Food Safety Risk Assessment for the Australian Dairy Industry

by
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Declaration

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A theory is not the truth. It points the way to a theory that points to the truth.

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Abstract

This thesis describes the development of a food safety risk assessment framework for the Australian dairy industry, through the collection of specific information regarding that industry and its collation and organisation into a structured and flexible spreadsheet model. The risk assessment model framework was developed for use as a tool for evaluating, identifying and prioritising research needs. Developed in Excel (Microsoft Corp.) with @Risk (Palisade Corp.) as an add-in, the model uses a stochastic approach to evaluate the likely concentration of hazards that may be present in liquid milk. Those hazards include: *Escherichia coli*, *Listeria monocytogenes*, *Salmonella* spp., *Campylobacter* spp., *Staphylococcus aureus* and *Yersinia enterocolitica*, *Bacillus cereus*, antibiotic and herbicide residues. The structure of the model allows for multiple hazards to be modelled in a single simulation. Flexibility of the spreadsheet model allows for manipulation of the input distribution parameters. This enables the evaluation of the effect on hazard concentration in liquid milk to be determined from specific contamination events at the farm level. The effect of pasteurisation on microbiological hazards was examined together with the validity of log-linear thermal inactivation kinetics. Model estimates for antibiotic residues show that there is less than 10^{-3} chance of exceeding the MRL when starting with an initial probability of 0.0016 that each cow is contaminated and 0.1 grams of residue is present in milk from each contaminated cow. Microbiological hazards are not expected to survive pasteurisation given the estimated concentrations of those hazards entering the milk supply from the farm level and the reliability of the pasteurisation process.

1. Literature Review

1.1 Introduction

The trend in the incidence of food borne illness (FBI) in developed countries is, at present, unclear. The US Centre for Disease Control (CDC) has recently reported a decrease in the proportion of FBI attributed to bacterial infection for the year 2001 (CDC, 2002). However, in general FBI has been increasing over the last 10-20 years (CDN, 2000). The increase in illness could be an artefact of better epidemiological data, better diagnostic techniques (including laboratory tests) or a true increase in the number of pathogenic organisms present in foods. Due to the increase in illness, various governmental, international and industry organisations are targeting the cause of the increase.

FBI causes economic and social consequences, and with changes in social trends, e.g. increased reliance of consumers on other people to prepare food, attempts at curbing the increase in FBI have led to new areas of research, including processing and production changes, the widespread implementation of hazard analysis and critical control point (HACCP) scheme on a larger scale and also the increasing emphasis on Risk Assessment, and in particular food safety risk assessments.

Risk assessment is a field of science that has grown in recognition and use over the last 30 years. It has application in many disciplines including: medicine, finance, cancer research, computing and microbiology (Haas et al, 1993; Soh et al, 1995; Brown et al, 1998; Cassin et al, 1998; Smith 1988)). Risk assessment is an applied science formed by the confluence of several disciplines. Risk assessment in microbial food safety therefore involves elements of microbiology, epidemiology, statistics, computing, pathobiology etc. In the management of food supply, risk assessment has been adopted as a structured process for organising scientific knowledge about hazards, so that inferences can be made about the likelihood of a particular food safety event occurring because of ingestion of a hazard and the impact of this in terms of severity of illness or some social or economic measure of consequence. The assessment may be either qualitative, where data is lacking and value judgements are required, or quantitative when there is sufficient data to describe the process mathematically and the likelihood of events described in terms of numerical estimates of probability (Waltner-Toews and McEwen, 1994a). The estimate of the probability of those events should include the variability and uncertainty of those estimates based on the information available regarding the events (Nauta, 2000).

The methodological basis of risk assessment has undergone close scrutiny in the last decade. Several approaches have been developed to provide consistency to the risk assessment process within each field of application. The International Life Sciences

Institute (ILSI, 2000) and the Codex Alimentarius Commission (CAC, 1998) have developed standardised frameworks for conducting microbial food safety risk assessments. The US Environmental Protection Agency has developed a framework for environmental risk assessments (EPA, 1998), and the Office International des Epizooties (OIE, 1998) has developed a risk assessment framework for appraising the risk of hazards to animal, plant and human health in imported foods and agricultural commodities. These frameworks are not intended to be absolute rules; rather they are aimed at being useful guidelines that cover the key aspects within the risk assessment process.

The concurrent existence of several frameworks for performing risk assessments creates potential for confusion. However the approach adopted by each framework is fundamentally the same, there being minor differences in detail. To avoid confusion arising from terminology this document adopts the framework and definition proffered by the Codex Alimentarius Commission (CAC, 1998). These have been implemented during international collaborations of scientists performing a range of risk assessments of pathogens in foods (USDA/FSIS, 1998; WHO/FAO, 2001) and therefore have the most credibility to adopt as a standard. The definitions are as follows:

Hazard Identification: The identification of chemical, microbiological or physical agents that may cause adverse health affects in humans through the consumption of, or exposure to, a particular food product or type.

Hazard Characterisation: A qualitative or quantitative description of the nature of the adverse reaction associated with the chemical, microbiological and physical hazards that may be present in the food.

Exposure Assessment: The qualitative or quantitative estimate of the likely intake of chemical, microbiological or physical hazards through the consumption of food, or other routes if applicable.

Risk Characterisation: The qualitative or quantitative evaluation of the probability, including uncertainty, of the potential harm and the severity of that harm to the health of the consuming population based on the above steps.

These four steps form the basis of risk assessments designed to comply with the internationally accepted approach proffered by the World Health Organisation (WHO) and the Food and Agriculture Organisation (FAO; CAC, 1998). Individual risk assessments may differ in the detail of the approach taken, but in broad terms comply with the above structure and process. To clarify the application of the above process when dealing with a food borne hazard a more detailed explanation of each step in risk assessment is provided in the following sections.

1.2 Risk Communication

Risk communication is as vital to the success of a risk analysis as the four components of risk assessment. Regardless of how accurate and reliable the prediction that the risk assessment provides, if decision and policy makers do not understand what those predictions mean and what their limits are then problems may arise in the application of the assessment. Risk communication is an interactive exchange of ideas, information and opinions between the risk managers and the risk assessors and the stakeholders (i.e. those affected by the risk), which should occur throughout the assessment process. This is not a once off process. There should be continual interaction and communication throughout the risk assessment process (Notermans et al, 1999).

1.3 Risk Management

With adequate communication of the findings of a risk assessment the final step in the process may occur; the management of those risks identified during the assessment, taking into account the current policy and regulations that exist (Notermans et al, 1999). This falls outside the hands of the scientific community and into the realm of the regulators and policy makers. There are three effects that may be brought about, although not exclusively: the managers decide to do nothing; action is taken to reduce the risks identified in the assessment, or initiation of further research. The first of these may be considered a frustrating outcome, however, having established the conditions that enable a particular risk from a hazard(s) to arise, any change in those conditions may be monitored and at a later date some action may be made. The second, would generally arise if the risk was considered by the managers to be too great, hence the need to take action to reduce it. The third acknowledges that even the most carefully constructed risk assessment contains untested assumptions that may be erroneous or simply critical to the outcome, and usually will have identified data gaps in our knowledge of a process that, if available, would enable a clearer picture to be obtained.

It cannot be stressed enough that during the development of the risk assessment the scientist(s) conducting the RA should remain unbiased, and any value based judgements and assumptions should be explicitly stated. The scientist should also have in mind a broad view of the assessment and not just focus on quantification. It is for this reason that there is required some kind of mediation between the policy makers, the scientific community and the public, that public concern is taken into account. This stands well with the concept of the risk assessment process, which at its ultimate end aims to reduce the risk of a particular hazard causing undue illness or death.

1.4 Uncertainty

With any attempt to determine the amount of hazard, especially microbiological, at the point of consumption one must consider the variability inherent in the process. Delignette-Muller and Rosso (2000) showed that both uncertainty and variability should be accounted for in any attempt to analyse the degree of exposure to *Bacillus cereus* in pasteurised milk at the point of consumption. Any model that is used to describe the process of growth and, or inactivation should address both uncertainty and variability (Nauta, 2000; WHO/FAO, 2002).

Before a risk assessment on a particular pathogen can be produced, extensive knowledge of the organism is required including: growth rates, optimal conditions, effects of bacteriostatic and bacteriocidal agents and ability to grow and or produce toxins in food. All these aspects produce a profile of the pathogen, and with this information a clearer picture can be gained as to the foods in which the bacterium is likely to survive and/or grow.

A large part of producing a risk assessment is the ability to describe all the aspects of the risk in terms of mathematical functions, to give a numerical value to the risk. The form that this takes is a model that can be either deterministic or stochastic. A deterministic model uses point estimates rather than a range of possible values and their associated probabilities as are used in stochastic modelling. From this background it is possible to make decisions that can affect a wide range of areas, from the incidence of illness to the introduction of diseases to a "clean" area. The latter point is especially pertinent with the current efforts to open trade between all countries in the world and to have a global standard for food (ICMSF, 1998).

The biggest stumbling bock for the evaluation of potential sources of contamination and the degree of that contamination is a lack of reliable and detailed data (Jaykus, 1996). However, as with other problems regarding a lack of data, a qualitative estimate may sometimes be used rather than a quantitative one.

1.5 Stochastic Modelling

A food safety risk assessment model attempts to estimate the likelihood and magnitude of an adverse health effect (Lammerding, 1997). A value can be placed on the relative risk of a particular pathogen being present and causing illness through the use of a mathematical model. Moreover that value may be a single point estimate, usually the mean, i.e. deterministic, or a range of possible values, stochastic (Vose, 1998). The difference between these two approaches is the exclusion or inclusion of variability into the estimate. Variability is an inherent aspect in risk assessment, closely tied both to the microbial and human populations, and what happens to those populations over time

(Buchanan et al, 2000). However, there is also an amount of information that is not known nor can ever be known. This is uncertainty. There are three types of models that may be used when attempting to model a system, primary, secondary and tertiary. Tertiary models are beyond the scope of this project. Primary models describe the effect of a single variable on the system, e.g. temperature on the rate of growth of microorganisms (van Gerwen and Zwietering, 1998). Secondary models attempt to include both variable and uncertain aspects of a process into the model, thus in this example giving a range of values for the growth rate at a specified temperature. A large part of stochastic modelling is to reduce the uncertainty, and more accurately describe variability (Cassin et al, 1998).

The range of possible values that any particular variable can take is described by a distribution function in stochastic models. As with the type of model used, distribution functions can be either discrete, taking only a set of specific values, or continuous, having a range of real values (Vose, 1998). Determining the result of mathematical operations between distribution functions is not an easy task, requiring a deep understanding of the mathematics behind the functions (Vose, 2000). To overcome the problem of the difficulty in working with distribution functions, stochastic modelling uses sampling from within each distribution to obtain a final predicted value. A process automated by computer software. Hence the final output of a stochastic model is limited by the technique used to sample the range of distributions for each variable and the number of samples taken. The more samples used, the better the accuracy of the predicted values. Two commonly used sampling methods that can be used to produce a predicted value from a model are Monte-Carlo and Latin Hypercube (Vose, 1998; Cassin et al, 1998). The Monte-Carlo sampling technique takes random samples from the entire distribution of possible values, whereas Latin Hypercube sampling divides the distribution into equal parts and takes an equal number of samples from each part of the distribution. In both cases the distribution function will be re-created with sufficient iterations, although the Latin Hypercube technique will take fewer iterations than the Monte-Carlo technique (Vose, 1996). An iteration in a stochastic model is selection of a single sample from each of the distributions in that model.

With modelling it is, in a limited way, possible to know the future, or at the least put it between the bounds of mathematically derived confidence limits. A model is useless if it fails to produce predicted values that are similar to known, observed values. A saying goes: garbage in, garbage out, and is applicable to modelling. What this means is, if the inputs for a model do not reflect the real or observed range of values, then the model will produce a worthless output. For this reason a large part of producing a model is to elucidate the range of possible values for each variable prior to constructing the model itself.

1.6 Hazard Identification

A hazard can be defined as an agent which is either infectious or otherwise that may cause an adverse health effect. In food safety, a hazard is a contaminant of or an element of the food itself. The hazard in food may cause an adverse health affects when ingested by a person. Hence, there is a very broad range of hazards that may possibly be present in a particular food. Comprehensive assessment of all the risks for a particular food product may thus be very time consuming and difficult and most risk assessments consider a subset of the possible classes of hazards.

There are three main groups of hazard that may be found in foods, these include microbiological, chemical, and physical. A fourth group, product tampering, may be included although this should be classed as a risk as the tampering will affect the level of hazard in the product. This risk falls outside the scope of this risk assessment, however it should not be discounted entirely due to potentially disastrous effects. The reader should be aware that this is another source of contamination of the product.

Hazard identification is mainly a qualitative evaluation of the risk issues being estimated in the risk assessment. For microbial risk assessment hazard identification is often a straightforward task as the agents responsible for causing adverse reaction are well described and their effects on consumers can be measured in terms of hours or days (Lammerding and Fazil, 2000). Hazard identification for microbial pathogens is more focussed on determining those organisms that are likely to be present in the product of concern, in this case dairy products, rather than determining if there is a possible health effect induced from the ingestion of the organism (Lammerding, 1997). Chemicals, however, represent a seemingly inexhaustible supply of hazards. Moreover the effects of these contaminants in foods on the exposed population is usually measured in terms of years or lifetimes, making the evaluation of the risk from these hazards a difficult task. As a result there have been risk assessments performed for single chemical hazards to determine whether they have a health effect (Waltner-Toews et al, 1994a; Welp and Brümmer, 1997).

van Gerwen (2000) provides a list of potential pathogens that may be present in liquid milk. The list contains the major pathogens, that is, those widely recognised and notable for their disease causing abilities, and minor ones, that is opportunistic pathogens that would normally be of little concern except to those with a predisposing factor such as a compromised immune system. The list of potential pathogens was compiled by using a set of defined "knowledge rules". Those rules reconciled the physiological requirements each potential pathogen has for its survival with the physical conditions encountered in liquid milk. The use of knowledge rules to identify a range of hazards is an acceptable way to begin constructing a list of potential pathogens, however, the list presented by van Gerwen is large containing over 70 different pathogenic

organisms. A description of each of these pathogens would be a lengthy process and for several of the organisms listed there is a paucity of information in the published literature regarding their characteristics and modes of transmission and virulence. It will be noted by the reader that in the Hazard characterisation section (1.3) there are not 70 organisms described, rather, several of the more significant organisms have been highlighted for discussion.

