



Title	Approaches for a probabilistic evaluation in predictive microbiology : Interpretation of stochastic bacterial inactivation process in a population and single cell level [an abstract of dissertation and a summary of dissertation review]
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学位論文内容の要旨

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学位論文題名

Approaches for a probabilistic evaluation in predictive microbiology: Interpretation of stochastic bacterial inactivation process in a population and single cell level

（予測微生物学における確率的評価のためのアプローチ：集団および単一細胞
レベルにおける確率的細菌不活化プロセスの解釈）

The trend of a consumers' demand for processed foods has been changing minimally processed and fresh-like products. Minimum processing may lead to insufficient control of pathogenic bacteria that would cause foodborne illness to human. Accurate bacterial cell behavior should be revealed to guarantee an acceptable safety level during food processing and storage. However, deterministic approach that has been used in the present food processing system is insufficient for reliable estimation of the bacterial survivors of inactivation treatment, because it predicts only mean behavior of bacterial cell population. For example, bacterial inactivation behavior has been described by log-linear model for simplification. Decimal log reduction time (*D*-value) calculated from log-linear model has long been widely used for microbial risk assessment and sterilization time estimation. The *D*-value ignored not only inactivation kinetics curvature but also individual cell heterogeneity, a significant source of variability for small amount cells. As a result, the worst-case scenario is generally used to estimate probability of survival bacterial population in order to avoid overly optimistic estimation. Thus, probabilistic and stochastic models should be introduced to make the realistic prediction with random variable including individual cell heterogeneity. In this study, we described stochastic behavior of bacterial inactivation via computer simulation and mathematical formulation and estimated time-to-inactivation and probability of a population containing survivors.

1. Monte Carlo simulation of stochastic inactivation of individual cells

We investigated an approach for simulating stochastic inactivation of bacterial cells and estimated the time-to-inactivation. The bacterial inactivation is normally described as a log-linear or log-Weibull model and random variable in initial cell number is often assumed as Poisson distribution. In our study, Weibull and Poisson distributions were used to provide individual cell inactivation time variability and initial number of cells

variability, respectively. We sampled random variable of number of initial cells and individual cell inactivation time from Poisson distribution and Weibull distribution by Monte Carlo simulation. The simulation results demonstrated that the time-to-inactivation significantly depends on kinetics curvature and initial number of cells. For example, with increases in the initial number of cells, the respective variance of the time-to-inactivation of log-linear, concave downward curve, and concave upward curve remains constant, decreases, and increases, respectively. The results of this study indicated that shape of kinetic model should be well considered for estimating time-to-inactivation.

2. Mathematical description for a stochastic evaluation of inactivation of individual bacterial cells

The stochastic mathematical description is a basic approach toward understanding random variable in bacterial inactivation. In this study, stochastic inactivation of individual cell in a bacterial population was calculated by using exponential distribution and Poisson process. In the first approach, we calculated the duration required for a specific reduction in the number of bacterial cells. We considered the process of individual cell inactivation as a random event described by exponential distribution. We calculated the timing of inactivation of individual cell in a population and summed up them until all the cells died. We formulated the duration required for a specific reduction in the number of bacterial cells as the convolution of exponential distributions. In the second approach, we calculated the process that the number of initial cells following a Poisson distribution decrease randomly one by one. We formulated the number of survival cells as a Poisson distribution. We calculated the probability of a population containing survivors after inactivation process with the D -value and the stochastic formulation. The stochastic formulation indicated that D -value over or underestimate the probability of a population containing survivors due to ignoring inactivation kinetics curvature. The stochastic formulation should be used for estimating the probability of a population containing survivors instead of D -value under the assumption that individual cell becomes death independently.

Our simulation and formulation offered a basic concept of stochastic evaluation for inactivation of bacterial individual cells. Our approach changes the descriptions of bacterial behavior from point estimation to random variable. The concept of the stochastic simulation and formulation would contribute to probabilistic inactivation modeling and microbial risk assessment to describe exposure to bacteria as random variable.