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Review Article

Quantitative prediction of microbial behaviour during food processing using an integrated modelling approach: a review

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Abstract

Microbiological safety of food relies on microbial examination of raw materials and final products, coupled with monitoring process parameters and hygiene standards. The concept of predictive microbiology was developed to evaluate the effect of processing, distribution and storage operations on food safety. The objective of this paper is to review the approaches proposed by researchers to quantify the effect of competitiveness or fluctuating conditions on bacterial behaviour. The main microbial models that quantify the effects of various hurdles on microbial kinetics are presented. To provide complementary information for microbial models, three areas have to be considered: process engineering that characterises and models mass and heat transfer; microbiology that characterises and models bacterial behaviour and metabolite production, and; applied thermodynamics that characterises and models the physico-chemical properties of a food product. Global modelling approaches, developed by integrating the previous models, are illustrated with recent results.

Keywords: Food; Manufacturing; Chilling; Modelling; Growth; Survival; Bacteria; Microbiology

Prévision quantitative du comportement microbiologique lors du traitement des produits alimentaires employant une approche intégrée de la modélisation: bilan

Mots clés : Produit alimentaire ; Fabrication ; Réfrigération ; Modélisation ; Croissance ; Survie ; Bactérie ; Microbiologie

1. Introduction

Traditionally, the microbiological safety of food has always relied on microbial examination of raw materials and final products, coupled with monitoring process parameters and hygiene standards. Challenge tests or inoculated pack experiments were established to simulate the effects

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of environmental conditions on food, in terms of growth and proliferation of spoilage and pathogenic microorganisms [1]. They can provide useful data for determining the safety and shelf life of food under a set of conditions. At the same time, HACCP (Hazard Analysis and Critical Control Point) was developed to help anticipate and identify potential microbial hazards in order to select those procedures or processes in the production system that prevented or controlled the hazard. HACCP can be considered as a better alternative to conventional inspection and end-product testing but information is needed on:

- product formulation, the microbial profile of the raw product, its pH and water activity (a_w), the presence of additives: are these factors capable of preventing bacterial growth?
- process steps: how does each step influence the contamination, survival, inhibition or growth of microorganisms?
- distribution and consumption conditions: how do they modify the quality and the safety of the products?
- means to control the process and the contamination level.

To answer these questions, it is necessary to better understand the responses of the microorganisms to the key controlling factors in the food environment, to build a cumulative knowledge base and to develop the means to interpolate calculated microbial responses [2]. The concept of predictive microbiology was developed to evaluate the effect of processing, distribution and storage operations on the microbiological safety of foods [3]. It uses mathematical models that correlate bacterial growth or death response to the environmental conditions of the food. Despite the progress made by predictive microbiology, some aspects have not been totally considered: competition between microorganisms in food or fluctuating conditions. During a process, environmental conditions may vary as a function of time or space in the food due to diffusion phenomena (heat and mass transfers). The prediction of conditions that prevent growth in such complex situations is not easy. Additional information is needed on how the competitive bacteria or the variables that control the process and the food affect the main environmental parameters (temperature, pH and a_w) used in predictive microbial models. Such information cannot be obtained through predictive microbiology alone. Mathematical models that integrate both heat or mass transfer phenomena and dynamic bacterial growth are rarely found in scientific literature [4].

The objective of this paper is to review the approaches proposed by researchers to quantify the effect of competitiveness or fluctuating conditions on bacterial behaviour. First, the mathematical microbial models that describe and quantify the effects of various hurdles on microbial growth kinetics are given in Section 2. Section 3 then presents the models that will provide complementary information for predictive bacterial models. Examples of integrative modelling approaches are presented in Section 4.

2. Predictive microbiology models

2.1. Introduction

A predictive food microbiological model is a mathematical expression that describes the growth, survival, inactivation or biochemical process of a microorganism. MacDonald and Sun [1] proposed a classification scheme of the models according to Whiting and Buchanan [5] (Table 1). Primary models describe the change of the bacterial number over time under environmental conditions and generate information about the microorganism such as generation time and lag phase duration. Secondary models describe the evolution of one or more parameters of a primary model in relation to one or more changes in environmental conditions. Tertiary models take modelling to its final form. They are applications to one or more primary or secondary models, incorporated into a user-friendly computer software package [1].

2.2. Primary models

2.2.1. Growth

In many cases, the growth of a homogeneous microbial population can be described by a curve (Fig. 1) with three phases: a lag phase during which the microbial cells adapt to their new environment, followed by an exponential growth phase during which the cells multiply exponentially and, finally, a stationary phase during which the maximum population density is reached. Environmental conditions, food composition and growth status of the microorganisms (lag, exponential, stationary phase) can affect the growth rate (Table 2). They are not the only sources of variations: strains of a same genus may grow differently under the same intrinsic and extrinsic conditions.

Historically, Malthus [6] developed the first model of population dynamics, followed by Verhulst [7], who introduced the logistic model. During the last decade, a large

Table 1
Classification of some models used (derived from MacDonald and Sun [1])

Primary models	Secondary models	Tertiary models
(modified) Gompertz function	Response surface models	Pathogen Modelling Programme
Logistic model	(modified) Arrhenius model	Growth Predictor
Baranyi model	Square root models	*Pseudomonas* Predictor
Rosso model	γ-models	Seafood spoilage and Safety Predictor
(modified) Monod model	*z* values	ComBase
D values of inactivation		Sym'Previus