Hazards identified as being of concern in this study, as elicited from discussions with experts and stakeholders in the Australian dairy industry, are shown in decreasing order of priority in Table 1.10. Included in the list are some hazards that have not been examined in this thesis, as there is insufficient information available to model the health risks arising from their occurrence in dairy products. The higher priority hazards are described briefly below.

1.7 Pathogens of concern in the dairy industry

Listeria monocytogenes

monocytogenes is a pathogen of concern, as can be perceived by Australia's and the FDA's policy of "zero tolerance" for the organism in ready-to-eat (RTE) foods (Shank et al, 1996; Duffes et al, 1999). It is ubiquitous in the environment, and relatively harmless for the majority of people. It does, however, have one of the highest mortality rates for all pathogenic bacteria, up to 30% (Gray and Killinger, 1996; Doyle et al, 1997). Incidence estimates for listeriosis range from 7.1 per million population per year in the US (Gellin et al, 1991) to between 0.1 and 11.3 per million per year in Europe (Notermans et al, 1998). In Australia there were 60 cases of listeriosis in 2000, ~3 cases per million population, with two outbreaks of food borne listeriosis with 13 cases in Australia between 1980 and 1995 (CDN, 2000). Table 1.1 outlines the main characteristics of listeriosis. Several dose response relationships have been developed for this pathogen and are outlined in section 1.8, below.

Escherichia coli

Escherichia coli O157:H7 was first recognised as a human pathogen in 1982 (Riley et al, 1983). Its importance as a human pathogen has grown over the last twenty years. There are many pathogenic strains of *E. coli*, each with different disease characteristics (Murray et al, 1998). Among the enterohaemorrhagic strains, the so-called verotoxigenic *E. coli* (VTEC) or shiga-toxin producing *E. coli* (STEC) group, *E. coli* O157:H7 is found predominantly overseas, whereas O111 is the most common strain found Australia, with some 23 cases reported between 1980 and 1995, including one death (CDN, 2000). Table 1.2 outlines the main characteristics of

enterohaemorrhagic *E. coli* infections. Dose response relationships have primarily focused on *E. coli* O157:H7 and there is a lack of information available regarding other *E. coli* strains to produce suitable dose response models.

Table 1.1 Characteristics of Listeriosis (CDC, 2001a)

Clinical Features	Manifestations are host dependent. In elderly and immunocompromised persons, sepsis and meningitis are the main presentations. Pregnant women experience a mild, flu-like illness often followed by foetal loss or bacteraemia and meningitis in their newborns. Immunocompetent persons may experience acute febrile gastroenteritis.
Etiologic Agent	*Listeria monocytogenes*
Incidence	Approximately 3 cases per million population annually in Australia.
Transmission	Contaminated food. Rare cases of nosocomial transmission have been reported.
Risk Groups	For invasive disease, immunocompromised individuals, pregnant women and their foetuses and neonates, and the elderly.

Table 1.2 Characteristics of verotoxigenic, or ST *E. coli* infections (CDC, 2001b)

Clinical Features	Acute bloody diarrhoea and abdominal cramps with little or no fever; usually lasts 1 week.
Etiologic Agent	Several, most recognised is *Escherichia coli* serotype O157:H7. Gram-negative rod-shaped bacterium producing Shiga toxin(s).
Sequelae	Haemolytic uremic syndrome (HUS): People with this illness develop kidney failure and often require dialysis and transfusions. Some develop chronic kidney failure or neurological impairment (e.g., seizures or blindness). Some require surgery to remove part of the bowel. Death (estimated 61 fatal cases annually; 3-5% with HUS die).
Costs	Estimated 20 cases annually in the Australia. The illness is often misdiagnosed; therefore, expensive and invasive diagnostic procedures may be performed. Patients who develop HUS often require prolonged hospitalisation, dialysis, and long-term follow-up.
Transmission	Major source is ground beef; other sources include consumption of un-pasteurised milk and juice, sprouts, lettuce, and salami, and contact with cattle. Waterborne transmission occurs through swimming in contaminated lakes, pools, or drinking inadequately chlorinated water. Organism is easily transmitted from person to person and has been difficult to control in child day-care centres.
Risk Groups	All persons. Children <5 years old and the elderly are more likely to develop serious complications.

Salmonella

The genus *Salmonellae* is now considered to contain a single species, *Salmonella enterica*, with seven distinct subgroups. This species contains over 2000 serovars all of which are capable of causing infection and disease in humans (Murray et al, 1998; Fazil et al, 2000). In Australia there were around 5700 reported cases of Salmonellosis in total in 2000 (CDN, 2000). Foodborne salmonellosis in Australia, between 1980 and 1995, caused 27 outbreaks with 1323 cases and one death (CDN, 2000). Table 1.3 outlines the main characteristics of salmonellosis. This highlights the importance of this organism in the food industry, as it covers many food types, countries and situations. Teunis et al (1999) reported that one of the biggest complications with modelling the dose response relationship for *Salmonellae* is the difference in strain virulence within the species. This strain difference makes it difficult to describe a dose response for *Salmonellae*, because it should be known for which strain the dose response has been derived. Consequently several dose response relationships have been developed for this pathogen; see section 1.8.

Table 1.3 Characteristics of *Salmonella* spp infections (CDC, 2001c)

Clinical Features	Fever, abdominal cramps, and diarrhoea (sometimes bloody). Occasionally progresses to sepsis.
Etiologic Agent	Enterobacteriaceae of the genus *Salmonella*. Approximately 2000 serotypes cause human disease.
Transmission	Contaminated food, water, or contact with infected animals.
Risk Groups	Affects all age groups. Groups at greatest risk for severe or complicated disease include infants, the elderly, and persons with compromised immune systems.

Campylobacter jejuni

Campylobacteriosis is one of the most common causes of intestinal disease (Medema et al, 1996) with estimates of incidence ranging between 1-2% in the Netherlands (Medema et al, 1996), ~1% in the US (Tauxe, 1992), and 1.1% in the UK (Kendall and Tanner, 1982). In Australia there were ~12000 notified cases of campylobacteriosis in the year 2000. Between 1980 and 1995 there were 5 outbreaks involving 109 cases of foodborne campylobacteriosis (CDN, 2000). The majority of cases of campylobacteriosis are sporadic. Table 1.4 outlines the main characteristics of *Campylobacter jejuni* infections. Several dose response models have been published, these are presented in section 1.8.

Table 1.4 Characteristics of *Campylobacter jejuni* infections (CDC, 2001d)

Clinical Features	Incubation periods of between 2 and 11 days, 3-5 the most common. In adults: onset quite fast. Duration ~<1week. Recurrence of symptoms in 25% of cases (Blaser et al, 1983). In children: vomiting in ~50% of cases, few patients with abdominal pain.
Etiologic Agent	*Campylobacter jejuni* and *C. coli* two most common causes of infection with this genus
Incidence	Milk implicated in a large number of infection outbreaks, from small localised outbreaks to large ones involving 100's of people. Incidence in raw milk is low 0.4% up to 8.1% (latter figure is from cattle herds known to be infected with Campylobacter).
Sequelae	Symptoms intestinal but sometimes flu-like prodromal period with associated malaise, headache, shivering, dizziness and myalgia. Intestinal symptoms more pronounced if following a prodrome. Diarrhoea – severe and prostrating to a few loose stools. Abdominal pain.
Transmission	Infective dose – as few as 500cells and up to 10^6 have been reported. Contamination of milk most likely though faeces. Only been associated with liquid milk rather than other dairy products.
Risk Groups	bimodal distribution, in the UK children between 1-4 yrs, and between 15-24yrs. Male homosexuals at greater risk to Campylobacter enteritis. Systemic infections mainly in those with underlying predisposition – malignant diseases such as leukaemia, immunosuppression, alcoholism, liver cirrhosis, diabetes, chronic renal failure and gastrectomony (Skirrow, 1984). Pregnancy is also a risk factor (Weinberg, 1984). Excluding pregnancy, systemic infections predominantly in males 45yrs or older.

Bacillus cereus

Bacillus cereus is a Gram-positive, spore-forming bacterium, found in most environments, from soil to the raw ingredients in foods. It is recognised as a food borne pathogen and is a significant causative agent in food born illness, due to either of two toxins produced by the organism (Dufrenne et al, 1995; Murray et al, 1998). In Australia between 1980 and 1995 there were 5 outbreaks of food borne *B. cereus* infections, involving 27 cases (CDN, 2000). More recently the organism has been implicated in an outbreak in Victoria (Vic. DHS, 2002). The two toxins produced by *B. cereus* cause differing illness. A heat stable toxin is associated with the emetic form of illness, and a heat labile toxin is associated with the diarrhoeal form (Murray et al, 1998). Table 1.5 outlines the characteristics of *B. cereus* intoxications.

Notermans et al (1997) describe the risk assessment process for *B. cereus* in pasteurised milk. From various sources, they state, that the likely level of the organism required to induce symptomatic illness is $>10^5$. This is a similar figure to that presented by Doyle et al (1997), who indicate that an infectious dose of this organism is between 10^5-10^7 and 10^5-10^8 will likely induce toxin production in the small intestine and in

food, respectively. Those authors did not derive a dose response relationship for the organism. A lack of information regarding this organism's ability to induce illness, indications that not all strains of *B. cereus* are toxin producers, and differences between the level of organism required to cause either emetic and diarrhoeic illness are highlighted as difficulties in developing a suitable dose response relationship for this organism.

Table 1.5 Characteristics of *Bacillus cereus* infections (adapted from Murray et al, 1998).

Clinical Features	Diarrhoeal and emetic food poisoning a result of two different toxins
Etiologic Agent	*Bacillus cereus* – toxin production.
Incidence	No cases of *B. cereus* poisoning have been reported for UHT milk, but is a common contaminant of dried milk, although the importance of this is under debate.
Sequelae	Diarrhoeal – incubation period of 8-16 hours, followed by abdominal cramps, and profuse diarrhoea. Vomiting and fever are occasional symptoms, recovery usually within 24 hrs. Emetic poisoning short incubation of 1-6 hours. Nausea followed by vomiting and malaise, recovery generally within 24 hours.
Transmission	Associated with the spoilage of fresh milk, this has changed recently due to the introduction of refrigeration for pasteurised products, and partly from reduced incidence of contamination of raw materials. Can still be readily isolated from pasteurised milk (Christiansson, 1989) and cream. Can also be isolated from UHT milk (Mostert et al, 1979; Westhoff and Dougherty, 1981)
Risk Groups	No particular groups are at risk, although the extremes of age and immunocompromised would have a relatively higher risk of infection. Most commonly associated with large-scale food preparation.

More complete lists of potential pathogens in dairy products are presented in Boor (1997) and van Gerwen (2000). A summary of the characteristics of disease caused by some of those organisms is given in Tables 1.6, 1.7, 1.8 and 1.9.

Table 1.6 *Staphylococcus aureus*: characteristics of disease

Clinical Features	Symptoms usually appear within 2-4 hours (Bergdoll, 1979). Symptoms generally persist for less than 24 hours
Etiologic Agent	*Staphylococcus aureus*
Incidence	USA of 131 outbreak and over 7000 cases (Holmberg and Blake, 1984). Reported cases of staphylococcal food poisoning from cheese limited to cheddar and similar varieties (ICMSF, 1980, 1986) and Swiss type cheese (Todd et al, 1981).
Sequelae	Nausea, retching, vomiting and less frequently diarrhoea. Fever has been found in ~16% of cases (Holmberg and Blake, 1984). With severe cases – dehydration, shock and collapse, accompanied by shallow breathing and weak pulse. Up to 10% of sufferers seek medial attention. Death rare. Symptoms may be confused with *B. cereus* emetic infection (Newsome, 1988)
Transmission	Milk from most species including cattle (Harvey and Gilmour, 1985), goats and sheep contain *S. aureus*. Greater numbers in mastitic milk, although less marked with this organism than other mastitis causing bacteria, *S. uberis* (Bramley et al, 1984). Presence in raw milk is generally not a problem, though from mastitic milk higher numbers of enterotoxigenic organisms may be present (Lombai et al, 1980). There have been examples of toxin production in milk prior to pasteurisation (Holmberg and Blake, 1984). Staphylococcus aureus can be isolated from a wide range of fermented milk products, usually in low numbers. The greatest numbers is generally in hard cheeses (cheddar etc) due predominantly to a poor starter culture.
Risk Groups	Wide variation among normal adults, but greatest susceptibility in the young and old. Unhealthy people are at greater risk, but no particular predisposing condition for staphylococcal infection.

