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# **A novel model developed for Quantitative Microbial Risk Assessment in the pork food chain**

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***Simone Megan Titus***

Institute of Veterinary, Animal and Biomedical Sciences  
Massey University  
Palmerston North, New Zealand

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Institute of Veterinary, Animal and Biomedical Sciences

Massey University

Palmerston North, New Zealand

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## 0.1 Abstract

Food-borne diseases contribute substantially to morbidity and mortality rates worldwide. The deleterious impact of these diseases on human health, concurrent with the associated socioeconomic cost has led to an increased demand for the production of safe food globally. Consequently, agencies such as the World Health Organization (WHO) and the Food and Agriculture Organization (FAO) have resolved to address this issue. In this vein, scientific, risk-based approaches which facilitate estimation of the probability of disease occurrence, the magnitude of the disease and efficacious control measures have been recommended for use internationally.

Many pathogens have been implicated as aetiological agents of food-borne disease. The WHO has identified non-typhoidal *Salmonella*, *Escherichia coli* and thermophilic *Campylobacter* as zoonotic food-borne pathogens of greatest importance. These pathogens can be transmitted to humans through pork consumption. This thesis therefore proposes a suite of novel, mechanistic, semi-stochastic, quantitative, modular process risk models describing the propagation of these three pathogens from the live pig at the abattoir, to pork chops sold at retail. The model is developed for use in risk-based, quantitative microbial exposure assessments in New Zealand and can be employed to explore different intervention strategies targeted at mitigating contamination levels of these pathogens on pork chops.

The models comprise multiple, coupled, differential and difference equations. These equations explicitly describe bacterial growth, inactivation, removal, cross-contamination and food partitioning occurring in continuous and discrete time in abattoirs and at retail. Distributions of pathogen numbers on the surface of carcasses, and prevalence levels are output by the models at different stages of abattoir processing and pork chop production. Both dressed pork carcasses exiting abattoirs in New Zealand and pork chops at retail are predicted to contain low surface contamination levels of the pathogens under consideration, while a small percentage is estimated to be highly contaminated.

Median contamination levels on dressed pork exiting the abattoir are predicted to be less than one cfu/cm<sup>2</sup>. Generally, there are large reductions in surface bacterial numbers for all three organisms from the time the live pig enters the abattoir, to sale of the pork chop at retail. The introduction of a second singeing procedure immediately post-evisceration in the abattoir is predicted by our models, to be an effective mitigation strat-

egy, with estimated reductions in median pathogen levels of 100%. This control measure is considered to be more effective than coverage of the anal region of the pig during evisceration. This latter mitigation strategy was predicted to result in 10% – 44% reduction of median pathogen contamination levels.

At retail, pork chops are also estimated to contain low numbers of these pathogens. Therefore handling of the raw pork chop soon after purchase from retail outlets may be associated with a low risk of contracting salmonellosis, colibacillosis and campylobacteriosis. This risk can be further reduced by placing pork chops in a blast chiller for 12 hours prior to display. When this mitigation strategy was modelled the outputs indicated a 15% – 61% reduction in the maximum pathogen levels on pork chops, 44 – 100% reduction in the 10<sup>th</sup> – 90<sup>th</sup> range and 14% – 50% reduction in pathogen prevalence levels.

Detailed investigation revealed the limitations of a specific modelling approach. We determined that the population-based modelling approach is not an appropriate alternative to the individual-based modelling approach when there is a large disparity in contamination levels between processed carcasses. Therefore the former technique should not be used in the presence of large heterogeneity with respect to the number of bacteria on the food unit of interest, or when bacterial populations input into the model are described with large variances.

This thesis demonstrates the application of a suite of novel risk models in the pork food chain. We propose use in quantitative microbial exposure assessments. The applicability of these models is not only limited to the pork chain or to the above mentioned pathogens, but by modification of parameters, the entire model, or portions thereof can be extrapolated to other animal species undergoing similar abattoir procedures with pathogens of analogous epidemiological patterns. Finally the information provided by the models can be instrumental in assisting risk managers in their decision-making and policy development undertakings and provide guidance to effectively and strategically funnel limited resources.

