

DEVELOPMENT OF AN INTEGRATED MODEL FOR HEAT TRANSFER AND
DYNAMIC GROWTH OF *CLOSTRIDIUM PERFRINGENS* DURING THE
COOLING OF COOKED BONELESS HAM

by

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A DISSERTATION

Presented to the Faculty of
The Graduate College at the University of Nebraska
In Partial Fulfillment of Requirements
For the Degree of Doctor of Philosophy

Major: Interdepartmental Area of Engineering

Under the Supervision of Professor Curtis L. Weller

Lincoln, Nebraska

May, 2004

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DISSERTATION TITLE

Development of an Integrated Model for Heat Transfer and Dynamic Growth of

Clostridium perfringens During the Cooling of Cooked Boneless Ham

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UNIVERSITY OF
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**DEVELOPMENT OF AN INTEGRATED MODEL FOR HEAT TRANSFER
AND DYNAMIC GROWTH OF *CLOSTRIDIUM PERFRINGENS* DURING THE
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Alejandro Amézquita, Ph.D.

University of Nebraska, 2004

Adviser: Curtis L. Weller

The Food Safety and Inspection Service (FSIS) of the U.S. Department of Agriculture requires meat processors to follow time-temperature compliance guidelines to meet stabilization performance standards. The FSIS has proposed that by following these guidelines, allowable growth of *Clostridium perfringens* is limited to a 1-log₁₀ multiplication during cooling after cooking of ready-to-eat meat products. Numerous small meat processors have difficulties complying with these performance standards. Several attempts, mainly focused on microbiological aspects, have been made to develop predictive models for growth of *C. perfringens* within the range of cooling temperatures of the guidelines. Conversely, studies dealing with heat transfer models to predict cooling rates in meat products, do not address microbial growth. Integration of heat transfer relationships with *C. perfringens* growth relationships during cooling of meat products has been very limited.

The objective of the current study was to integrate a heat transfer model and a *C. perfringens* growth model into a user-friendly computer program for accurate prediction

of cooling rates and potential growth of the microorganism during cooling of cooked boneless ham.

The heat transfer component was developed in Matlab[®] 6.5 using finite element analysis to model two-dimensional axisymmetric transient heat conduction. Validation used experimental data collected in commercial meat-processing facilities. For *C. perfringens* growth, a dynamic model was constructed using Baranyi's non-autonomous differential equation. The bacterium's growth model was integrated into the computer program by using predicted temperature histories as input values.

For cooling cooked hams from 66.6°C to 4.4°C using forced air, the maximum deviation between predicted and experimental core temperature data was 2.54°C. Predicted *C. perfringens* growth curves obtained from dynamic modeling were in good agreement with validated results for three different cooling scenarios. Mean absolute values of relative errors were below 6%, and deviations between predicted and experimental cell counts were within 0.37 log₁₀ CFU/g. For a cooling process which was in exact compliance with the FSIS stabilization performance standards, a mean net growth of 1.37 log₁₀ CFU/g was predicted.

This study introduced the combination of engineering modeling and microbiological modeling as a useful quantitative tool for general food safety applications, such as risk assessment and Hazard Analysis and Critical Control Points plans.

PREVIEW

***To my parents, Fabio and Mercedes, and
especially to my newly-born nephew, Ricardo.***

ACKNOWLEDGMENTS

I wish to thank my advisor, Dr. Curtis L. Weller, for all the support he gave me during my doctorate's program. I appreciate his guidance and patience at difficult moments during the program. I am particularly grateful to Dr. Weller for being so dynamic and effective at reviewing my dissertation under a tight timeline, allowing me to meet the deadlines established by the Office of Graduate Studies. I would also like to thank the other members of my supervisory committee, Dr. Milford A. Hanna, Dr. David D. Jones, Dr. Harshavardhan Thippareddi and Dr. Dennis E. Burson, for their valuable inputs. I am especially thankful to Dr. Thippareddi for letting me "abuse" his laboratory during the development of the *Clostridium perfringens* growth model.

Special thanks to Dr. Lijun Wang, post-doctoral research associate in the Department of Biological Systems Engineering, for his thoughtful inputs and expert opinion during the development of the heat transfer model. Also, special thanks to Dr. Erin Blankenship, assistant professor in the Department of Statistics for her great assistance with statistical analyses and helpful discussions about non-linear models. Other UNL faculty members who provided me with expert opinions and technical support, and with whom I am indebted as well, are Dr. Mehrdad Negahban and Dr. Florin Bobaru, from the Department of Engineering Mechanics, and Dr. Kevin D. Cole and Dr. George Gogos from the Department of Mechanical Engineering.