Table 1.7 Characteristics of Group A Streptococcal infections (CDC, 2001f)

Clinical Features	Non-invasive disease (strep throat, cellulitis); invasive disease (necrotizing fasciitis (NF), streptococcal toxic shock syndrome (STSS), bacteraemia, pneumonia); nonsuppurative sequelae (rheumatic fever, post-streptococcal glomerulonephritis). STSS is a severe illness characterized by shock, multiple organ failure. NF presents with severe local pain, destruction of tissue. Rheumatic fever is a leading cause of acquired heart disease in young people worldwide.
Etiologic Agent	Group A *Streptococcus*; STSS and NF occur more often among persons infected with group A *Streptococcus* spp serotypes M-1 and M-3 or toxin- producing strains.
Incidence	Approximately 10,000 annual cases of invasive disease (3.7/100,000 population) occurred in 1998; approximately 5% are STSS and 5%-8% are NF. Over 10 million noninvasive GAS infections (primarily throat and skin infections) occur annually.
Sequelae	Death in 10%-13% of all invasive cases, 45% of STSS, 25% of NF cases. Organ system failure (STSS) and amputation (NF) also may result.
Transmission	Person to person by contact with infectious secretions.
Risk Groups	Invasive disease: elderly, immunosuppressed, persons with chronic cardiac or respiratory disease, diabetes, skin lesions (i.e. children with varicella [chicken pox], intravenous drug users) African-Americans, American Indians. Noninvasive disease: children (especially elementary school age) at highest risk.

Table 1.8 Characteristics of Group B Streptococcal infections (CDC, 2001g)

Clinical Features	In neonates: sepsis, pneumonia and meningitis. In adults: sepsis and soft tissue infections. Pregnancy-related infections: sepsis, amnionitis, urinary tract infection, and stillbirth.
Etiologic Agent	*Streptococcus agalactiae* or group B streptococcus (GBS).
Incidence	Approximately 18,000 cases occur annually in the United States; approximately 7,500 occurred in newborns before recent prevention. The rate of neonatal infection has decreased from 1.7 cases per 1,000 live births (1993) to 0.6 cases per 1,000 live births (1998).
Sequelae	Neurological sequelae include sight or hearing loss and mental retardation. Death occurs in 6% of infants and 16% of adults.
Transmission	Asymptomatic carriage in gastrointestinal and genital tracts is common. Intrapartum transmission via ascending spread from vaginal and/or gastrointestinal GBS colonization occurs. Mode of transmission of disease in non-pregnant adults is unknown.
Risk Groups	Risk Groups Adults with chronic illnesses (e.g., diabetes mellitus and liver failure), pregnant women, the foetus, and the newborn are at risk. For neonatal disease, risk is higher among infants born to women with GBS colonization, prolonged rupture of membranes or pre-term delivery.

Table 1.9 Characteristics of *Yersinia enterocolitica* infections (CDC, 2001e)

Clinical Features	Children - fever, abdominal pain, and diarrhoea, which is often bloody. Adults - right-sided abdominal pain and fever. Symptoms develop within 4-7 days. Duration of illness 1-3 weeks, maybe longer
Etiologic Agent	Most illness caused by *Y. enterocolitica*. *Y pseudotuberculosis* causes similar illness though not as common.
Incidence	1 per 100000 people, more common in children and during winter
Transmission	Animal reservoir primarily pigs, also rodents, rabbits, sheep, cattle, horses, dogs, and cats. Contaminated milk or untreated water, contact with infected animals, faecal-oral infections and rarely through contaminated blood

Table 1.10 – Ranking of Hazards Associated with Dairy Products

Hazard Ranking	Hazard
High	Enterococci; EHEC/VTEC; Salmonella spp.; *Listeria monocytogenes*; herbicides; aflatoxins
Medium	*Yersinia* spp.; *Campylobacter* spp.; *Bacillus cereus*; *Staphylococcus aureus*; *Cryptosporidium* spp; antimicrobials; antiparasitics – flukicides and anthelminthics ; mycotoxins Pesticides – Organochlorines, Organophosphates and pyrethroids
Low	Q Fever; Toxoplasmosis; *Brucella abortis*; *Pseudomonas pseudomallei*; *Clostridium botulinum*; *Clostridium perfringens*; BST and other hormones; Blue-green algae; Heavy metals and Iodine
For consideration if time is available	*Mycobacterium paratuberculosis*; *Bacillus anthracis*; Viruses; agent causing bovine spongiform encephalopathy (BSE); enzootic bovine leucosis (EBL)

Of these hazards it was resolved (see section 2.1) that those to be included in the risk assessment model be: *Escherichia coli*, *Salmonella* spp, *Listeria monocytogenes*, *Bacillus cereus*, *Campylobacter jejuni*, *Yersinia enterocolitica*, antibiotics and herbicides in general (there was insufficient information to focus on a particular one).

1.8 Hazard Characterisation – Dose Response Assessment

Hazard characterisation, as mentioned previously, is the qualitative or quantitative description of the adverse health effects resulting from contact with those hazards identified in the hazard identification (Farber et al, 1996; Buchanan et al, 2000). Buchanan et al (2000) mentions the infectious disease triangle, stating the importance of three aspects of the likelihood of developing illness from a foodborne pathogen. These three aspects include the interaction between the host, the pathogen and the food matrix, which together determine if illness is manifested in the host. The three points in the disease triangle are:

- The disease causing characteristics of microorganisms; infections, toxico-infectious or toxigenic.
- The characteristics of the host; the very young, the old, immunocompromised, immune or naive.
- The food matrix: the food may confer some resistance from the host's non-specific and immune system defences to the pathogen, it may either hamper or enhance the pathogenicity of the organism.

A further consideration emerges from Buchanan et al (2000): that of variability within each aspect of the disease triangle.

It is not necessary here to describe the wide and varied forms of pathogenicity of microbiological hazards or to give a detailed examination of the chemical hazards (This alone could constitute a third of this thesis). For clarity, however, a brief discussion of the various forms of dose response models that have been developed for both microbiological and chemical hazards shall be given, and then an examination of each prioritised hazard together with their dose response relationship, if that exists.

1.8.1 Dose Response Assessment

Dose response modelling is not a new concept. One journal article, describing mathematically the infectivity of the tobacco mosaic virus (Furomoto and Mickey, 1967), is more than 30 years old and forms the theoretical basis of many of the models used currently. The basis of dose response modelling for food safety risk assessments, that is determining/predicting human health effects to known levels of hazards in a mathematical form, has not changed. There have been a large variety of dose response papers published. These consider topics including: cancer research (Edler and Kopp-Schneider, 1998), chemical safety (Krewski and van Ryzin, 1981; Welp and Brümmer, 1997), microbiology (Buchanan et al, 2000; Haas et al, 2000; Havelaar et al, 2000), water safety research (Regli et al, 1991; Haas et al, 1993), discussions on dose response modelling (Coleman and Marks, 1998; Buchanan et al, 2000), and papers discussing the advantages and disadvantages of different dose response models (Holcomb et al, 1999; Teunis and Havelaar, 2000; WHO/FAO, 2002).

There are many different ways to model the health reaction to the ingestion of known hazards. For microbial dose response models there are predominantly two end points that are modelled: the probability of infection and the probability of illness. A third endpoint that may be mentioned, though rarely modelled, is the probability of mortality at a given dose, or it may be presented as severity with mortality included. Most studies only examine one of the end points, whereas a few try to make some connection between infection and the probability of developing illness from that infection.

Dose Response Modelling Theory

The aim of dose response modelling is to determine the probability of a defined adverse health reaction from the ingestion of a particular hazard. Of the dose response models that have been developed, there are two broad categories: those models that assume a threshold, below which no infection occurs, and hit-theory models, which assume that every individual cell or toxic particle is capable of causing infection in the host (Furomoto and Mickey, 1967; Turner, 1975; Coleman and Marks, 1998). Much debate over which type of model is the most suitable has occurred. The majority of models used are hit-theory models, which are in a class of a larger group of mechanistic models. A single hit model assumes that a single particle is capable of causing an adverse health reaction. The log-logistic, log-probit and Weibull (-Gamma) models are among the hit theory models used (WHO/FAO, 2002). There has been confusion about which models are and are not hit theory models. For example the exponential model has often been considered a threshold model due to the sigmoidal shape of the response curve, which suggests that below some level there is no response, however, Buchanan et al (1997) show that when the log is taken of the probability of response, there is a linear relationship between the log dose and the log probability. This precludes the possibility of a threshold existing for this model. Moreover, for another widely used model, the Beta-Poisson model, it has been demonstrated (Teunis and Havelaar, 2000) that although it is assumed to be a single hit model, it is not.

What follows is a brief discussion on the various forms of dose response models that exist in the published literature, the relationship between different models, and problems associated with each.

The underlying theme of hit-theory models assumes that each ingested pathogen or unit of hazard is capable of causing disease, with some probability (Vose, 1998). This is a Binomial process; hence the probability of infection is given by:

$$P_{inf} = 1 - (1 - p)^n \qquad (1)$$

Where P_{inf} is the probability of infection, n is the amount of hazard ingested (trials), and p is the probability that each organism ingested will survive to cause infection.

The simplest of the dose response models that are used in the literature is the exponential model. The exponential model assumes that each organism entering the host is capable of causing infection, i.e. a single hit is required to cause infection, that each ingested cell acts independently of others, and that the organisms are distributed randomly throughout the contaminated food. The model is expressed in the form:

$$P = 1 - e^{-rd} \qquad (2)$$

Where r is probability of an individual cell causing infection and d is the dose (number of organisms ingested).

The cells ingested in each dose are assumed to follow a Poisson distribution, randomly distributed, and the dose is the mean of the sample taken from that distribution (Powell et al, 2000). A further assumption in the exponential model is that r is a constant. This represents the host-microbe interaction, or the proportion of organisms surviving the host's defences to cause infection (Regli et al, 1991; Powell et al, 2000).

If r is not a constant, by taking a general case it's value can be approximated (Vose, 1998). The Beta-Poisson model does this where it is assumed that r follows a Beta distribution (r = Beta(a, b)). This may be explained in terms of the ingested cells and the host's immune response. For each individual cell in the dose, each may be considered independent, that is they all have equal probability of surviving to cause infection once inside the host. However, the number of cells in the dose that survive and are able to initiate infection can be described by a Beta distribution (Holcomb et al, 1999; Powell et al, 2000). The general form of the Beta-Poisson model is expressed as:

$$P = 1 - (1 + d/b)^{-a} \quad (3)$$

This only holds for when b is much larger than a, and hence the probability of an individual cell causing infection is low (Vose, 1998). The more common form of this is to express b in terms of the median effective dose (ED_{50}) or median Infective dose (ID_{50}), that is, the number of ingested organisms required to cause infection in half of the exposed population, where:

$$b = ED_{50}/(2^{1/a} - 1) \quad (4)$$

Hence the Beta-Poisson model (3) can be expressed as:

$$P = 1 - (1+ (d/ED_{50})^* (2^{1/a} - 1))^{-a} \quad (5)$$

Another approximation of the Beta-Poisson model may be made. Where b approaches 0, the model (3) reduces to its Poisson form:

$$P = 1 - e^{-r} \quad (6)$$

The Beta-Poisson model is a special case of a third, more flexible three-parameter model, the Weibull-Gamma model:

$$P = 1 - (1 + (d^x/b))^{-a} \quad (7)$$

Where a, b and x are parameters affecting the shape of the curve.

This reduces to the Beta-Poisson model when $x = 1$. Moreover, the Weibull-Gamma reduces to the Log-Logistic when $a = 1$.

Other models have been used to describe the dose response relationship for microbial pathogens. The general forms for these models are listed in Table 1.11.

Table 1.11 Dose response models used for microbial pathogens, general form

Model	Parameters	Equation
Logistic	alpha, beta	$e^{alpha + beta*ln(dose)} / 1 + e^{alpha + beta*ln(dose)}$
Gompertz – log	alpha, beta	$1 - e^{-e^{\wedge}(alpha + (beta*ln(dose)))}$
Gompertz – Power	alpha, beta, power	$1 - e^{-e^{\wedge}(alpha + (beta\wedge power))}$
Log-Normal (Probit)	alpha, beta	Normal_cdf(alpha + beta * $\log_{10}$(dose)
Multihit	gamma, k	Gamma_cdf(gamma * dose, k)

cdf = cumulative distribution function

There are several considerations before a dose response model is used to predict the probability of a health outcome. Firstly, the model should fit the observed data adequately, and it should be as simple as possible (a more parsimonious model is one that has fewer fit parameters than another which fits the data equally). The model chosen should also be applicable over the range of conditions for the data to which it is being applied (Holcomb et al, 1999). In the event that there is no suitable dose response model available, with the exception of developing a new one, it has been proposed that linear risk extrapolation can often be accepted as the default for dose-response curves (Waltner-Toews and McEwen, 1994a).

Due to the broad range of models and hazards that have had a dose response relationship described, the succeeding section details some models that have been developed for microbial pathogens and presents a short treatise on the concept of chemical dose response assessment.

1.8.2 Microbial Dose Response Assessment

There are several pathogens on which a greater amount of risk assessment research has been focussed, namely *E. coli* O157, *Salmonella*, *Listeria monocytogenes* and to a lesser extent *Campylobacter jejuni.* Consequently for these pathogens there are several papers that describe dose response models that have been developed. One of the basic premises of these models is that at an increasing dose the chance of becoming ill increases to maximum at some point, that is, the response has an asymptote.

For each of the identified microbiological hazards a discussion on the various dose response models proposed to describe infectivity curves is presented. There are some microbial pathogens that have not had a dose-response curve defined. This is mainly due to a lack of data to describe the curve with any degree of certainty.

Listeria monocytogenes

Haas et al (1999) developed and validated a dose response relationship for infection for *Listeria monocytogenes*. Data used were based on animal feeding studies conducted by Audurier et al (1980) and Golnazarian et al (1989). Haas et al (1999) used three different sets of data when fitting the parameters for the dose response models. Hass et al (1999) compares the use of the exponential and the Beta-Poisson dose response models to fit the data used. Those authors found that the Beta-Poisson model had the best fit to all sets of data, including the pooled dataset. A summary of the fit parameters is shown for the pooled dose response data (Table 1.12).