## 0.2 Acknowledgements

This PhD was truly a journey, a process - a process of developing a new way of thinking and working; exponentially increasing my knowledge in the field of study; a test of tenacity; determination; personal maturity; tolerance; patience; enduring the seemingly innumerable storms and yet, constantly attempting to maintain my inner peace. My journey through this process has been filled with summits, excitements, thrills, irritations and troughs of utter frustration and agony. But, I came to finally learn not to let the PhD master me, but to master it; not to let it overwhelm me but to take each step at a time, each day at a time until the mountain becomes a plain before me. With this perception, half the battle was already won.

No man is an island and this work could not have been completed without the assistance of many people. I would therefore like to thank the following people for their support and help: All the staff and students in the EpiCentre, IVABS and the Statistics Department that assisted me from 2004 - 2007; the computer software developers in the EpiCentre; the New Zealand Pork Industry Board; Landmeat, Freshpork and Taranaki Abattoirs; The Roger Morris Foundation for providing the needed funds; the New Zealand Commonwealth Scholarship for financially supporting me while I was in New Zealand, the Government of Trinidad and Tobago that allowed me the opportunity to further my education; Graham McBride, a mathematician; my supervisors Nigel French, Mark Stevenson and Roger Morris and special thanks to Jonathan Marshall, another mathematician.

Anyone who has chatted with me for a while would realize that even though I have been in New Zealand, my heart never left the Caribbean. This acknowledgement would not be complete without my emphatically extending heartfelt and deepest thanks to those persons whose support commenced prior to my embarking on the PhD, extended throughout the duration of the study, never waning, and will persist after its completion. It is the support from these persons, extending over thousands of miles, that was so very critical to the completion of my thesis. I thank my friends from the Caribbean, particularly Angela Kerr and leaving the best for last, my dearest parents — Mr. and Mrs. Irwin and Albertha Titus, whose love and support knows no bounds. Mom, Dad, your contribution was invaluable.

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supported me, for enabling me to complete the task of finishing the thesis. He is truly faithful and helped me 'keep it together when everything around me seemed to indicate that things were falling apart'. It was His contribution that was the single most significant contributor to my success. Now I can happily say 'Return to rest O my soul, For the Lord has dealt bountifully with you.'. For 'all things work together for good to those who love Him and are called according to His purpose'.

## 0.3 Nomenclature

CAC	Codex Alimentarius Commission
cfu	colony forming units
cm	centimetre
FAO	Food and Agriculture Organization
g	gram
kg	kilogram
ml	millilitre
mm	millimetre
MPRM	Modular Process Risk Model
NZ	New Zealand
NZFSA	New Zealand Food Safety Authority
OIE	Organisation International des Epizooties or World Organisation for Animal Health
QMRA	Quantitative Microbial Risk Assessment
RA	Risk Assessment
sd	Standard deviation
UK	United Kingdom
USA	United States of America
WHO	World Health Organization





## 0.4 Glossary

In this thesis the following terms are defined as stated below:

- **Contamination:**

The presence of bacteria on the surface of the pig carcass, which may or may not be associated with faecal material; or the presence of unwanted material on the surface of an object.

- **Cross-contamination:**

The movement of bacteria from one object to another.

- **Deterministic Model:**

A model that predicts point estimate outputs and does not incorporate the element of chance or contain randomly varying components.

- **Inactivation:**

The action of rendering an organism non-pathogenic.

- **Infection:**

Bacterial colonisation of the gastro-intestinal tract and associated tissues.

- **Model:**

A simplified representation of a realistic phenomenon.

- **Stochastic Model:**

A model in which the element of chance is explicitly described so that each realization of the model can output different results for the same initial values.



