

Mathematical Modeling of Listeria Overgrowth Phenomena

Hedia Fgaier and Herman Eberl
Department of Mathematics and Statistics
University of Guelph, Canada

Abstract

The objective of this paper is to present a mathematical model in terms of differential equations for the interaction between the two strains *L. monocytogenes* and *Listeria innocua* (*L.welshimeri*) where *L. monocytogenes* was overgrown during enrichment by other species present in the original sample, (e.g. *Listeria innocua* or *L.welshimeri*). The model is utilized to shed light into the phenomena of false negative in food testing and to confirm experimental observations that suggest that the overgrowth could partially be explained in terms of a nutritional competition. Therefore, we established that the growth of both strains is based on a substrate *S* present in the system and assumed that this substrate is the only limiting substrate. We used the Monod kinetics that assumes that at low concentrations the growth rate is first-order with respect to substrate concentration, while at higher concentrations the growth rate is independent of *S* concentration. The parameters in the model consist of the substrate concentration at which the growth rate is half the maximum, the maximum growth rate of the strain, and two additional parameters that describe the lag phase. We conducted successfully a parameter identification study using a sequential quadratic programming approach based on the data provided. We solved the model numerically and validated it against the experimental measurements.

We used the prepared model to study the effect of initial count on the growth of strains. We found out that the initial bacteria count has an effect on the growth of strains. The strain with the greater initial count is the one that grows more than the other strain and keeps a higher microbial count at later times. Therefore the false negative takes place especially when the initial count of the non pathogenic (*L.innocua* or *L.welshimeri*) strain is greater than the initial count of *Listeria* (*L. monocytogenes*).

The model indicated that the physiological state affects also the growth of strains. Changing the values of the physiological adaptation parameters and keeping the same values of the other parameters, the system was able to move from the case where *L.innocua* is the higher count competitor to the case where *L. monocytogenes* is the higher count competitor. Therefore, we can conclude that false negative is an issue and this depends on the initial count of the bacteria and their initial physiological state. We suggest also that one can maybe change the *L. monocytogenes* medium in the benefit of *L. monocytogenes*.

The findings of this paper lead us to conclude that false negative is an issue and this depends on the initial count of the bacteria and their initial physiological state. We suggest also that one can change the *L. monocytogenes* medium in the benefit of *L. monocytogenes*. In a chemostat set-up, we performed various numerical simulations to test for the presence of both at very small flow rates and very large flow rates (washout). The washout flow rate obtained numerically was larger than the one obtained theoretically. This is an additional validation to the numerical scheme used in this work. Through simulations we were able to determine the flow rates for which one species survives and the washout rate at which both species get extinct. It remains to compare these results against experimental measurements and to validate further the competition phenomena based on the Half Fraser case.

Keywords

Optimization, parameter estimation, microbial competition, food testing, pathogen detection