Buchanan et al (1997) developed a risk assessment model for listeriosis using German smoked fish data, as an example of the development of purposefully conservative risk assessment models based on annual disease statistics and food survey data. The dose response model used in that assessment was an exponential dose response model with parameter R being as conservative as the data would allow. The R-value estimated in the paper is defined as the probability that the ingestion of a single cell of *L. monocytogenes* would produce an active case of listeriosis. This approach estimates a "worst case", thus allowing the current tolerance to this organism's presence in foods to be evaluated. The dose response model was used to estimate an adverse health effect, that is morbidity.

Lindqvist and Westöö (2000) used a similar approach as Buchanan et al (1997) to develop a conservative dose response relationship for *Listeria monocytogenes* based on annual disease statistics and food survey data in Sweden. They selected two models: the exponential and the Weibull-gamma. The fitted parameters for the exponential model are shown in Table 1.8.2.1. The parameter values used in the Weibull-gamma model were those estimated by Farber et al (1996).

Farber et al (1996) developed a dose response model for *Listeria monocytogenes* based on the Weibull Gamma model. The parameter values fitted to the model are not presented, however, those authors attempted to distinguish between high and low risk populations, through the use of the infectious dose (ID) at two levels, ID_{10} and ID_{90}. The ID_n is that dose causing illness in the stated (n) percentage of the population, i.e. in the above case, 10% and 90% of the population respectively.

The United Nation's World Health Organisation (WHO) and the Food and Agriculture Organisation (FAO) conducted a risk assessment for *Listeria*

monocytogenes in ready to eat foods (WHO/FAO, 2001). An exponential model was used for the dose response relationship, with different parameter values for susceptible and less susceptible exposed populations.

Table 1.8.2.1 Dose response model parameters for *Listeria monocytogenes*

Author	Model	Parameter	Value
Haas et al (1999)	Exponential	k	1.77×10^{4}
	Beta-Poisson	α	0.25
		N_{50}	2.76×10^{2}
Buchanan et al (1997)	Exponential	R	1.179×10^{-10}
Lindqvist ad Westöö (2000)	Exponential	R	5.6×10^{-10}
Farber (1996)	Weibull-gamma	b	$10^{10.98}$ (high risk)
			$10^{10.26}$ (low risk)
WHO/FAO (2001)	Exponential	R	1.06×10^{-12} (susceptible)
			2.37×10^{-14} (normal)

N_{50} signifies the dose at which half the exposed population will become infected
R is the probability that the ingestion of a single cell causes the adverse health reaction

A comparison of the different dose response relationships that have been derived for *Listeria monocytogenes* is shown (Fig 1.1). The curves presented are those that could be regenerated from the information presented in the papers listed above.

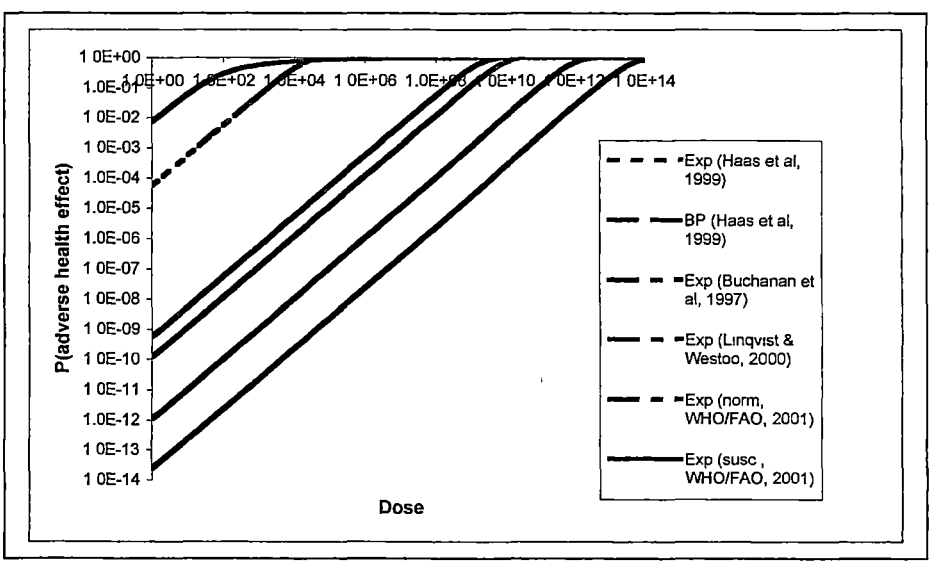

Fig 1.1 Comparison of different dose response models for *Listeria monocytogenes*. Exp: exponential dose response model, BP: Beta-Poisson dose response model. Norm and Susc refer to the exposed population being either normal or susceptible to infections with this organism

Escherichia coli

Haas et al (2000) developed a dose response relationship for *E. coli* O157:H7 based on an animal model for this organism from data produced by Pai et al (1986). This data was fitted to the beta-poisson dose response relationship, with validation based on outbreak data from the US. In this study the beta-poisson model goodness of fit (GOF) was compared with that of the exponential model. Haas et al (2000) state that although Shigella can be used in surrogate dose response modelling for *E. coli* O157, the dose response relationship they present does not support the use of surrogacy between the two organisms. Intra-specific variability is inherent in all organisms, inter-specific variability, however, is greater. Regardless, there have been attempts to model the dose response relationship for pathogenic *E. coli* with surrogate microorganisms, for example *Shigella* spp (Cassin et al, 1998). The dose response curves are reproduced in Fig 1.2.

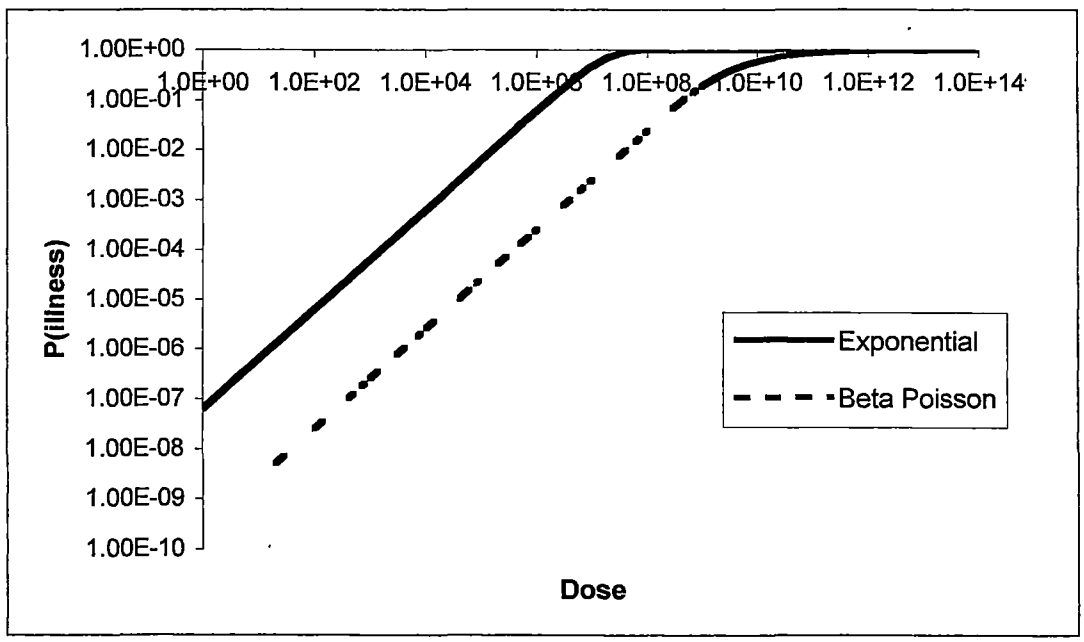

Figure 1.2 Comparison of the Exponential and the Beta-Poisson dose response curve for *E. coli* O157:H7. Redrawn from equations presented by Haas et al (2000).

Cassin et al (1998) describe another dose response relationship for *E. coli* O157:H7. This model is based on human feeding trials for *Shigella dysenteriae* and *Shigella flexneri.* It assumes that the pathogenicity of shiga-toxin producing *E. coli* is similar to that of the *Shigella* species. The difference between their dose response relationship and that produced by Haas et al (2000), with the exception of surrogacy, lies in the model used. Cassin et al (1998) use a beta-binomial model as opposed to the beta-poisson model used by Haas et al (2000). Also Cassin et al (1998) describes a method for adjusting the model to cover portions of the population with varying susceptibility to illness from this pathogen.

An animal model was used to study the infectivity of *E. coli* O157 in rats (Havelaar et al, 2000). The experimental design did not provide sufficient data to allow the development of a dose response relationship. Furthermore Havelaar et al (2000) did not highlight the problems associated with extrapolating an animal model-based dose response relationship to humans. Because of a lack of data in the published literature based on animal models for *E. coli* O157 infection a description of the dose response relationship has not been included in this thesis.

Powell et al (2000) described the development of two different sets of dose response models for *E. coli.* The first used *Shigella dysenteriae* as a surrogate for Shiga-toxin producing *E. coli* strains, the second used data from enteropathogenic *E. coli* (EPEC) strains. The data were derived from human feeding trials with enteropathogenic *E. coli* (EPEC) and *S. dysenteriae* Type 1 (Levine et al, 1973; Levine et al, 1978; Bieber et al, 1998). Three models for each data set were fitted: the exponential, the Beta-Poisson, and the Weibull-Gamma models. The fit parameters for those models are given in Table 1.13. Moreover, the aim of that paper was to describe an "envelope" dose response model for *E. coli* O157:H7. An envelope model describes the highest and lowest dose response limits for infectious strains of *E. coli*, and then a mean dose response curve is fitted. The model chosen for the envelope was the beta-Poisson, with the upper and lower bounds defined by the surrogate pathogen (upper) and EPEC (lower) model. The median value for the envelope was again a beta-Poisson DR model, with epidemiological data from various sources, primarily concerned with ground beef in the USA. That model was the most complete, in terms of explanation of the process involved in generating the dose response curve, and provided a means of determining the variability in probability of infection between strains of *E. coli.* The dose response curves generated from the equations presented by Powell et al (2000) are presented (Fig 1.3. overleaf).

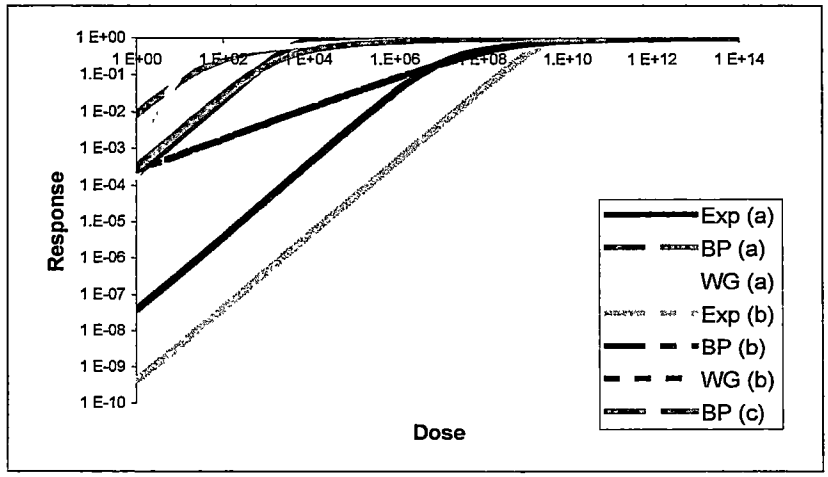

Figure 1.3 Comparison of the dose response curves for *E. coli* O157:H7 presented by Powell et al (2000). *a*, *b* and *c* refer to datasets used to derive the dose response curve (see table 1.13). Exp = exponential, BP = beta-Poisson, WG = Weibull-Gamma

Haas et al (2000) show a greater degree of uncertainty in the low and high dose regions of the curve with the beta-Poisson model than does the beta-binomial mode used by Cassin et al (1998). The beta-binomial model used by Cassin et al (1998) gives a N_{50} of ~3.2×10^3, whereas Haas et al's (2000) model gives the N_{50} at ~6.3×10^5. The reasons for this difference may arise from several sources; the data used, the method of parameter fitting for determining the relationship; the strain of the bacterium used, or the differences between the general form of the dose response curve described by the beta-Poisson and beta-binomial models.

Salmonella

Teunis et al (1999) used the data collected from human feeding studies for *Salmonella enterica* serovar Meleagridis to develop a dose response relationship for this pathogen. The authors attempted to model both the dose response for infection and the dose response for illness resulting from infection. Teunis et al (1999) used the beta-Poisson dose response relationship to model the probability of infection. Fitting of the dose response data resulted in the Beta-Poisson dose response model reducing to a simple exponential model. Summarised in Table 1.14 are the parameter values fitted to the dose response models.