## 0.5 Symbols and Units

Symbol	Description	Units
$\alpha$	rate of pathogen movement from water to carcass in scalding	minute <sup>-1</sup>
$\beta$	rate of pathogen movement from carcass to water in scalding	minute <sup>-1</sup>
$\delta$	rate of pathogen movement from dehairing machine to carcass	minute <sup>-1</sup>
$\epsilon$	pathogen inactivation rate on carcass in singeing	minute <sup>-1</sup>
$\theta$	rate of pathogen movement between carcasses in storage/chilling	hour <sup>-1</sup>
$\kappa$	pathogen inactivation/growth rate on pork chop	day <sup>-1</sup>
$\lambda$	transmission parameter	minute <sup>-1</sup>
$\mu$	rate of pathogen movement from carcass to the dehairing machine	minute <sup>-1</sup>
$\tau_1$	pathogen inactivation rate on carcasses in scalding	minute <sup>-1</sup>
$\tau_2$	pathogen inactivation rate in water in scalding	minute <sup>-1</sup>
a	probability that each cfu of bacteria moves from the carcass exterior to the knife (pork chop models)	cfu <sup>-1</sup>
$a_{f,s}$	probability that each cfu of bacteria moves from the faeces to the knife (abattoir models)	cfu <sup>-1</sup>
area	relative proportion of pork chop surface area with respect to the half carcass	%
$a_{x,s}$	probability that each cfu of bacteria moves from the carcass exterior to the knife (abattoir models)	cfu <sup>-1</sup>
b	probability that each cfu of bacteria moves from the knife to the carcass exterior (pork chop models)	cfu <sup>-1</sup>
$b_{e,S}$	probability that each cfu of bacteria moves from the knife to the carcass exterior (pork chop models)	cfu <sup>-1</sup>
c	probability of inactivation from the knife per cfu of bacteria (pork chop models)	cfu <sup>-1</sup>

Symbol	Description	Units
$c_{e,S}$	probability of inactivation from the knife per cfu of bacteria (abattoir models)	$\text{cfu}^{-1}$
$c_{x,S}$	probability of inactivation and removal from carcass exterior (abattoir models)	$\text{cfu}^{-1}$
d	probability of bacterial inactivation and removal from carcass exterior (pork chop models)	$\text{cfu}^{-1}$
$g_f$	concentration of bacteria in faeces	$\text{cfu/g}$
$h$	smoothing parameter	
$k$	kernel function	
r	pathogen inactivation rate on carcass in storage/chilling	$\text{hour}^{-1}$
$r_{p,c}$	pathogen inactivation rate on pork chop in storage/chilling	$\text{hour}^{-1}$
t	time	$\text{minute}^{-1}$
$t_D$	decimal reduction time	$\text{minute}^{-1}$
time	time	$\text{days}^{-1}$
x	pork chop contamination level after cross-contamination	cfu
y	pathogen numbers on skin of the pork chop after partitioning when $z > 30,000$	cfu
$y_1$	pathogen numbers on skin of the pork chop after partitioning when $z < 30,000$	cfu
z	bacteria numbers on half carcass	cfu
A	probability that bacteria are present on area of carcass in contact with knife for evisceration cut	$\text{cfu}^{-1}$
$A_{f,d}$	faecal quantity output from pig in dehairing	g
B	pathogen numbers in faeces released from carcass in dehairing	cfu

Symbol	Description	Units
$C$	probability of transfer of bacteria from carcass surface to the knife	$\text{cfu}^{-1}$
$C_1$	pathogen numbers on halved carcass in storage	cfu
$C_2$	pathogen numbers on another halved carcass in storage	cfu
$E$	probability of bacteria on the region to be trimmed coming into contact with knife	$\text{cfu}^{-1}$
$F$	probability of transfer of bacteria to knife	$\text{cfu}^{-1}$
$G$	probability that bacteria are present on area of carcass in contact with knife during halving	$\text{cfu}^{-1}$
$H$	probability of transfer of bacteria to knife	$\text{cfu}^{-1}$
$Inf$	probability of inactivation of bacteria on carcass skin	$\text{cfu}^{-1}$
$I$	number of infected animals	pigs
$M$	pathogen numbers on dehairing machine	cfu
$N_{e,S}$	bacterial load in environment	cfu
$N_{f,d}$	pathogen concentration in the faecal material in dehairing	cfu/g
$N_{f,l}$	pathogen concentration in infected faeces in lairage	cfu/g
$N_{f,S}$	pathogen numbers in leaking faeces from a carcass	cfu
$N_{p,l}$	total number of bacteria in a pen in the lairage	cfu
$N_{saw}$	pathogen number on saw after cutting pork chop	cfu
$N_{x,c}$	pathogen number on pork chop after partitioning	cfu
$N_{x,pc}$	pathogen number on skin surface of the pork chop after cross-contamination process	cfu
$N_{p,i}$	pathogen number on skin surface of the pork chop in intervention strategy	cfu
$N_{x,S}$	bacterial load on carcass surface	cfu

