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A modified Gompertz model to predict microbial inactivation under time-varying temperature conditions

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Abstract

Development of effective heat treatments is crucial to achieve food products' safety, and predictive microbiology is an excellent tool to design adequate processing conditions.

This work focuses on the application of a modified Gompertz model to describe the inactivation behaviour under time-varying temperature conditions at the surface of a food product. Kinetic studies were carried out assuming two different heating regimes, typically used in surface pasteurisation treatments, and compared with isothermal conditions. Parameters were estimated on the basis of generated pseudo-experimental data. It was concluded that the heating period greatly affects microbial inactivation and parameter estimation. If a slow heating treatment is used, the process time should be extended to achieve a given microbial load when compared to a fast heating process. This is explained by the fact that, in the slow heating rate process the temperature was below the lowest temperature for inactivation for a much longer time, in comparison with the fast heating regime.

Keywords: Predictive microbiology; Gompertz model; Inactivation kinetics; Time-varying temperature

1. Introduction

The bacterial spoilage of foods and the survival of pathogens are of major importance to the food process industries, because it directly affects the consumer's health and safety. As the critical boundary for contamination is the exposed surface, heat treatments at food surface can be an effective mean of controlling pathogens. This makes effective surface pasteurisation systems critical to produce safe products (Kozempel, Goldberg, Radewonuk, & Scullen, 2000). Consequently, thermal decontamination must be designed to provide an adequate margin of safety against food-borne pathogens. However, it is difficult to determine the exact amount of microbial inactivation when these treatments are applied (James & James, 1997). Kinetic models are mathematical expressions that relate a particular measured response with time, under specific environmental conditions. In predictive microbiology (Roberts & Jarvis, 1983), these models should be developed to predict the behaviour of pathogens or spoiling microorganisms populations under stress factors (e.g., high temperature, particular ranges of pH and a_w), precisely and accurately, being of main importance for the food industry in the development of reliable surface pasteurisation systems. Nevertheless, modelling microbial kinetics, that lead to reliable predictions of safety and shelf life of foods, is only recently used (MacDonald & Sun, 1999). An overview of the models used in literature to describe microbial inactivation was done by Xiong, Xie, Edmondson, Linton, and Sheard (1999). Those models describe linear and non-linear curves, with lag and/or tailing phases. Among non-linear models, the Gompertz equation and its modified forms have been successfully applied to describe inactivation of *Listeria monocytogenes* at isothermal conditions (Bhaduri et

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Nomenclature

a	parameter of the relationship of L with T (s)	T	temperature (K)
b	parameter of the relationship of L with T (K^{-1})	T_{ref}	reference temperature (K)
c	parameter of the relationship of k with T (s^{-1} K^{-2})	*Greek symbols*	
d	parameter of the relationship of k with T (K)	ε	error term
e	level of the pseudo-experimental error	*Subscripts*	
N	microbial cell density (cfu g^{-1})	exp	pseudo-experimental value
N_0	initial microbial cell density (cfu g^{-1})	sim	simulated value
N_f	residual microbial cell density (cfu g^{-1})	*Abbreviations*	
K	maximum inactivation rate constant (s^{-1})	cfu	colony forming unit
L	time parameter or shoulder (s)	MSE	mean sum of squares of the residuals
R^2	coefficient of determination	SHW	standardised half width (%)
t	time (s)		
t'	dummy variable		

al., 1991; Linton, Carter, Pierson, & Hackney, 1995; Linton, Carter, Pierson, Hackney, & Eifert, 1996; Xiong et al., 1999).

Actually, the majority of predictive approaches are based on un-realistic isothermal conditions (Peleg, Penchina, & Cole, 2001; Reichart, 1994). Yet, it is well known that temperature may vary extensively throughout the complete process. The kinetic parameters, estimated under time-varying temperature conditions, may differ from the ones predicted at constant temperatures. Using the later ones, in situations in which the temperature varies with the time, may affect the predictive ability of the model. This can be particularly important when the safety of a product is the final goal. In order to appropriately describe the real microbial behaviour, surface thermal models should be designed to include the variations of temperature along the total process time. This could be enhanced by the numerical integration approach. A non-isothermal kinetic model was developed by Van Impe, Nicolaï, Martens, De Baerdemaeker, and Vandewalle (1992) by differentiating a modified Gompertz equation with respect to time, in combination with an Arrhenius-type equation to describe the microbial load as a function of both time and temperature. Geeraerd, Herremans, and Van Impe (2000) also referred the need of applying differential equations, as well as the design requirements, and compared the most relevant models used to describe the inactivation microorganisms kinetics under time-varying environmental conditions.

The objective of this work was to develop a model to predict the survival of microorganisms on the surface of a food product, able to deal with typical temperature profiles during air surface decontamination treatments. The Gompertz model was applied by differentiating the isothermal model with respect to time. The regression procedure was tested using pseudo-experimental data generated considering time-varying temperature conditions. The influence of the heating period on microbial inactivation was also studied.

2. Model description

The mathematical model used to describe inactivation of microorganisms was based on modifications of the Gompertz equation (Zwietering, Jongenburger, Rombouts, & Van't Riet, 1990). The inactivation model considered, valid for isothermal conditions, is:

$$\log N = \log N_0 - \log\left(\frac{N_0}{N_f}\right) \times \exp\left(-\exp\left(\frac{k\exp(1)}{\log\left(\frac{N_0}{N_f}\right)}(L-t)+1\right)\right) \quad (1)$$

Herein, N represents the microbial cell density at a certain process time (t), L is the time parameter (or shoulder) and k the maximum inactivation rate constant. N_0 and N_f are the initial and residual microbial cell density, respectively.

By differentiating Eq. (1) with respect to time, one can generally obtain an expression applicable for time-varying temperature conditions:

$$\log N = \log N_0 - \int_0^t \left[k\exp(1)\exp\left(\frac{k\exp(1)}{\log\left(\frac{N_0}{N_f}\right)}(L-t')+1\right) \times \exp\left(-\exp\left(\frac{k\exp(1)}{\log\left(\frac{N_0}{N_f}\right)}(L-t')+1\right)\right)\right] dt' \quad (2)$$