Whiting and Buchanan (1997), using an exponential dose response relationship, predicted that with an increase in prevalence of *Salmonella* Enteritidis in flocks of chickens the probability of illness increases. They used parameter values derived by Rose et al (1996). In Whiting and Buchanan (1997), the use of the dose response

Table 1.13 Summary of models for dose response relationship for *E. coli* O157:H7

Author	Model	Parameter	Value
Haas et al (2000)	Exponential	$P_I(D)$	$1 - \exp(-D/k)$
		K	1.6×10^7
	Beta-Poisson	$P_I(D)$	$1 - [(1 + D/N_{50}(2^{1/\alpha} - 1))^{(-\alpha)}]$
		α	0.49
		ED_{50}	5.96×10^5
Cassin et al (1998)	Beta-binomial	$P_I(D)$	$1 - (1 - P_I(1))^D$
		$P_I(1)$	Beta (α, β)
		α	0.267
		β	$\ln \beta \sim$ Normal (5.435, 2.47)
Powell et al (2000)	(a)		
	Exponential	r	2.052×10^{-4}
	Beta-Poisson	α	0.157
		β	9.169
		ED_{50}	742
	Weibull gamma	α	0.040
		β	239.327
		x	3.514
	(b)		
	Exponential	r	4.070×10^{-10}
	Beta-Poisson	α	0.221
		β	3112348.268
		ED_{50}	68494661
	Weibull gamma	α	1.944
		β	7409.340
		x	0.418
	(c)		
	Beta-Poisson	α	0.221
		β	8722.480
		ED50	16643

$P_I(D)$ is the probability of illness given a dose of D organisms
$P_I(1)$ is the probability of illness given a dose of 1 organism
(a) denotes the model fit parameters for *S. dysenteriae*
(b) denotes the fit parameters for EPEC
(c) The median value for the envelope dose response model
ED_{50} is the dose required to cause symptomatic illness in half the exposed population

model is not purely to demonstrate the goodness of fit of the model but as part of a demonstration of the risk assessment process, and its ability to quantitatively describe the production of eggs and the associated contamination with *Salmonella* Enteritidis. The parameter value for the dose response model is shown (Table 1.14) and the curve generated is also presented (Fig 1.4).

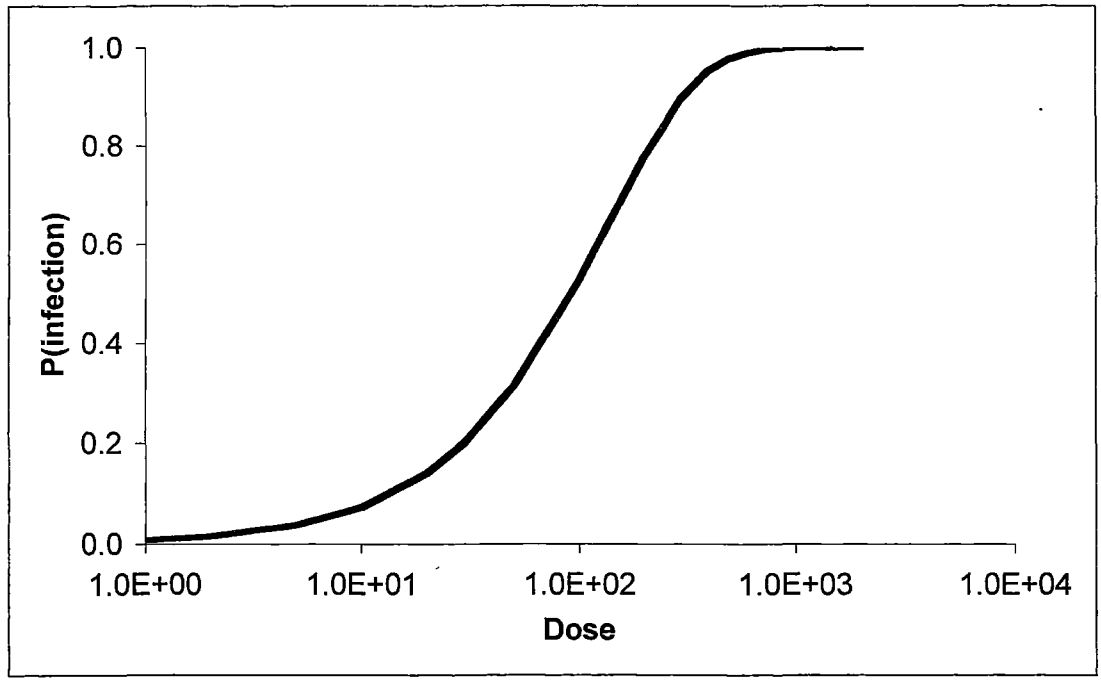

Figure 1.4 Dose response curve for *Salmonella* Enteritidis in liquid eggs. (Reproduced from Whiting and Buchanan, 1997)

Brown et al (1998) also produced a risk assessment for *Salmonella* in chickens. Those authors do not identify which serotype of *Salmonella* they chose for developing the risk assessment; neither do they give adequate explanation of the model.

An animal model was used to study the infectivity of *Salmonella* Enteritidis in rats (Havelaar et al, 2000). The data presented in that paper indicate a high infectivity of the rats by *Salmonella* Enteritidis, however the authors did not describe a mathematical dose response relationship for this bacterium in rats. Lack of data precludes a description of the dose response relationship.

Fazil et al (2000) compare three different dose response models, in a report for the FAO/WHO on the hazard characterisation, for *Salmonella*. The first details Fazil's (1996) beta-Poisson dose response model for infection for non-typhoid Salmonella on both naïve and exposed people, based on feeding study data. The second outlines the dose response model developed in the USDA/FDA (1998) *Salmonella* Enteritidis risk assessment model. Based on epidemiological data concerning Salmonella Enteritidis, the model proposed by the USDA/FDA study (1998) is a beta-Poisson model for illness. The third model outlined was presented in risk assessment paper developed by Health Canada (Paoli, 2000; Ross, 2000). For that risk assessment a re-parameterised Weibull model was used. The fit parameters for each of the models are shown in Table 1.14.

Table 1.14. Parameter values for dose response models for *Salmonella*

Author	Model	Parameter	Value
Whiting and Buchanan (1997)	Exponential	r	0.00752
Teunis et al (1999)	Beta-Poisson	_	0.89
		_	4.4×10^{5}
	Illness model	P(ill|inf)	$1-(1+\_\_)^{-r}$
		_	1
		_	_D
		_	1.0×10^{-16}
		r	3.4×10^{8}
Fazil et al (2000)	Beta-Poisson	_	0.3136
		_	3008
	Beta-Poisson (naïve)	_	0.4059
		_	5308
USDA-FSIS (1998)	Beta-Poisson (normal)	_	0.2767
		_	Normal(21.159, 20) min: 0, max: 60
	Beta-Poisson (susceptible)	_	0.2767
	-	_	Normal (2.116, 2) min: 0, max: 6
Health Canada (see Fazil et al, 2000)	Re-parameterised Weibull	_	Normal(-1.22, 0.025)
		Concentration	Lognormal(0.15, 0.1)
		Amount Consumed	Pert(60, 130, 260)
		Attack Rate	6.6%
	Susceptible	a_s	231
		b_s	987
	Normal	a_n	749
		b_n	5966

P(ill|inf) is the probability of becoming ill given that the person is infected.
D is the dose of the ingested organism.
Normal, Naïve, and Susceptible refer to the exposed population's immune status

Campylobacter jejuni

Medema et al (1996) used human feeding trial data to develop a dose response model for infection by *Campylobacter jejuni.* The exponential and beta-Poisson models were again used to produce dose response curves. The beta-Poisson dose response

model fitted the data 'adequately', whereas the exponential model provided a poorer fit to the data. Maximum likelihood estimates (MLE) of the fit parameters are presented in Table 1.15. The fit of the model parameters was found to be dependent on a range of host-microbe factors, including the presence or absence of flagellated strains of *C. jejuni*, however, no improvement in fit was found when the distinction between the flagellated and non-flagellated strains was made.

Teunis et al (1999) also produced a dose response model for infection with *C. jejuni* based on human feeding trials. No comparison was made between the fit of different dose response models to the data. Table 1.15 presents a summary of the fitted parameters. The data set used by Teunis et al (1999) is the same as used by Medema et al (1996). Consequently the estimated model parameters are almost identical. Figure 1.5 shows a comparison of the models produced by Teunis et al (1999) and Medema et al (1996).

Holcomb et al (1999) compared six dose response models for infection with *C. jejuni* based on data sets selected from a literature search. The MLE of the fit parameters for each of the models is given in Table 1.15.

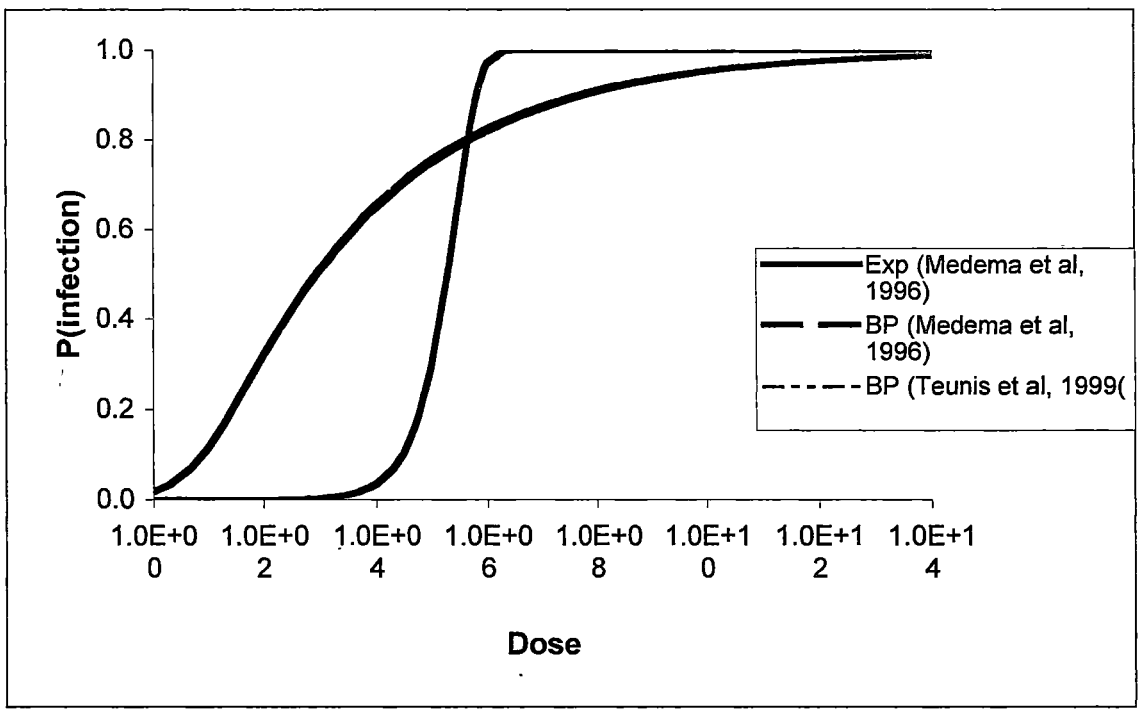

Figure 1.5 Comparison of the dose response curves for *Campylobacter jejuni* are based on the equations presented by Medema et al (1996) and Teunis et al (1999). The Beta-Poisson (BP) models are so similar they overlap in the figure above.

Table 1.15. Dose response parameters for *Campylobacter jejuni*

Author	Model	Parameter	Value
Medema et al (1996)	Exponential	r	3.52×10^{-6}
	Beta-Poisson	_	0.145
		_	7.59
Teunis et al (1999)	Beta-Poisson	_	0.15
		_	7.9
Holcomb et al (1999)	Log-logistic	_	0.41
	Log-normal	b_0	-0.83
		b_1	0.29
	Simple exponential	k	0.26
	Flexible exponential	_	0.29
	Beta-Poisson	_	0.12
		_	2.46
	Weibull-gamma	_	0.05
		_	9.99

Bacillus cereus

Notermans et al (1997) describe the risk assessment process for *B. cereus* in pasteurised milk. From various sources, they conclude, that the likely level of the organism required to induce symptomatic illness is $>10^5$. This is a similar figure to that presented by Doyle et al (1997), who indicate that an infectious dose of this organism is between 10^5-10^7 and 10^5-10^8 will likely induce toxin production in the small intestine and in food, respectively. Those authors did not derive a dose response relationship for the organism. A lack of information regarding this organism's ability to induce illness, indications that not all strains of *B. cereus* are toxin producers, and differences between the level of organism required to cause either emetic and diarrhoeic illness are highlighted as difficulties in developing a suitable dose response relationship for this organism.

1.8.3 Problems associated with microbial dose response models

Foremost among the problems associated with the construction of dose response models for microbial pathogens is a lack of data. This prevents the accurate estimation of the response curve. For those curves that have been defined there are large uncertainty bounds, especially in the low dose region of the curve, but also in the high dose region, and there are no suitable mechanistic models currently available that describe this region (Haas et al, 2000; Teunis and Havelaar, 2000; WHO/FAO, 2002). Moreover, the source of data for constructing the dose response models is another

potential problem. Several dose response models that have been developed are based on either surrogate organisms (Pai et al, 1986; Haas et al, 2000; Powell et al, 2000), from data collected from feeding trial studies (Cassin et al, 1998; Haas et al, 1999), or from animal feed trial studies (Holcomb et al, 1999).

The use of surrogate organisms is problematic, as the models don't usually define the difference between the organisms for which the model is constructed for and the one used in the experiment; intra-specific variability is inherent in all organisms, however, inter-specific variability is greater. Human feeding studies generally use a small healthy sample from a population and that sample is not representative of the population as a whole, thus reducing the validity of the constructed dose response model when applied to people not from the experimental group (Vose, 1998). Extrapolation from the dose response models developed from animal feeding studies also presents a problem as their applicability to humans is in question.

1.8.4 Dose Response Assessment for Chemical Hazards

This section considers chemical contaminants that may be present in dairy products and their associated health risks. Those considered included hormones, heavy metals, pesticides, herbicides and antibiotics. With the exception of heavy metals and hormones, the health effects from contact with these chemicals is relatively unknown. This is due to the difficulties of defining causal relationships when there is a long and variable time interval between 'exposure' and the possible onset of detectable health effects (Lammerding and Fazil, 2000).