Very special thanks to Carolina Estrada for the countless long hours she spent in the lab assisting me with the project, for keeping me on track at all times, for being supportive, patient and caring, and for being truly an awesome partner in crime. Thanks

also to Marcos Sánchez for his valuable guidance on microbiological techniques, for the plethora of enriching discussions about each other's research projects, and for being a good friend. Thanks to student workers and staff in Dr. Thippareddi's lab, especially to Jayne Stratton for her cooperation during my lab work.

Finally, thanks to the USDA – CSREES Integrated Research, Education, and Extension Competitive Grants Program – National Food Safety Initiative for funding a portion of my research project.

PREVIEW

PREFACE

This dissertation consists of three chapters and three appendices. Chapter 1 is a comprehensive review of literature that assimilates research concerned with modeling of microbial growth under time-varying temperature conditions. Chapters 2 and 3 are written as individual research articles. Chapter 2 is concerned with heat transfer modeling, using finite element analysis, to predict cooling rates of large ready-to-eat meat products under various air-chilling conditions. Experimental validation of the heat transfer model under actual processing conditions is also included in Chapter 2. Chapter 3 presents a methodology by which the heat transfer model developed in Chapter 2 is integrated with a dynamic *Clostridium perfringens* growth model. Chapter 3 also includes experimental validation of the integrated model for heat transfer and dynamic growth in a cured ham matrix. Appendix A presents a detailed derivation of the finite element method for a two-dimensional axisymmetric transient heat conduction problem with combined convective, radiative and evaporative boundary conditions. Appendix B includes all the computer programs written in Matlab[®] 6.5 Release 13 for the solution of the heat transfer model and for integration of this model with the dynamic *C. perfringens* growth model. Finally, Appendix C includes experimental data collected during the course of the research project, as well as a typical SAS program utilized for non-linear regression of *C. perfringens* growth data.

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PREVIEW

CHAPTER 1

MODELING MICROBIAL GROWTH UNDER TIME-VARYING TEMPERATURE CONDITIONS IN FOOD PROCESSING: A REVIEW

This review will be published as:

Amézquita A, Weller CL. 2004. Modeling microbial growth under time-varying temperature conditions in food processing: A review. Submitted to: Comp. Rev. Food Sci. Food Saf.

PREVIEW

MODELING MICROBIAL GROWTH UNDER TIME-VARYING TEMPERATURE CONDITIONS IN FOOD PROCESSING: A REVIEW

ABSTRACT

The concept of predictive food microbiology encompasses various traditional disciplines such as mathematics, statistics, and microbiology with the purpose of developing kinetic or probability models that describe the responses of microbial populations to environmental (controlling) factors. Of particular interest within this emerging field, is the modeling of microbial dynamics under fluctuating environmental conditions, especially with respect to temperature, as it is normally encountered during food processing. This poses a challenge when modeling growth, particularly because both the lag and exponential phases need to be considered in model development. Factors such as the effect of previous growing environmental conditions on the initial physiological state of microbial cells have presented a considerable challenge for researchers in this area. Furthermore, considering temperature the most influential factor on microbial population dynamics in food processing environments, accurate predictions of product temperature histories and profiles are necessary inputs for appropriate model development. Nevertheless, integrated models of heat transfer and dynamic microbial growth are lacking. This paper presents a comprehensive and critical review of existing modeling techniques in the context of microbial growth under time-varying temperature conditions, and introduces a proposed optimized methodology for effective integration of engineering and microbiological modeling as a quantitative tool to support food safety management strategies such as HACCP and microbiological risk assessment.

INTRODUCTION

Predictive food microbiology is a research area that combines mathematical, statistical and microbiological principles to predict quantitatively the behavior of microbial populations in foods (Ross and others 2000). Predictive microbial models find their most significant application in the area of food safety (McMeekin and others 1997; Soboleva and others 2000), providing quantitative information necessary for the development of safety assurance systems such as the Hazard Analysis and Critical Control Points (HACCP) system (Baker 1995; Elliot 1996; Panisello and Quantick 1998; Ross and McMeekin 1995), and for the establishment of Food Safety Objectives (FSO) in the context of Microbiological Risk Assessment (MRA) (Buchanan and Whiting 1996; Foegeding 1997; McNab 1997; Ross and McMeekin 2003; Soboleva and others 2000; Walls and Scott 1997).

Predictive microbial models are generally summarized in the form of mathematical equations. These equations are derived starting from the general principle that microbial populations respond to environmental factors in a reproducible fashion, and that by characterizing food environments in terms of those factors with greatest influence on microbial growth and survival, it is possible to predict the responses of those populations in similar food matrices, based on past observations (Ross and McMeekin 1994; Ross and others 2000). In the past decade, two books have been published that comprehensively review the development, validation and application of predictive food microbiology (McKellar and Lu 2004a; McMeekin and others 1993).

For many years, researchers in the area of predictive microbiology have preferred the use of sigmoidal functions to fit microbial growth data collected under non-varying