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

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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 carcases 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^2. 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^{th} – 90^{th} 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.

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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
α	rate of pathogen movement from water to carcass in scalding	minute^{-1}
β	rate of pathogen movement from carcass to water in scalding	minute^{-1}
δ	rate of pathogen movement from dehairing machine to carcass	minute^{-1}
ϵ	pathogen inactivation rate on carcass in singeing	minute^{-1}
θ	rate of pathogen movement between carcasses in storage/chilling	hour^{-1}
κ	pathogen inactivation/growth rate on pork chop	day^{-1}
λ	transmission parameter	minute^{-1}
μ	rate of pathogen movement from carcass to the dehairing machine	minute^{-1}
τ_1	pathogen inactivation rate on carcasses in scalding	minute^{-1}
τ_2	pathogen inactivation rate in water in scalding	minute^{-1}
a	probability that each cfu of bacteria moves from the carcass exterior to the knife (pork chop models)	cfu^{-1}
$a_{f,s}$	probability that each cfu of bacteria moves from the faeces to the knife (abattoir models)	cfu^{-1}
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^{-1}
b	probability that each cfu of bacteria moves from the knife to the carcass exterior (pork chop models)	cfu^{-1}
$b_{e,S}$	probability that each cfu of bacteria moves from the knife to the carcass exterior (pork chop models)	cfu^{-1}
c	probability of inactivation from the knife per cfu of bacteria (pork chop models)	cfu^{-1}

Symbol	Description	Units
$c_{e,S}$	probability of inactivation from the knife per cfu of bacteria (abattoir models)	cfu^{-1}
$c_{x,S}$	probability of inactivation and removal from carcass exterior (abattoir models)	cfu^{-1}
d	probability of bacterial inactivation and removal from carcass exterior (pork chop models)	cfu^{-1}
g_f	concentration of bacteria in faeces	cfu/g
h	smoothing parameter	
k	kernel function	
r	pathogen inactivation rate on carcass in storage/chilling	hour^{-1}
$r_{p,c}$	pathogen inactivation rate on pork chop in storage/chilling	hour^{-1}
t	time	minute^{-1}
t_D	decimal reduction time	minute^{-1}
time	time	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	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	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	cfu^{-1}
F	probability of transfer of bacteria to knife	cfu^{-1}
G	probability that bacteria are present on area of carcass in contact with knife during halving	cfu^{-1}
H	probability of transfer of bacteria to knife	cfu^{-1}
Inf	probability of inactivation of bacteria on carcass skin	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^{-1}
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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