Optimising food process and formulation through Sym'Previus, Food safety Management

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Abstract

Sym'Previus network gathers expertises in predictive microbiology from major food companies, French technical centres and public research institutes. Based on the most recent concepts in predictive microbiology, Sym'Previus proposes an assistance in food safety management.

Sym'Previus predictive tool is composed of a database and an advanced simulation software. The database provides several informations on microorganisms behaviour in/on foods as well as natural contaminations encountered in foods. The specifically developed querying system, called MIEL, allows a flexible and structured search for a given microorganism, food matrix or food category selected (Buche *et al.*, 2005). New perspectives about this database system are presented in Hignette *et al.* (2007). Secondly, a user-friendly software simulates microorganisms growth in food matrix or heat destruction after industrial treatment. Sym'Previus is an easy way to access predictive microbiology tools for food companies. At the present time, the software describes the effect of temperature, pH and water activity on bacterial growth and thermal destruction in a wide range of food categories, such as cereals, egg products, dairy product, meat, ready-to-eat food. Sym'Previus simulations mainly contains pathogens species (36 strains of 4 major pathogens), but allows prediction for any other species as soon as cardinal values are known.

Keywords

Microorganism behaviour in food, food safety, Simulation software, process and formulation optimisation

Context

Numerous predictive models have been proposed, these last decades, to describe growth rate and growth boundaries of a given microorganism. Although many models are specifically developed in broth, some are based on biological parameters or growth limits called cardinal values. In the 1990's, predictive microbiology strongly developed and particularly concerning growth. The enlargement of "secondary models" and the introduction of the gamma-concept of Zwietering (1992) oriented this discipline towards new models. In the same way, Rosso (1995) proposed the cardinal models, noted CTPM (equation 1), which describes growth rate (μ_{max}), i.e. the main parameter of growth kinetics as a function of cardinal values. At first, these models were used to take into account the temperature and pH effect, but were rapidly extended to the effect of water activity by the same authors in 1998.

$$g(X, \Theta_2) = \sqrt{\mu_{opt}(X) \cdot CM_n(X)}$$

$$CM_n(X) = \begin{cases} 0 & , X \leq X_{min} \\ \dfrac{(X - X_{max}) \cdot (X - X_{min})^n}{(X_{opt} - X_{min})^{n-1} \cdot \left[(X_{opt} - X_{min}) \cdot (X - X_{opt}) - (X_{opt} - X_{max}) \cdot ((n-1) \cdot X_{opt} + X_{min} - n \cdot X)\right]} & \\ & , X_{min} < X < X_{max} \\ 0 & , X \geq X_{max} \end{cases}$$

Where

	X	environmental factor (temperature, pH or water activity)
	X_{min}	minimal cardinal value
	X_{opt}	optimal cardinal value
	X_{max}	maximal cardinal value
	n	fixed parameter without signification

$$\Theta_2 = \left(\mu_{opt}(X), X_{min}, X_{opt}, X_{max}\right)$$

LeMarc (2001), and then Augustin *et al.* (2005) proposed a new independent γ-function to take the interaction between environmental factors into account. which only requires cardinal values from other γ-functions (T_{min}, T_{opt}, pH_{min}, pH_{opt}, aw_{min}, aw_{opt}).

$$\sqrt{\mu_{max}} = \sqrt{\mu_{opt} \cdot \gamma_T \cdot \gamma_{pH} \cdot \gamma_{aw} \cdot \gamma_{int\ eraction}}$$

Because Cardinal values are independent from the growth medium, these physiological parameters are estimated in broth. To appreciate the intraspecific variability, the behaviour of many strains need to be studied. For instance, parameters of twelve *Listeria monocytogenes* have been acquired by Sym'Previus labs to calculate the associated confidence band which includes biological variability.

Including food matrix in growth simulation

The Models used by Sym'Previus present the main advantage to be suited to food products : from a growth kinetic determined in food, Sym'Previus estimates characteristic parameters , μ_{opt}, associated with a given association of microorganism/food. It is then possible to simulate growth for other conditions of temperature, pH or water activity.
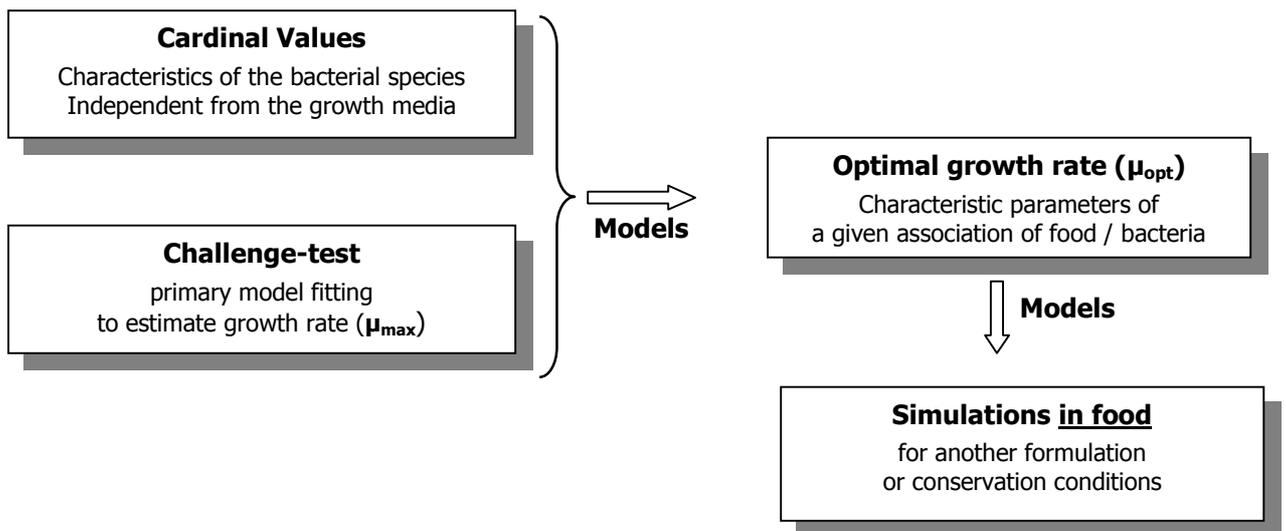

