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A suitable model of microbial survival curves for beer pasteurization

Sencer Buzrul*

Food Engineering Department, Middle East Technical University, 06531 Ankara, Turkey

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Abstract

Published isothermal inactivation data indicated that beer can undergo under- or over-processing depending on the target log reduction and the shape of the survival curve of a microorganism if traditional first-order model is used. This was demonstrated for a mold, yeasts and lactic acid bacteria by use of a more flexible and convenient model than the first-order model, namely Weibull model. The parameters of the Weibull model can be reduced from two to one with a very a slight loss of goodness-of-fit. The validity of the proposed model should also be checked for mixed populations of microorganisms in beer and non-isothermal treatments for beer. Beer can be the first product to validate the proposed model in industrial base since it has been free from problems with pathogenic microorganisms. If the model provides the requirements then it can also be used in other food products. This will minimize the energy expenditure for pasteurization and provide minimal processing to achieve a better food quality.

Keywords: Beer; Under-processing; Over-processing; Weibull; First-order model; Minimal processing

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1. Introduction

Beer is the one of the most consumed beverage in the world and it continues to be a popular drink. The brewing industry has an ancient tradition, but it is a dynamic sector open to modern technology and scientific progress. Brewers are very concerned that the finishing techniques they use are the best in terms of product quality, safety and cost effectiveness (Buzrul, Alpas, & Bozoglu, 2005a).

The microbial stability of the final product is achieved by heat pasteurization. The stability of the final product up to several months can be provided if beer spoilage organisms are inactivated. Currently, heat treatment is either done by flash pasteurization, where beer is first pasteurized and then packaged aseptically usually into metal kegs, or by tunnel pasteurization, in which beer is first filled into sterile glass bottles and then pasteurized through tunnel pasteurizers (Buzrul, 2003; Buzrul et al., 2005a).

The commercial rule of thumb has been to use a time–temperature relationship of 15 min at 60 °C i.e., 15 pasteurization units (PU), where 1 PU is defined as exposure to 60 °C for 1 min. Nevertheless, even though the cycle of pasteurization (heating up, holding, and cooling down) is fully understood and fully considered in the use of lethality curves and pasteurizer recorders to assess killing before and after attainment of the maximal temperature, a wide variance occurs in the temperature of pasteurization and numbers of PUs used among the breweries. Although laboratory tests indicate that values from 1 to 5 PU are effective in achieving commercial sterility, 8–30 PU are generally used, perhaps to have a built-in safety factor in case of possible resistant contaminants (Tshang & Ingledew, 1982) and although the thermal process applied in beer pasteurization is a low-temperature process, it is desirable to apply the minimal thermal process in order to reduce undesirable organoleptic changes (adverse effect of heat on beer flavor, reduction of carbon dioxide solubility due to heat etc. ...) in the final product (Reveron, Barreiro, & Sandoval, 2005) and to minimize the energy expenditure for pasteurization of beer (Tshang & Ingledew, 1982).

The objective of this study is to demonstrate over- and under-processing of beer during isothermal heat treatments by using a more flexible and convenient model than the traditional first-order model, and therefore give a new idea

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*Corresponding author. Tel.: +90 312 210 5625; fax: +90 312 210 2767.
E-mail address: sbuzrul@metu.edu.tr.

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to the brewers in order to obtain minimally processed beer.

2. Materials and methods

Survival curves of different microorganisms in beer published by L'Anthoën and Ingledew (1996); Reveron et al. (2005) and Tshang and Ingledew (1982) served as the database for this study. The data were scanned and digitized using a software program WinDIG 2.5 (written by Mr. Dominique Lovy, Geneve, Switzerland). The parameters of the models were obtained by linear and non-linear regression using the SigmaPlot 2000 Version 6.00 (Chicago, IL, USA).

2.1. The model

It has been theorized that at constant temperature the inactivation of bacteria is exponential with time i.e., first-order kinetics. Many thermal processing calculations used in food processing are based on this assumption. The model results in the following equation:

$$\log_{10} S(t) = -\frac{t}{D(T)}\ (t \geqslant 0), \tag{1}$$

where $S(t)$ is the survival ratio which is defined as the ratio between the number of survivors after an exposure time t, $N(t)$ and the initial number, N_0, i.e., $S(t) = N(t)/N_0$. $D(T)$, is the temperature-dependent D value or decimal reduction time; time required for one log reduction in number of cells.

