

9th International Conference on Predictive Modelling in Food

Predicting the behaviour of *Yersinia enterocolitica* and *Listeria monocytogenes* in Italian style fresh sausages under drying period

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Abstract

Italian style fresh sausage is a traditional pork product that is frequently consumed raw, usually after drying. So far, the prediction of the behaviour of microorganisms in varying environments has been carried out through separate growth or death models. The aim of this study is to show how to combine these, in order to describe the kinetics of *Yersinia enterocolitica* and *Listeria monocytogenes* in sausage during the drying period.

During this time, the storage temperature and the pH are fairly constant, while the water activity decreases, being the primary cause of shifting the organisms' kinetics from growth to inactivation. The water activity takes up values from growth (R_G), uncertainty (R_0) and death (R_D) regions. In the uncertainty region, neither growth nor death is predicted. Among the native flora, lactic acid bacteria may have significant effect on these kinetics.

Here we show how to generate predictions for such scenarios, from data that are generated in constant environments. Thus the predictions in our dynamic environments are extrapolations and could be problematic if the environmental fluctuation is extreme. Our approach can be used to predict bacterial growth/death kinetics under temporal variation of storage environments, which is vital when assessing the safety of fresh sausage. We envisage similar applications to other RTE meat products, too.

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Peer-review under responsibility of Department of Food Science, Faculty of Food Engineering, University of Campinas.

Keywords: dynamic environment; kinetics; *Listeria monocytogenes*; *Yersinia enterocolitica*; predictive microbiology; sausage

1. Introduction

Italian style fresh sausage is a traditional pork product. It can be consumed cooked or raw. The consumption of raw sausage is most frequent in regions of Central Italy, usually after a variable drying period. According to regulation CE 853/2004¹ the process should be considered to be a meat preparation, but since the drying period can change the

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physical characteristics of the meat, the result could be a “salami-style” meat product. In Italy, sausages are usually self-checked or “intended to be cooked” products. In some Italian regions, as high as 5% of them are eaten raw².

Codex Alimentarius recommends to move food control activities from a hazard-based and final testing to a more risk-based management approach^{3,4}. This has made statistical and mathematical tools specifically designed to predict microbial behaviour more and more necessary. The use of predictive models is also recommended by EC regulation 2073/2005⁵, currently in effect in the EU. This regulation makes it possible for food business operators to use “predictive mathematical modelling established for the food in question, using critical growth or survival factors for the micro-organisms of concern in the product”. Though predictive models cannot completely replace lab testing or the judgement of an expert food microbiologist, but they aid informed decisions on food safety issues⁶.

So far, the prediction of the behaviour of microorganisms in varying environments has been carried out through separate growth or death models. The aim of this paper is to show how to develop models to predict the kinetics of these pathogens in dynamic environments shifting from growth to inactivation regions. The parameters of existing predictive models for *Y. enterocolitica* and *L. monocytogenes*⁷ will be used for demonstration.

2. Materials and methods

2.1 Primary models of growth and death

For constant, growth-supporting environments, the log counts data can be fitted by the explicit (4-parameter sigmoid curve) version of the model of Baranyi and Roberts⁸:

$$y(t) = y_0 + \mu A(t) - \text{Ln} \left(1 + \frac{e^{\mu A(t)} - 1}{e^{y_{\max} - y_0}} \right)$$

$A(t)$ being

$$A(t) = t - \lambda + \frac{\text{Ln}(1 - e^{-\mu t} + e^{-\mu(t-\lambda)})}{\mu}$$

where

- $y(t)$ describes the temporal variation of the natural logarithm of the bacterial concentration, the time being denoted by t ;
- y_0 is the natural logarithm of the initial bacterial concentration (i.e. at $t=0$);
- y_{\max} is the natural logarithm of the maximum population density the given environment and resources are able to carry;
- μ is the maximum specific growth rate (the maximum of the dy/dt rate), characteristic of the growth environment.
- λ is a lag parameter (the time point where the actual specific rate is $\mu/2$).

This is an algebraic solution of the more general, dynamic model of Baranyi and Roberts⁸:

$$\begin{cases} \frac{dy}{dt} = \frac{1}{1+q} \mu (1 - e^{y_{\max} - y}) \\ \frac{dq}{dt} = \nu q \end{cases} \quad (1)$$

where $q(t)$ is a certain quantification of the actual physiological state of the cells that continuously improving according to linear kinetics, immediately after the inoculation, and the specific rate depends on $\ln(q)$ according to a

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