Figure 1 : microbial growth Simulations according to Sym'Previus models, taking the food matrix into account.

What about lag time?

A stochastic approach of bacterial growth is essential as food contamination with pathogens generally occurs with very few cells. bacterial behaviour must then be studied at the level of cell to improve predictions of the growth of these micro-organisms in foods. Guillier and Augustin (2006) modelled the lag time distributions of individual *Listeria monocytogenes cell* for 22 initial physiological states, 18 growth conditions, and 11 strains yielding 54 combinations in total. The proposed models allow the prediction of individual cell lag time distributions of *L. monocytogenes* for different growth conditions. In practise, population lag time is estimated from one challenge-test to estimate the distribution of individual cell lag times for tested temperature, pH and water activity conditions. From this distribution of individual lag time, it also possible to predict the distribution of individual cell lag times and population lag time in another conditions, or for another inoculum size.
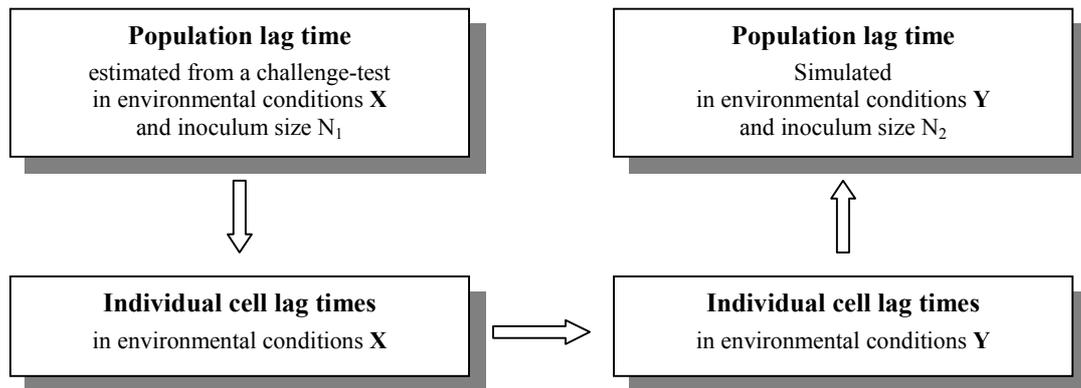
This approach allows the prediction of the lag phase duration whatever growth conditions and initial bacterial concentration based on a single growth experiment performed with high initial concentration for a given physiological state.

Simulation of Thermal Destruction

Thermal resistance of bacterial populations is characterized by two main parameters : D-value and p (Mafart *et al.* 2002). In the same way as the γ-concept for growth prediction, D-value is described thanks to a modular model, where environmental factors are independently taken into account.

$$\frac{1}{\delta} = \frac{1}{\delta^*}.\lambda_T(T).\lambda_{pH}(pH).\lambda_{aw}(a_w)... \qquad \text{Where} \qquad \lambda_X = \left(\frac{X - X_{ref}}{z_X}\right)^n$$

δ Decimal Reduction Time at temperature T, pH and aw

δ^* Decimal Reduction Time at standard condition of T, pH, aw obtained in the food matrix

X Environmental factor (temperature, pH or water activity)

X_{ref} Standard value of the factor X

z_X distance of X from X_{ref} which leads to a ten fold reduction in δ value, and quantifies the influence of the factor X on the bacterial heat resistance

n shape parameter

If a destruction curve is available for a given food product, it is also possible to simulate the heat destruction in this particular food in other heat treatment or formulation conditions. Added to temperature profile of pasteurisation or sterilisation process, the process effectiveness can be translated into decimal reduction number, and associated risk to observe microorganisms survival.

Is Sym'Previus operational ?

All models applied in Sym'Previus are already validated in a wide variety of food matrices.and applications of this advanced predictive software are wide spread. It is nowadays already used to :
- predict bacterial growth in several conditions
- predict the growth probability of microorganisms in foods
- evaluate contamination level at shelf-life
- optimise formulation (additive, pH, salt)
- optimise new process conditions (heat treatment time)
- evaluate the impact of cold chain breaks, and test different storage scenarios
- help to identify Critical Control Points in a process
- Identify targeted bacteria limitating shelf-life

Constant improvements and updates ensure Sym'Previus state of the art position in the field of simulation tools. These evolutions mainly concern :
- prediction of the growth probability in any food products,
- modelling of the non-thermal factors acting on the microbial decrease

In the same way, Sym'Previus extends models to other microorganisms (pathogens or spoilage bacteria).

Finally, simulations based on risk analysis approach could take into account the initial contamination distributions estimated from industrial monitoring data sets, individual cell lag times distributions and growth simulations could predict the probability to exceed critical limits of microorganisms concentrations in food.

Sym'Previus offers an English and French version available online at www.symprevius.org

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