Symbol	Description	Units
$N_{x,storage}$	pathogen number on halved carcass from abattoir	cfu
$p_{cut}$	probability of pathogen present on skin surface of the pork chop	
$P_d$	pathogen numbers on carcass in dehairing	cfu
$P_k$	pathogen numbers on carcass in scalding	cfu
$P_s$	pathogen numbers on carcass in singeing	cfu
$Prob$	probability of an animal being infected in lairage	
R	probability of removal of bacteria on the carcass skin	cfu <sup>-1</sup>
S	number of susceptible animals	pigs
$S_0$	pathogen numbers on carcass before singeing	cfu
$S_t$	pathogen numbers on carcass after singeing	cfu
T	temperature	°C
$T_{f,l}$	total infected faecal material in lairage	g
W	pathogen numbers in water in scalding	cfu
$w_{f,s}$	mass of leaking faeces	g
X	cross-contamination	
Y	inactivation	

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# Contents

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0.1	Abstract . . . . .	iii
0.2	Acknowledgements . . . . .	v
0.3	Nomenclature . . . . .	vii
0.4	Glossary . . . . .	ix
0.5	Symbols and Units . . . . .	xi
<b>1</b>	<b>Introduction</b>	<b>1</b>
<b>2</b>	<b>Literature Review</b>	<b>3</b>
2.1	Introduction . . . . .	3
2.2	Microbial risk assessment . . . . .	4
2.3	Steps involved in risk analysis . . . . .	5
2.4	Quantitative microbial risk assessment . . . . .	11
2.4.1	Model types . . . . .	11
2.5	Simulation modelling . . . . .	19
2.5.1	Simulation sampling . . . . .	20
2.6	Sensitivity analyses . . . . .	21
2.7	Second order modelling . . . . .	23
2.8	Parameter estimation . . . . .	24
2.9	Modelling techniques . . . . .	25
2.9.1	Bayesian belief network approach . . . . .	25
2.9.2	Probabilistic scenario analysis (PSA) . . . . .	27
2.9.3	Process risk model . . . . .	28
2.9.4	Modular process risk model . . . . .	28
2.10	Applications of risk analysis . . . . .	30
2.11	Risk profiles . . . . .	31
2.11.1	Salmonella . . . . .	31



2.11.2	Campylobacter . . . . .	36
2.11.3	Escherichia coli O157:H7 . . . . .	38
2.11.4	Summary . . . . .	41
2.12	Overview of Production processes . . . . .	41
2.12.1	Abattoir . . . . .	41
2.12.2	Further processing processes . . . . .	44
2.13	Conclusion . . . . .	44
<b>3</b>	<b>Modelling pathogen dynamics in the pig abattoir</b>	<b>47</b>
3.1	Abstract . . . . .	47
3.2	Introduction . . . . .	48
3.3	Model Description . . . . .	50
3.4	Results . . . . .	69
3.5	Discussion . . . . .	80
3.6	Acknowledgements . . . . .	86
3.7	Appendix . . . . .	86
<b>4</b>	<b>Modelling pathogen dynamics during Scalding in the Pig Abattoir</b>	<b>119</b>
4.1	Abstract . . . . .	119
4.2	Introduction . . . . .	120
4.3	Model Description . . . . .	121
4.4	Results . . . . .	129
4.5	Discussion . . . . .	140
4.6	Appendix . . . . .	144
<b>5</b>	<b>An example of assessing model uncertainty</b>	<b>147</b>
5.1	Abstract . . . . .	147
5.2	Introduction . . . . .	148
5.3	Model Description . . . . .	149
5.4	Results . . . . .	154
5.5	Discussion . . . . .	159
5.6	Appendix . . . . .	161

