pH_{\min}$ = The lowest pH value for the growth of microorganism

In addition to the above factor, the water activity A_w and μ_m square root also exist the linear relationship:

$$\mu_m = b_3^2 (Aw - Aw_{\min})^2 \quad (6)$$

wherein,
b_3 = The coefficient
Aw = Water activity
$Aw_{\min}$ = The minimum water activity

The establishment of dynamic model is as follows: according to the Eq. (1), the derivative can be obtained through x to the time t and it can obtain:

$$dx / dt = a \times \exp[-\exp(b-ct)][-\exp(b-ct)](-c)$$
$$= c \times y \ln(a / y) \quad (7)$$

According to the formula (2), we can obtain:

$$x = a \times \exp\{-\exp[(\mu_m e / a) \times (\lambda - t)+1]\}$$
$$= a \times \exp\{-\exp(e / a + 1 - \mu_m et / a)\} \quad (8)$$

The derivative can be obtained through x to the temperature T and it can obtain formula (9):

$$dx / dT = a \times \exp\{-\exp(e / a + 1 - \mu_m et / a) \times [-\exp(e / a - \mu_m et / a + 1)]$$
$$\times (e / a - \mu_m et + 1)\}$$
$$= x \times [-\exp(e / a - \mu_m et / a + 1)](-et / a) \times \mu_m$$
$$= x \times (\ln y - \ln a) \times (-et / a) \times [b_1^2 (T - T_{\min})^2]$$
$$= (2b_2^1 et / a) \times (T - T_{\min}) \times y \ln(a / y)$$
$$(9)$$

Similarly, the derivative can be obtained on pH and Aw according to the Eq. (5) and (6) and it can obtain:

$$dx / dpH = (2b_2^2 et / a) \times (pH - pH_{\min}) \times x \ln(a / x) \quad (10)$$

$$dx / dAw = (2b_3^2 et / a) \times (Aw - Aw_{\min}) \times x \ln(a / x) \quad (11)$$

For most microorganisms, it is hard to determine the function relationship between the growth rate and the oxygen, therefore, the microorganism in the food can be divided into the aerobic and anaerobic classes. The established model group adopts four-stage Runge-Kntta method to seek the numerical solution, the parameter shall be determined here. When considering four environmental factors of temperature, pH, water activity and oxygen, assuming they are independent, taking the determination of b_2 and $pH_{\min}$ as an example: if the temperature, water activity and preservative remain unchanged, the research on the influence of pH on most salmonella growth can adopt the Eq. (5) to measure the salmonella growth rate when pH is 5.4, 5.8, 6.0, 6.5, 7.0. b_2 and $pH_{\min}$ can be analyzed and determined with linear regression.

The similar method can be used to determine b_1, $T_{\min}$, b_3 and $Aw_{\min}$.

EXPERIMENT AND RESULTS

Through the experiment in the laboratory, the microorganism type in the product can be determined and the dominant bacteria in the product can be determined through comparing and analyzing the microorganism in these types. Through the experiment on the growth and reproduction situation of main micro-flora under different times and different temperature conditions, a large number of experimental data can be obtained and formed a microbial database (Demarigny, 2012). Through the pilot study in the huge mathematical models, the best mathematical model fitted with the colony growth situation can be determined. Inputting the microbial database in the computer and evaluating the parameter in the mathematical model with the function library in MATLAB can obtain the simulated function library. The simulated function can be called by other programming language in order to form a more friendly human-computer interface and rapidly predict the microbial in the product.

For MATLAB software system is very huge, it will occupy a large number of hard disk space after completing the installation and it is not conducive to the use of non-professional developer, therefore, MATLAB also provides a good program calling interface chao for other different software development system. Combined with VC 6.0 software development system, the implementation process of user program development can be offered. With VC 6.0 application framework, MFC 4.2 can quickly generate the user interface and the programmer only needs to focus on the processing and display of the data. For MATLAB has dealt with the experimental data, the programmer only needs to conduct how to call the dynamic link library and manage the mathematical model database and the final result can be displayed with the user-friendly manner. In this way, it can greatly reduce the burden of the programmer, shorten the development cycle and it is easy for the software maintenance and upgrade. Meanwhile, VC is a Microsoft product closely connected with Windows, therefore, the developed program can achieve the cross-platform usage in Win9x, Win200 and Winxp system (Wu *et al.*, 2012).

In the simulation process, the most critical is to determine the mathematical model. Using the existing huge function library in MATLAB can rapidly fit the data, thus mutually connecting the experimental data with extrapolation and broad predictability.

It is easy to use and learn MATLAB, such as MATLAB code simulates the Compertz and "square root":

```
% construct Gompertz function:
LogN = A×exp {—exp [-B (t—M)]} +LogN0
```

```
function y = Gompertz (x0 step_time)
y = x_0 (1) ×exp {-exp [—x_0 (2) ×a]} +x_0 (4)
Wherein, a = step_time—x_0 (3).
% use Levenberg Marquardt algorithm to fit
Gompertz function:
Options = Optimset ("Levenberg Marquardt", "on")
x = lsqcurvefit ('Gompertz', x_0 step_time, input X)
y = Gompertz (x, step_time)
```

Wherein, input X is the number of bacteria related with time obtained from the experiment, x_0 is the initial number of bacteria, step_time is the fitting step size. Seen from the code, MATLAB can set different algorithms and fit any function.

The experiment can prove that the MATLAB can simulate and realize the prediction and forecast process of microbial model in the computer. On one hand, it can rapidly obtain an important reference data, on the other hand, it can provide an objective standard for the measurement to help the scientific researcher and manager to design and evaluate the product. Through the simulation, it can also save the money and shorten the test cycle. Meanwhile, compared with other development software, MATLAB has a good program interface, MATLAB function library can be easily called by other development softwares, thus forming a more convenient and practical user interface and becoming user-friendly.

CONCLUSION

Combined with the microbial fermentation feature of fruit and vegetable and existing empirical models, this study adopts the method of ordinary differential equation and establishes the dynamic mathematical model on the influence of the environmental factors of temperature, pH and water activity on the food microbiology growth. The established dynamic mathematical model can be used to predict the total bacterial count, food storage time and food preservation temperature under certain parameters. The algorithm is validated through MATLAB and the experiment can show that the method can simulate the microbial fermentation process of fruit and vegetable under different conditions, thus providing an important technical means for the preservation and corrosion prevention of fruit and vegetable.

REFERENCES

Davis, R.A., 2008. Parameter estimation for simultaneous saccharification and fermentation of food waste into ethanol using Matlab Simulink. Appl. Biochem. Biotech., 147(1-3):11-21.

Demarigny, Y., 2012. Fermented food products made with vegetable materials from tropical and warm countries: Microbial and technological considerations. Int. J. Food Sci. Technol., 47(12): 2469-2476.

Gobbetti, M., R. Di Cagno and M. De Angelis, 2010. Functional microorganisms for functional food quality. Crit. Rev. Food Sci., 50(8): 716-727.

Peilong, X. and S. Yipeng, 2013. Study on fresh keeping effect of chitosan antistaling agent for several kinds of fruits. Adv. J. Food Sci. Technol., 5(12): 1577-1579.

Wu, H., S.A. Tassou, T.G. Karayiannis and H. Jouhara, 2012. Analysis and simulation of continuous food frying processes. Appl. Therm. Eng., 53(2): 332-339.