With the exception of large doses of any particular chemical hazard, there appears to be a threshold below which there is no observable adverse effect; this is known as the NOAEL. There are other measures of hazard used for chemical contaminants. These include the maximum residual limit (MRL), the limit of reporting (LOR), the effective maximum residual limit (EMRL), and the lowest observed adverse effect level (LOAEL). These measures of risk for chemicals are used to determine a tolerable daily intake (TDI) or allowable daily intake (ADI). That is, that average level of the substance that may be ingested regularly over the entire lifetime of the consumer without causing an effect (WHO, 1996). This value is determined by dividing either the NOAEL or the LOAEL by an uncertainty factor (UF).

The UF is a means to incorporate in the TDI possible errors in extrapolation from animal feeding studies to the effects that may arise in humans. Extrapolation of models from animal bioassay data for chemicals to affects in humans may involve errors of several orders of magnitude (Smith, 1988). Typically the UF ranges from between 10 to 1000. Values greater than 10 000 are considered to indicate that the risk assessment

performed for that chemical would have produced TDI values of little meaning. Uncertainty factors are described in Table 1.16.

Chemicals that are considered for a TDI include only those that are non-carcinogenic. Carcinogenic chemicals are treated differently. It is generally considered that carcinogenic chemical compounds cause mutations in somatic cells as opposed to the gametes in humans. Thus, any amount of exposure to these genotoxic substances is considered a risk, as there is no threshold limit (WHO, 1996). There are, however, substances that may cause tumour development that are not genotoxic. These may have a threshold limit, but the mechanisms surrounding cancer development from these substances is not well understood.

Table 1.16 Uncertainty factors for determining tolerable daily intake for chemicals (Reproduced from WHO, 1996)

Source of uncertainty	Factor
Interspecies variation (animals to humans)	1–10
Intraspecies variation (individual variations)	1–10
Adequacy of studies or database	1–10
Nature and severity of effect	1–10

Again the typical method for determining the toxicity, or carcinogenicity of the compounds under consideration involves a combination of animal tests and epidemiological data gathered from people exposed to the chemical on a regular basis. Several different classes of carcinogenic compounds are distinguished, from those that are known human carcinogens, to those that are probably not carcinogenic (Table 1.17).

To most consumers the idea of consuming any amount of carcinogenic substance in food is unacceptable. For this reason the government of the United States of America changed the laws regarding food production by introducing the 'Delaney clause'. This was intended to prevent carcinogenic substances from entering the food supply. However, since the clause was added to the legislation there has been much controversy and public debate over which substances can and cannot cause cancer. Moreover the question arises, do we have sufficient information available to define unequivocally which substances will cause cancer and at what dose (Merrill, 1997)?

Table 1.17 Classes of carcinogenic compounds (reproduced from WHO, 1996)

Group 1. The agent (mixture) is carcinogenic to humans.
The exposure circumstance entails exposures that are carcinogenic to humans.
This category is used when there is sufficient evidence of carcinogenicity in humans. Exceptionally, an agent (mixture) may be placed in this category when evidence in humans is less than sufficient but there is sufficient evidence of carcinogenicity in experimental animals and strong evidence in exposed humans that the agent (mixture) acts through a relevant mechanism of carcinogenicity.

Group 2
This category includes agents, mixtures, and exposure circumstances for which, at one extreme, the degree of evidence of carcinogenicity in humans is almost sufficient, as well as those for which, at the other extreme, there are no human data but for which there is evidence of carcinogenicity in experimental animals. Agents, mixtures, and exposure circumstances are assigned to either group 2A (probably carcinogenic to humans) or group 2B (possibly carcinogenic to humans) on the basis of epidemiological and experimental evidence of carcinogenicity and other relevant data.

Group 2A. The agent (mixture) is probably carcinogenic to humans.
The exposure circumstance entails exposures that are probably carcinogenic to humans.
This category is used when there is limited evidence of carcinogenicity in humans and sufficient evidence of carcinogenicity in experimental animals. In some cases, an agent (mixture) may be classified in this category when there is inadequate evidence of carcinogenicity in humans and sufficient evidence of carcinogenicity in experimental animals and strong evidence that the carcinogenesis is mediated by a mechanism that also operates in humans. Exceptionally, an agent, mixture, or exposure circumstance may be classified in this category solely on the basis of limited evidence of carcinogenicity in humans.

Group 2B. The agent (mixture) is possibly carcinogenic to humans.
The exposure circumstance entails exposures that are possibly carcinogenic to humans.
This category is used for agents, mixtures, and exposure circumstances for which there is limited evidence of carcinogenicity in humans and less than sufficient evidence of carcinogenicity in experimental animals. It may also be used when there is inadequate evidence of carcinogenicity in humans but there is sufficient evidence of carcinogenicity in experimental animals. In some instances, an agent, mixture, or exposure circumstance for which there is inadequate evidence of carcinogenicity in humans but limited evidence of carcinogenicity in experimental animals together with supporting evidence from other relevant data may be placed in this group.

Group 3. The agent (mixture or exposure circumstance) is not classifiable as to its carcinogenicity to humans.
This category is used most commonly for agents, mixtures, and exposure circumstances for which the evidence of carcinogenicity is inadequate in humans and inadequate or limited in experimental animals. Exceptionally, agents (mixtures) for which the evidence of carcinogenicity in inadequate in humans but sufficient in experimental animals may be placed in this category when there is strong evidence that the mechanism of carcinogenicity in experimental animals does not operate in humans.
Agents, mixtures, and exposure circumstances that do not fall into any other group are also placed in this category.

Group 4. The agent (mixture) is probably not carcinogenic to humans.
This category is used for agents or mixtures for which there is evidence suggesting lack of carcinogenicity in humans and in experimental animals. In some instances, agents or mixtures for which there is inadequate evidence of carcinogenicity in humans but evidence suggesting lack of carcinogenicity in experimental animals, consistently and strongly supported by a broad range of other relevant data, may be classified in this group.

These considerations aside, what follows is a list of potential chemical contaminants in dairy products. Some may be of more importance depending on the conditions at the dairy farm, whereas others are included for completeness. Where possible MRLs for each chemical is given.

Hormones

Hormones are used within the cattle and dairy industry to increase growth rate, feed conversion and milk production, and can be either endogenous or synthetic (Waltner-Toews and McEwen, 1994d). Among the most widely known is Bovine somatotropin (BST), used in cows for increasing milk production. It is not available in Australia but widely used in the US. For hormones that may, but not necessarily, be used the ADI and withdrawal times have not been established for testosterone, progesterone, oestrogen and somatotropin, but these are generally not used in Australia. These hormones are used as feed supplements. The reason for not establishing the ADI is based on the premise that these are naturally occurring compounds, tissue residue levels are within the normal range, and hence health problems are minimal. The main risk from these hormones is from humans ingesting implants not removed prior to or during the carcass dressing process (Waltner-Toews and McEwen, 1994d).

Xenobiotic, manmade, hormones used worldwide include trenbolone acetate (TBA), melangestrol acetate (MGA), zeranol and the stilbenes. Trenbolone, is a synthetic steroid compound that is not considered genotoxic. The MRL in edible tissue is 0.7μg/kg for β-hydroxytrenbolone and 7.0 μg/kg for α-hydroxytrenbolone, it's two main derivatives (Waltner-Toews and McEwen, 1994e). The ADI is established from hormonal studies in pigs, and set at 0 – 0.02 μg/kg/day.

MGA is an orally active progestrogen, used in heifers as a feed additive. The MRL has been set at 25 μg/kg (25ppb) in edible tissue.

Somatotropin (ST) is also known as "growth hormone" and has been subject to much debate, although it is not currently used in Australia. Known since the 1920s, it can increase milk production and has been used (or licensing sought) with dairy cows. ST is not anabolically active in humans when given orally. BST (bovine somatotropin) occurs naturally in milk and with care treated and untreated animals have the same residual levels present in milk. However insulin-like growth factor is present in the meat of treated cattle at twice the normal level. No evidence exists that these increased IGF-1 levels pose a health risk.

Correct usage of xenobiotic substances should not leave a residue with an affect in humans from the consumption of contaminated tissue. However, incorrect use of the hormonal substances may lead to undesirably high residue levels that may have an adverse health affect in humans (Waltner-Toews and McEwen, 1994d).

Pesticides/Herbicides

Food was estimated to comprise up to 90% of the exposure source of insecticides for the general population of Ontario, with milk, eggs and meat accounting for >40% of food related exposure, with fish a further 25%. (Waltner-Toews and McEwen, 1994b). Hence agricultural insecticides are of particular concern for public health. These include: Organochlorines (including DDT and its relatives, hexachlorohexane derivatives, cyclodienes and polychloroterpenes), organophosphates and carbamates (Waltner-Toews and McEwen, 1994b). Cattle may be contaminated with various organochlorines including dieldrin, heptachlor, hexochlorobenzene (HCB) and chlordane as a result of pesticide use during crop production,. pasture production, horticulture, and the treatment of buildings and fittings (Waltner-Toews and McEwen, 1994b). These agricultural chemicals bioaccumulate in the body fat of animals and can be conveniently detected by assaying the milk fat chemicals are persistently found in the milk fat. The ability of these chemicals to bioaccumulate in animals and persist in the environment makes them a long-term residue hazard in all animal production systems. Consequently they have largely been banned from agricultural use in Australia and they cannot legally be applied to animals.

Fenthion, a cholinesterase inhibitor used as a pesticide, may also be present. The oxidative metabolites are more potent than the parent compound. Persistence of fenthion in milk of treated cattle rises to a maximum after ~8hr and falls to below 0.05 mg/kg within 24 hours, which at the time of writing, was the maximum allowable limit for this pesticide in raw milk (O'Keeffe et al, 1983).

Antibiotics and antiparasitic drugs

Problems associated with antibacterial residues in food include – direct toxicity, allergic reactions, development of resistant bacteria, and interference with starter cultures for fermented foods (Waltner-Toews and McEwen, 1994d). A large number of antibacterial and antiparasitic drugs are available for use with animals, however, not all have been reported as residues in foods. Moreover, they are found in very small concentrations in foods, generally far below the level required to cause an adverse reaction in humans. A list of the antibacterial and antiparasitc drugs that have been found in foods of animal origin is shown in Table 1.18. These are not specific to milk or dairy products.

In Australia antibacterial residues in milk have decreased in prevalence and amount in the last 30 years, despite increases in testing sensitivity (ANRSP, 1999). Australia reported as low as 0.07% failure to comply with regulations regarding the use of

antimicrobials and their presence in dairy farm vats, tankers and milk factory silos (ANRSP, 1999).

Table 1.18 Antibacterial and antiparasitic drugs found in foods from animal origin (from Waltner-Toews and Mc Ewen, 1994e)

Tetracycline	Relatively non toxic to humans and animals
Effects of	At therapeutic doses – peripheral blood changes, discolouration of the bones and teeth, and allergic reactions in humans Low doses (20mg oxytetracycline/person/day) – may affect the anaerobic faecal microflora in humans
ADI, MRL etc	ADI of 0 – 0.003 mg/kg body wt (humans)
β-lactam antibiotics	Relatively non-toxic at therapeutic doses Recent additions to this family of antibiotics have higher toxicity – imipenum and some cephalosporins
Effects of	Responsible for the majority of allergic reactions to antibiotics.
Rate of adverse effect	4-15/100 000 courses of treatment, 1-5/100 000 penicillin courses Those with reactions may have high sensitivity. Overall sensitivity is between 3 and 10% of the population
ADI, MRL etc	Doses below 0.01 μg /ml of penicillin are not important allergenically
Sulphonamides	Toxic
Effects of	Effect on thyroid function, hypersensitivity reactions (skin rashes), rare cases of agranulocytosis and aplastic anaemia
ADI, MRL etc	ADI 0 – 0.004 mg/kg body weight/day A rough estimate due to insufficient data
Aminoglycosides and others	All are toxic, this family includes - streptomycin, dihydrostreptomycin, gentamicin and neomycin. Nitrofurans – furazolidone and nitrofurantoin
Effects of	Urinary, vestibular and auditory damage, Allergic reaction to therapeutic doses Nitrofurans are toxic and have mutagenic and carcinogenic potential
ADI, MRL etc	Neomycin 0.5, Streptomycin 0.2 (mg/kg)
Antiparasitic drugs	closantel, ivermectin, levamisole, albendazole, dimetridazole, ipronidazole, ronidazole and carbadox
Effects of	Some evidence for carbadox and some of its metabolites being carcinogenic and genotoxic Dimetridazole and ipronidazole increase mammary tumours in rats. Levamisole associated with haematological abnormalities in humans

With the hazards identified, their effects characterised and where possible a dose response assessment performed, the likely exposure to those hazards and the magnitude of that exposure is required before an estimate of the risk from each hazard can be elucidated. The following section describes the process of exposure assessment.

1.9 Exposure Assessment

Exposure assessment is the characterisation of the likelihood of encountering a particular hazard in a food product and the magnitude of that encounter (Lammerding, 1997). The process of assessing the degree to which humans are exposed to a particular hazard is potentially complex. The steps involved vary according to the terms of reference of the risk assessment, the extent to which the work is quantitative, and the biological and physical processes that affect the concentration of hazard in the process being examined. The amount of that product acting as the vehicle that is consumed during a particular timescale needs to be known, i.e. the consumption pattern of the identified vehicle. Consumption patterns are the frequency of consumption of a product or group of products and the likely range of the amount consumed. The age and gender of the consumer can also be of importance because consumption and immune status varies according to age and gender. Finally an estimate of the likely magnitude of the exposure is required. This is based on the estimation of the likely contamination events and the magnitude of those events in the context of where they occur during the production of the food. A profile of the health, disease, and immune status, of the consuming population should also be known.

The consumption pattern data and the health profile will not be discussed here, the reader is referred to the Materials and Methods, Results and Conclusion for the former and Appendix B for the latter.