<b>6</b>	<b>Evaluation of pathogen mitigation strategies in pig abattoirs</b>	<b>167</b>
6.1	Abstract . . . . .	167
6.2	Introduction . . . . .	168
6.3	Model Description . . . . .	169
6.4	Results . . . . .	172
6.5	Discussion . . . . .	179
<b>7</b>	<b>Modelling pathogen dynamics during pork chop production</b>	<b>183</b>
7.1	Abstract . . . . .	183
7.2	Introduction . . . . .	184
7.3	Model Description . . . . .	185
7.4	Results . . . . .	192
7.5	Discussion . . . . .	199
<b>8</b>	<b>General discussion</b>	<b>205</b>
8.1	Introduction . . . . .	205
8.2	Model development and techniques used . . . . .	206
8.3	The model . . . . .	209
8.4	Future Applications . . . . .	212
8.5	Conclusion . . . . .	213
	<b>Bibliography</b>	<b>215</b>
<b>A</b>	<b>General appendix</b>	<b>A-1</b>



---

## List of Figures

---

2.1	Codex Alimentarius Commission schematic for Risk Analysis. . . . .	6
3.1	Schematic of modelled abattoir. . . . .	52
3.2	Schematic diagram of pathogen dynamics occurring during Evisceration.	54
3.3	Composite diagrams of pig abattoir modules described by differential equations. . . . .	58
3.4	Predicted bacterial numbers on pig carcasses at different stages in the abattoir. . . . .	74
3.5	Predicted distributions of pathogens at storage . . . . .	75
3.6	Time Series of predicted surface contamination levels of <i>Salmonella</i> on pig carcasses at various abattoir stages . . . . .	76
3.7	Outcome of the second order analysis for <i>Salmonella</i> . . . . .	77
3.8	Outcome of the second order analysis for <i>E. coli</i> . . . . .	78
3.9	Outcome of the second order analysis for <i>Campylobacter</i> . . . . .	79
3.10	Lairage and Killing module of abattoir model. . . . .	113
3.11	Scalding module of abattoir model. . . . .	114
3.12	Dehairing module of abattoir model. . . . .	115
3.13	Singeing and Evisceration modules of abattoir model. . . . .	116
3.14	Storage module of abattoir model. . . . .	117
4.1	Schematic of modelled scalding process. . . . .	122
4.2	Rate of change of pathogens on the carcass . . . . .	133
4.3	Phase plane plots showing pathogen dynamics (a). . . . .	134
4.4	Phase plane plots showing pathogen dynamics (b). . . . .	135
4.5	Tornado plot of sensitivity analyses results for the semi-stochastic scalding model. . . . .	136