According to this model, all the cells in a population have equal time-independent probability of mortality (Buzrul, Alpas, & Bozoglu, 2005b). A plot of $\log_{10} S(t)$ versus heating time will be linear. D values are usually determined by calculating the negative slope's reciprocal of the best-fit line using least-squares linear regression procedure (Linton, Carter, Pierson, & Hackney, 1995).

Different forms of the Weibull model were presented in literature (Buzrul & Alpas, 2004; Peleg, 2002; van Boekel, 2002); however, decimal logarithm form (Eq. (2)) seems suitable since its parameters have physical significance (Couvert, Gaillard, Savy, Mafart, & Leguérinel, 2005).

$$\log_{10} S(t) = -\left(\frac{t}{D_1(T)}\right)^{n(T)}. \tag{2}$$

The parameter $D_1(T)$ is the temperature-dependent-scale parameter (it was called transformed scale parameter by Collado, Fernández, Cunha, Ocio, and Martinez (2003)) and it represents the first reduction time that leads to a 10-fold reduction of the surviving population (i.e., time required to reduce the number of cells from N_0 to $N_0/10$) regardless of the value of the parameter $n(T)$ which is the temperature-dependent shape parameter.

Such a model presents the main advantage of being very simple and sufficiently robust to describe both monotonic downward concave (shoulder) survival curves ($n > 1$) and monotonic upward concave (tailing) survival curves ($n < 1$). Traditional first-order model (Eq. (1)) is then a special case ($n = 1$) of the Weibull model.

Although the Weibull model (Eq. (2)) is a simple and flexible model to describe microbial inactivation, it has two major drawbacks: First, assessment of parameters requires a non-linear regression. Secondly, n value is structurally strongly correlated with D_1 values. That is to say, both parameters are dependent; an error on D_1 will be balanced by an error on n in the same way. Such an autocorrelation causes certain instability of parameter estimates (Mafart, Couvert, Gaillard, & Leguerinel, 2002). In addition, the Weibull model (Eq. (2)), with one more parameter, is intrinsically more complex than the traditional first-order model (Eq. (1)); (Chen & Hoover, 2004). Thus, it seems worthwhile to fix n value characteristic to a strain for the overall data (whole set of kinetic for each microorganism), so that D_1 values can be estimated from a linear regression (Mafart, et al., 2002). Therefore, Eq. (3) was proposed for non-linear survival curves of microorganism (Chen & Hoover, 2004; Corradini, Normand, & Peleg, 2005; Mafart et al., 2002; van Boekel, 2002):

$$\log_{10} S(t) = -\left(\frac{t}{D_1(T)}\right)^{n_{\text{fixed}}}, \tag{3}$$

where n_{fixed} is a constant.

3. Results and discussion

The survival curves of *Aspergillus niger* are shown in Fig. 1. The dashed lines indicate data were fitted with the Weibull model with a variable $n(T)$ (Eq. (2)), solid lines indicate data were fitted with the reduced Weibull model with a fixed n ($n_{\text{fixed}} = 1.2$ for *A. niger*) (Eq. (3)). The figure demonstrates that the degree of fit was comparable and therefore the reduced model, i.e., with a fixed power n

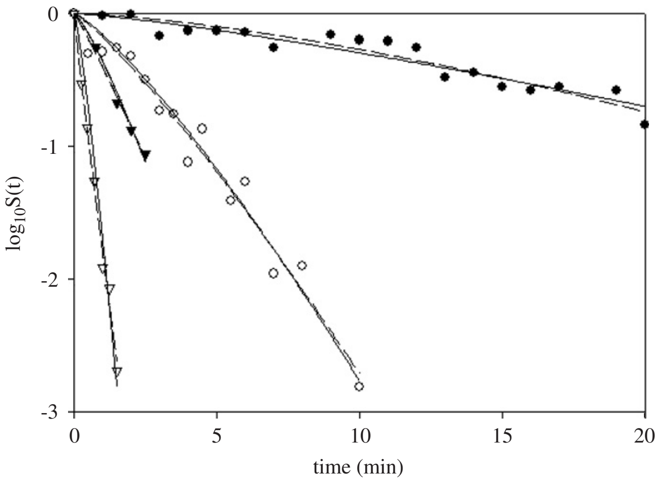

Fig. 1. Isothermal inactivation curves of *Aspergillus niger* in beer: (●), 50; (○), 52; (▼), 54; (▽), 56 °C; dashed lines indicate data were fitted with the Weibull model (Eq. (2)) with a variable n, solid lines indicate data were fitted with the reduced Weibull model (Eq. (3)) with a fixed n ($n_{\text{fixed}} = 1.2$ for *A. niger*) (Data source: Reveron et al., 2005).