For the majority of food processing operations a chemical hazard will neither be destroyed nor generated within the food. Microbial hazards have the potential to either grow or die between the time that the food is harvested to the time that it is consumed (Ross, 1999; Whiting and Buchanan, 1997); hence the necessity of trying to establish the steps and processes involved in the production of food between the farm and the consumer, or in the farm-to-fork continuum. Where possible it is better to include growth and inactivation steps within the exposure assessment rather than making assumptions that preclude possible growth or inactivation of microbiological pathogens. However, in some situations there might not be enough information about a particular farm-to-fork pathway to establish the likely growth and inactivation. In these situations it may be more useful to identify the steps involved and use a more qualitative description of the process until such time as a quantitative description is possible (Lammerding and Fazil, 2000).

The sources of hazards, either intrinsic to the process of from an external addition, need to be identified, together with the likely amount or concentration of the hazard entering from that source. This is what exposure assessment adds to the risk assessment process (Jaykus, 1996; Lammerding, 1997). There may be a huge array of potential sources for any particular hazard. What is required is some mediation between

the risk assessor and the risk manager to refine the scope of the exposure assessment regarding the inclusion of these sources (Lammerding, 1997).

1.10 Risk Characterization

Risk characterisation is the final step in the formal part of a risk assessment. It is the synthesis of the exposure assessment and the dose response assessment to arrive at an estimate of the risk, i.e. the likelihood that a population will suffer an adverse effect, and its severity, associated with a particular hazard (Buchanan et al, 2000). Moreover, risk characterisation is a statement about the assessor's confidence in the analysis. The characterisation of risk may be either quantitative or qualitative (Jaykus, 1996, Lammerding, 1997). Also the nature of the risk characterisation should reflect the uncertainties within the assessment, data gaps, potential problems with the assessment process, and the affect that critical assumptions in the exposure and dose response assessments have on the interpretation of the results (Buchanan et al, 2000).

The form that the risk characterisation takes, qualitative or quantitative, is largely dependent on the way that the other steps in the risk assessment were performed. For a quantitative risk assessment, the risk characterisation will take the form of a numerical estimate (Lammerding, 1997). The arrival at a numerical estimate derives from either the simulation of all possible results, through the sampling from distribution functions describing some or all factors in the model, via Monte Carlo analysis (Buchanan et al, 2000) or by using a deterministic approach. A stochastic approach is considered preferable to a deterministic one because it is possible to incorporate both uncertainty and variability directly. The main problem with using this type of analysis is the interpretation and presentation of the results. Even with a numerical estimate of risk, it may be more useful to offer a qualitative description of that risk rather than give a mean value with confidence intervals. This method will, however, reduce the value of the overall assessment, and with proper communication and interpretation of the results it is more beneficial to use a fully quantitative estimate (Lammerding, 1997).

1.11 Project Objective

This project is part of industry-funded research to produce a food safety risk assessment model for the Australian dairy industry. The objective of this project was to develop a model for assessing the likelihood and severity of adverse health outcomes in people who consume Australian dairy products. The purpose of the model was both to estimate the risk of illness from the consumption of dairy products, and to identify research needs for food safety within the Australian dairy industry.

To gain a better understanding of the Australian dairy industry, discussions were held with representatives of dairy manufacturing companies and other dairy industry

stakeholders in the project and visits were made to dairy farms and processing factories. Concurrently, SafeFood NSW was conducting a risk assessment for the NSW dairy industry. It was beneficial to both parties to collaborate and pool resources to achieve a common objective. It was hoped that upon completion of the project the model would be useful both as a research tool in the broader Australian dairy industry and for meeting the state specific requirements of the dairy regulator in NSW.

The overall aim of the project was to provide a food safety risk assessment framework for the Australian dairy industry, through the collection of specific information regarding that industry and its collation and organisation into a structured and flexible spreadsheet model. The model was primarily concerned with the estimation of the likely hazard concentrations in liquid milk, whereas the remainder of the overall project was concerned with the description of these hazards in other dairy products, their potential health effects in humans and a description of the health status of the consuming population in Australia.

2. Materials and Methods

2.0 Characterisation of the dairy industry

A range of characteristics of the Australian dairy industry can conceivably affect the risk of human illness arising from the consumption of dairy products. Thus a strategy was adopted where the characteristics of the NSW dairy industry could be assessed and used as a basis for a model that could be scaled (extrapolated) to encompass the entire industry in Australia. The NSW dairy industry was regarded as suitable because it encompasses a wide range of dairy production systems due to the variety of climatic and geographic regions in that state in which milk is produced and marketed. Information was gathered from a survey sent to 70 dairy processing factories in NSW. The survey requested data from each of the factories regarding; the volumes of finished product per year; the volume of raw materials used annually; the number of farms supplying the factory; the number of cows on those farms, including the proportion of those "in milk"; the types of microbiological tests performed on the product and around the factory; results of those tests, including frequency of failures, the products implicated and the hazard concerned; the pasteurisation time and temperature conditions and the number of pasteurisers used at the factory (both high temperature short time and batch pasteurisers); degree of compliance with mandated farm pick-up temperatures (i.e. 4°C regulation) and the maximum temperature of milk collected from the farm. The questionnaire is presented in Appendix A.

2.1 Hazard Identification

There are more than 70 potential microbial contaminants of milk, of these there are several that are clearly pathogenic and others that may be potentially pathogenic (van Gerwen, 2000). It is impractical to consider all within a single risk assessment. Therefore (as noted in section 1.7) a meeting between the risk assessment team and stakeholders in the project was held to discuss the pathogens of most current concern to the dairy industry. The stakeholders were representatives of major dairy product manufacturers in Australia, the Dairy Research and Development Corporation (DRDC), and controlling authorities which included quality control officers, project managers, production managers and research officers. The pathogens of most concern to the industry were identified, prioritised, and those associated with specific product groups were listed as the highest priority. At the same time stakeholders discussed chemical and physical hazards of greatest priority.

2.2 Hazard Characterisation

Each of the potential hazards identified was considered in detail, identifying modes of transmission, aetiology and virulence. This information was presented in the literature review under hazard identification (1.7) and hazard characterisation (1.8).

2.2.1 Growth kinetics of pathogenic microorganisms

The growth kinetics of several bacterial pathogens included in the risk assessment, i.e. *Escherichia coli*, *Listeria monocytogenes*, *Staphylococcus aureus*, *Bacillus* spp. and *Salmonella* spp were collated. For these pathogens a published mathematical growth model existed (Gibson et al, 1988; Buchanan and Phillips, 1990; Ross and McMeekin, 1991; Benedict et al, 1993; Buchanan et al, 1993a; Buchanan et al, 1993b; Tienungoon, 1998; Ross et al, in press). The models used are temperature based with growth conditions that of liquid milk (pH 6.5, a_w 0.995).

The growth rate of the microbiological hazards modelled, as predicted from the USDA's Pathogen Modelling Program and University of Tasmania's Microbiology group, are presented in table 2.2.1.1. Predictions were generated for a limited range of temperatures. The mean estimated growth rate for each microorganism from the models, without confidence intervals, was used in the model.

Table 2.2.1.1 Growth rate estimates (generations/hour) for microbiological hazards from Pathogen Modelling Program (a) and University of Tasmania microbiology group (b)

(a)							
Temp	*E. coli*	*Salmonella*	*L. monocytogenes*	*Y. enterocolitica*	*C. jejuni*	*B. cereus*	*S. aureus*
0	-	-	-	-		-	-
1	-	-	-	-		-	-
2	-	-	-	-		-	-
3	-	-	-	-		-	-
4	-	-	0.084	-		-	-
5	0.000	-	0.102	0.115		0.067	-
6	0.000	-	0.123	0.137		0.081	-
7	0.000	-	0.147	0.164		0.096	-
8	0.000	-	0.175	0.192		0.115	-
9	0.130	-	0.208	0.227		0.137	-
10	0.159	0.110	0.250	0.263		0.161	0.074
11	0.192	0.145	0.294	0.313		0.192	0.093
12	0.227	0.189	0.345	0.357		0.222	0.116
13	0.270	0.244	0.400	0.417		0.263	0.143
14	0.323	0.313	0.455	0.476		0.303	0.179
15	0.385	0.385	0.526	0.526		0.357	0.217
16	0.435	0.476	0.588	0.588		0.417	0.263
17	0.526	0.588	0.714	0.667		0.476	0.313
18	0.588	0.714	0.769	0.714		0.526	0.385
19	0.667	0.833	0.909	0.833		0.625	0.455
20	0.769	1.000	1.000	0.909		0.714	0.526
21	0.909	1.111	1.111	1.000		0.769	0.625
22	1.000	1.250	1.250	1.111		0.909	0.714
23	1.111	1.429	1.429	1.111		1.000	0.833
24	1.250	1.667	1.429	1.250		1.111	0.909
25	1.429	1.667	1.667	1.250		1.250	1.111
26	1.429	2.000	1.667	1.429		1.429	1.250
27	1.667	2.000	2.000	1.429		1.667	1.429
28	1.667	2.000	2.000	1.429		1.667	1.429
29	2.000	2.500	2.000	1.429		2.000	1.667
30	2.000	2.500	2.500	1.667		2.000	1.667
31	2.000	-	2.500	1.667		2.500	2.000
32	2.500	-	2.500	1.667		2.500	2.000
33	2.500	-	2.500	1.667		2.500	2.000
34	2.500	-	2.500	1.667		2.500	2.500
35	2.500	-	3.333	1.667		3.333	2.500
36	2.500	-	3.333	1.667		3.333	2.500
37	2.500	-	3.333	1.667		3.333	2.500
38	3.333	-	-	1.667		3.333	2.500
39	3.333	-	-	1.429		3.333	2.500

- indicates that temperature was outside the range of the model's prediction

(b)							
Temp	*E. coli*	*Salmonella**	*L. monocytogenes*	*Y. enterocolitica*	*C. jejuni**	*B. cereus*	*S. aureus*
0	0.000	0.000	0.000		0.000		0.000
1	0.000	0.000	0.000		0.000		0.000
2	0.000	0.000	0.003		0.000		0.000
3	0.000	0.000	0.010		0.000		0.000
4	0.000	0.000	0.021		0.000		0.000
5	0.000	0.000	0.036		0.000		0.000
6	0.000	0.000	0.056		0.000		0.000
7	0.000	0.000	0.080		0.000		0.000
8	0.049	0.000	0.108		0.000		0.000
9	0.077	0.080	0.141		0.000		0.000
10	0.112	0.115	0.178		0.000		0.000
11	0.154	0.156	0.219		0.000		0.000
12	0.202	0.204	0.265		0.000		0.000
13	0.256	0.259	0.314		0.000		0.156
14	0.317	0.319	0.368		0.000		0.203
15	0.385	0.386	0.427		0.000		0.257
16	0.459	0.460	0.489		0.209		0.318
17	0.539	0.539	0.556		0.258		0.384
18	0.626	0.626	0.627		0.312		0.457
19	0.720	0.718	0.703		0.372		0.537
20	0.820	0.817	0.782		0.436		0.622
21	0.926	0.922	0.866		0.506		0.715
22	1.039	1.034	0.954		0.580		0.813
23	1.158	1.152	1.047		0.660		0.918
24	1.284	1.276	1.144		0.746		1.029
25	1.415	1.407	1.245		0.836		1.146
26	1.553	1.544	1.350		0.931		1.270
27	1.696	1.687	1.459		1.032		1.400
28	1.845	1.836	1.572		1.138		1.537
29	1.998	1.991	1.688		1.249		1.679
30	2.157	2.152	1.807		1.365		1.827
31	2.319	2.317	1.927		1.486		1.981
32	2.483	2.488	2.046		1.612		2.141
33	2.649	2.661	2.159		1.744		2.304
34	2.813	2.837	2.259		1.880		2.470
35	2.974	3.013	2.333		2.022		2.635
36	3.128	3.185	2.355		2.168		2.795
37	3.270	3.349	2.289		2.319		2.941
38	3.392	3.497	2.072		2.475		3.059
39	3.488	3.618	1.629		2.634		3.123

*Denotes that the model estimates are derived from a generic exponential growth model equation

2.2.2 Thermal death kinetics of pathogenic microorganisms

A literature search was conducted to find a suitable method to model the effect of pasteurisation on bacterial pathogens that may be present in raw milk. Papers that described either mathematically, or through laboratory experiments, the thermal death kinetics of several bacterial pathogens were considered. The pathogens included were *Escherichia coli*, *Listeria monocytogenes*, *Staphylococcus aureus*, *Campylobacter* spp, *Bacillus* spp. and *Salmonella* spp. For the remaining pathogens (section 1.3), there was insufficient published information to construct thermal death models.

Papers that described the D or z value were of particular importance. The D-value is the time, in seconds, taken to reduce a population of bacterial cells by one log cycle at a given temperature, also known as the decimal reduction time (Mackey and Bratchell, 1989; Murphy et al, 2002). This assumes that the temperature is beyond the maximum temperature for growth of that organism. The z-value is the temperature increase required to reduce the D-time tenfold (Murphy et al, 2002). Where possible data concerning dairy products, and in particular liquid milk, were used to determine the fit parameters of the log-linear inactivation curve. Where no specific data for milk existed a composite curve consisting of pooled data for that organism is used as a surrogate (Appendix C presents the entire dataset from the published thermal inactivation times and temperatures and references).

2.3 Exposure Assessment

Assessment of the likely intake of chemical, microbiological or physical hazards through the consumption of milk and milk products and the consequences of those exposures was performed in two parts. Firstly, by estimating the consumption of dairy products, both frequency and serving size, by Australians and secondly by producing a health profile of the Australian population (Appendix B). These two pieces of information make it possible to predict the number of pathogens being ingested, given that the concentration of cells or toxins in the product is known.