4.6	Cumulative probability distribution of <i>Salmonella</i> on carcasses pre and post scalding. . . . .	137
4.7	Predicted contamination levels on pig carcasses and the scald tank water at 55°C. . . . .	138
4.8	Predicted contamination levels on pig carcasses and the scald tank water at 60°C. . . . .	139
5.1	Schematic of trimming process. . . . .	151
5.2	Quantile-quantile plots of the predicted distributions of carcass contamination levels after trimming from initial input Lognormal distributions (A). . . . .	155
5.3	Quantile-quantile plots of the predicted distributions of carcass contamination levels after trimming from initial input Lognormal distributions (B). . . . .	156
5.4	Quantile-quantile plots of the predicted distributions of carcass contamination levels after trimming from initial input ZIP distributions (A). . .	157
5.5	Quantile-quantile plots of the predicted distributions of carcass contamination levels after trimming from initial input ZIP distributions (B). . .	158
6.1	Modules and processes in a New Zealand abattoir. . . . .	170
6.2	Predicted <i>Salmonella</i> numbers on the surface of pig carcasses at different stages in the abattoir with and without mitigation strategies. . . . .	176
6.3	Predicted <i>E. coli</i> numbers on the surface of pig carcasses at different stages in the abattoir with and without mitigation strategies. . . . .	177
6.4	Predicted <i>Campylobacter</i> numbers on the surface of pig carcasses at different stages in the abattoir with and without mitigation strategies. . . .	178
7.1	Modules and Processes in pork chop production. . . . .	186
7.2	Parameters, variables and compartments modelled using difference equations for the further processing models. . . . .	188
7.3	Plots of the predicted distributions of contamination levels on pork chops at retail. . . . .	196
7.4	Spaghetti-looking graphs demonstrating the results of the second order modelling for the further processing models. . . . .	197

7.5	Tornado plot of sensitivity analysis for further processing models. . . .	198
A.1	. . . . .	A-15
A.2	. . . . .	A-16



---

## List of Tables

---

2.1	Overview of different analytical approaches for conducting risk analyses.	5
2.2	Overview of model types, applications, advantages and disadvantages used in microbial quantitative assessments. . . . .	18
2.3	Overview of sampling types used in microbial quantitative risk assessments. . . . .	21
3.1	Overview of model parameters for difference equations in the abattoir models. . . . .	54
3.2	Inputs and parameter values used in the model for <i>Salmonella</i> spp. . . .	65
3.2	Inputs and parameter values used in the model for <i>Salmonella</i> spp. . . .	66
3.2	Inputs and parameter values used in the model for <i>Salmonella</i> spp. . . .	67
3.2	Inputs and parameter values used in the model for <i>Salmonella</i> spp. . . .	68
3.3	Summary of predicted model outputs of pathogens on carcasses on completion of various stages of abattoir stages. . . . .	73
3.4	Results of quantitative faecal testing . . . . .	87
3.5	Results of carcass testing. . . . .	88
3.6	Results of abattoir observational studies . . . . .	89
3.7	Inputs and parameter values used in the model for <i>Campylobacter</i> . . . .	104
3.7	Inputs and parameter values used in the model for <i>Campylobacter</i> . . . .	105
3.7	Inputs and parameter values used in the model for <i>Campylobacter</i> . . . .	106
3.7	Inputs and parameter values used in the model for <i>Campylobacter</i> . . . .	107
3.8	Inputs and parameter values used in the model for <i>E. coli</i> . . . . .	108
3.8	Inputs and parameter values used in the model for <i>E. coli</i> . . . . .	109
3.9	Inputs and parameter values used in the model for <i>E. coli</i> . . . . .	110
3.9	Inputs and parameter values used in the model for <i>E. coli</i> . . . . .	111



4.1	Threshold values and corresponding dominant pathogen processes in scalding. . . . .	125
4.2	Parameter and initial values used in scalding models. . . . .	132
4.3	Effect of parameter and variable modification on carcass contamination levels post-scalding. . . . .	132
5.1	Overview of description of model parameters for individual and population-based model approaches. . . . .	151
6.1	Summary of descriptive statistics of the predicted number of, and reduction in pathogens on carcasses for mitigation scenarios in the abattoir. .	174
6.2	Results of the LHS/PRCC sensitivity analyses of the baseline models for <i>Salmonella</i> , <i>E. coli</i> and <i>Campylobacter</i> . . . . .	175
7.1	Overview of description of model parameters for the Further Processing models. . . . .	188
7.2	Values for model parameters describing cross-contamination, inactivation/removal in the Further Processing models. . . . .	191
7.3	Predicted contamination levels on pork chops during further processing.	195
7.4	Predicted numbers of <i>Salmonella</i> , <i>E. coli</i> and <i>Campylobacter</i> on pork chops estimated from the mitigation strategy. . . . .	195