2.3.1 Consumption Patterns of Dairy Products in Australia

The consumption of dairy products by age and state were examined. These consumption patterns detailed the amount and frequency of consumption of particular dairy product group. They were obtained through discussions with industry representatives and the collection and collation of information found in the Australian Bureau of Statistics National Nutrition Survey (ABS, 1997) and from the annual and

monthly statistics published by the Australian Dairy Corporation (ADC, 2000) and the Australian Dairy Industry Council (ADIC, 2000).

2.4 Risk Characterisation

To characterise the distribution of risk to humans of consuming in milk the range of hazards considered that may be present, the model was run using Monte Carlo simulation (see section 1.8). Each time the model was set to run for 30 000 iterations. For each iteration the model selects a value from each of the distribution functions within the model and calculates the final output based on calculations between each of these sampled values. The results from each iteration are stored and at the end of the simulation presented in a table that lists each of the outputs from the model, the individual results for each iteration (if requested) together with a summary based on descriptive statistics (mean, standard deviation, maximum, minimum, skewness, kurtosis, etc).

2.5 Model Development

The information gathered in the previous steps (section 2.2 and 2.3) was used to develop the risk assessment model. Several pathogens were modelled, and the flexibility built into the model allows for the risk from one or several different pathogens to be modelled during any single simulation. The objective of the model was to estimate the likely contamination of raw milk at the farm level with hazards, both microbiological and chemical, and to estimate the likelihood and frequency of exposure to those hazards in the finished dairy product. The model is a synthesis of the hazard identification and characterisation, exposure assessment and characterisation of the dairy industry. This section describes the development of the simulation model up to pasteurisation.

Sources of Hazards at the Farm Level

Fault tree analysis (AS/NZS, 1995) revealed that the model would be best configured with the individual cow assumed to be the primary source for milk contamination. That is, each cow is the source of milk for the model/industry, and contamination of the milk from that cow occurs by exposure of the individual cow to feed, pasture and environment etc. There are other sources of contamination conceivable prior to the cow, and from sources other than the cow, but a workable model can be best considered by considering each cow as being the initial source for all milk contamination (Fig 2.1). Other sources of contamination in raw milk are listed in Table 2.1.

Overview

A description of the model follows, detailing the input variables and distributions, the mathematical operations used and the outputs of the model. For clarity each stage in the model is described separately, and where possible the values used for the distribution parameters is omitted, to allow the logic and sequential steps of the model to become apparent to the reader. The input values for the distribution parameters are detailed in the Chapter 3. The logical steps and assumptions included in the description of the model are described in detail so that it is possible to reconstruct the model accurately, thus fulfilling one of the principles of risk assessment: transparency. A general overview of the model is shown (Fig 2.2) indicating the different stages, or modules, within the overall risk assessment model. There are three modules that have not been fully developed, but are included for completeness and to give an indication where further research is needed. For each model parameter that is used in the calculation of any other value, the parameter's identifier is given in italics. The model was developed on a Microsoft Windows based computer running Excel 2000 (Microsoft Corporation) and @Risk v4.05 and later @Risk v4.5 (Palisade Corporation).

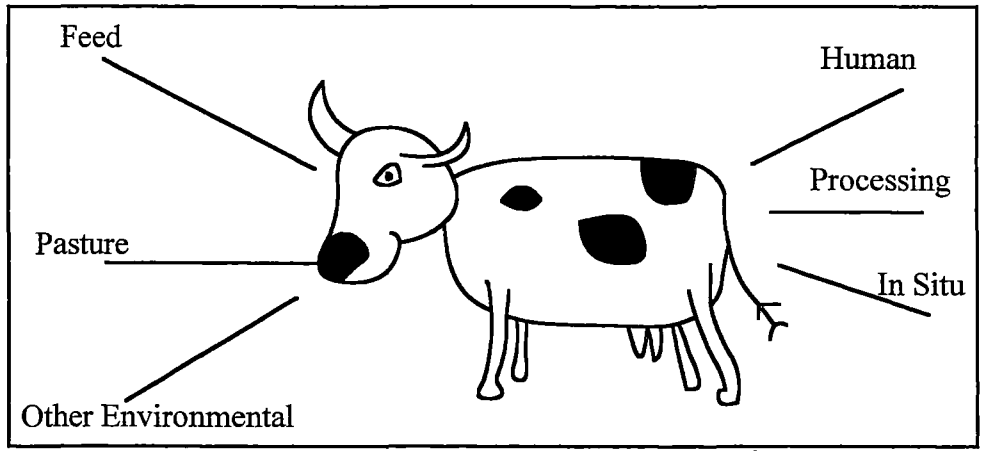

Fig 2.1 Contamination sources centre at the individual cow

Table 2.1 Sources of milk contamination (Varnam and Evans, 1991)

Bovine faeces	Defecation into milk Contamination of udder via bedding etc Contamination of milker's hands etc Contamination of milking equipment after dropping on floor Oral antibiotics passing through to faeces contaminating milk
Udder infection	Undetected sub-clinical mastitis or asymptomatic infection Use of mastitic milk Antibiotics passed through udder into milk
Milking Personnel	Direct transfer from unwell person to milk Indirect transfer from unwell person via contamination of milking equipment
Environmental sources	Udder contamination from stream or pond water, infected pasture etc. Chemical contaminants on pasture or other feed passing though to milk

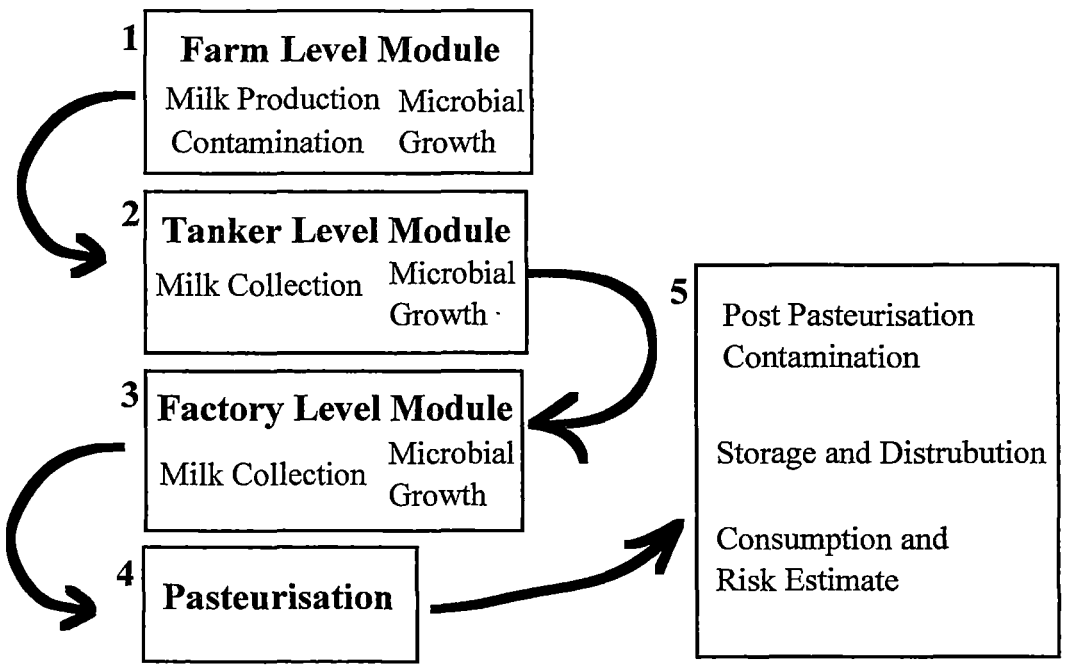

Fig 2.2 Overview of dairy risk assessment model structure. Modules 1-4 are complete; module 5 comprises the remaining three aspects of the risk assessment (These will be conducted subsequently as apart of the overall project described in section 1.11).

2.5.1 Farm Level Module

Objective:

This module predicts the volume of raw milk produced from herds of different sizes each day. It also estimates the bacterial and chemical contamination of raw milk from each herd prior to collection by the milk tanker. In the case of microbial hazards it estimates the potential growth of these organisms present during storage in the farm milk vat.

Inputs:

Variable Description	Identifier
Probability that the farm is "Large" in size	P(LF)
Probability that the farm is "medium" in size	P(MF)
Herd Size	HS
Probability that the herd is contaminated with hazard	P(HC) P(ChemHaz)
Number of cows contaminated	CHs
Number of cows within a herd that are not contaminated	UCHs
Probability that the udder is contaminated given that the herd is contaminated with the hazard	P(UC|HC)
The number of cells contaminating milk produced from each contaminated cow	CHb
The amount of chemical contamination from each contaminated cow (grams)	CCL
Mean daily milk production per cow (L)	μ_d
Variance of daily milk production (L)	σ_d^2
Volume of milk produced by a herd (L)	HM
The contamination level on each udder	UCL
Temperature of the farm milk vat (°C)	T_{FV}
Time milk spends in the farm milk vat (hours)	t_{FV}
Generation time of the pathogen (hours)	GT
Number of bacteria present in the milk vat	Nø

Assumptions made in this part of the model include that:

- There is no seasonal variation in milk production
- The hazard status of the cows does not affect the volume of milk produced from these animals. A contaminated cow produces the same volume of milk as a healthy one.

- The mean volume of milk produced per cow per day is the same regardless of the breed of cow.
- The size of the herd does not affect the milk production of individual cows.
- Milk production and hazard status of each cow is allocated independently of the other cows in the same herd (i.e. no clustering within herd based on features such as age or position in the milking queue is modelled)
- That milk in the vat prior to collection is at a constant temperature.
- Hazards present in the raw milk are distributed evenly throughout the entire volume of milk.
- Udder contamination is transferred into milk at the time of milking.
- There is no lag phase for pathogens present in the farm milk vat
- All bacterial cells of a given species grow at the same rate, i.e. the population of cells is in the same growth phase at all times.
- The number of cells contaminating the udders of infected cattle is a constant value.

Size of Farm

Three farm sizes or classes have been modelled, 'small', 'medium' and 'large' to reflect the various sizes of farms present. This distinction is based only on the size of the herds that they contain. A 'large farm' is defined as a farm that has a mean herd size of 390 ($\sigma = 75$), and is modelled by a normal probability distribution. Similarly for medium and small farms, 174 ($\sigma = 30$), and 70 ($\sigma = 15$) cows respectively were used. Fig 2.3 shows the range of total herd sizes in each farm size group, as per the survey data (section 2.0). For each farm being modelled, the size of the farm is determined using a Bernoulli trial (Vose, 2000) with the probability that the farm size is large given by *P(LF)*.

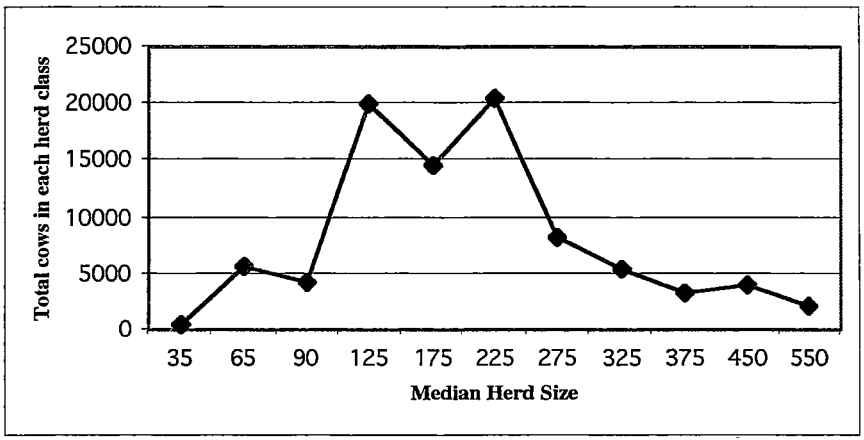

Fig 2.3 Total cows in each farm size (NSW Survey data)

Farm Size (0,1) ~ binomial (1, *P(LF)*)

If the return value, farm size, equals 1, then the farm is Large, if the return value equals 0, then the farm is not large.

If the farm is not large then there is a chance that it will be medium in size. Using the a similar process as with the above, a Binomial distribution with sample size 1, the probability that the farm is medium sized *P(MF)* is used.

Farm size (0,1) ~ binomial (1, *P(MF)*)

If the farm is neither large nor medium in size, then it is assumed to be small, the only remaining farm size class.

Once the "population" of farms has been generated, the size of the herd on each farm is determined using a normal distribution by referring to the specified mean and standard deviation for that population.

HS ~ normal (mean, std dev)

The size of each herd is used in further calculations, as detailed below.

Herd Contamination

There is the chance that any given herd may or may not be contaminated with any particular hazard. The status of the herd is determined using a Bernoulli trial where the probability of success is *P(HC)* (in the model this is generated as a binomial random variate with n=1 and p = *P(HC)*). A herd is contaminated if it contains at least one cow with the pathogen or hazard present. For each iteration a herd is 'created' and a test is performed which determines if that herd is contaminated for that iteration, given by:

HC(0,1) ~ binomial (1, *P(HC)*)

HC takes a value of 1 if the herd is contaminated, or 0 if the herd is not contaminated. The presence of both microbiological and chemical hazards are determined in this manner, however for chemical hazards:

HC(0,1) = HC(Chem) ~ binomial (1, *P(ChemHaz)*)

This process takes place for each hazard being modelled. Thus, any given herd may be free from all hazards, or may be contaminated by a single hazard or by multiple hazards. The model simulates nine hazards during a single run, thus for each farm in the model seven microbiological hazards and two chemical hazards are modelled.

Number of Contaminated and Uncontaminated Cows

If a herd is contaminated, the number of cows within that herd which have contaminated udders is determined by sampling from a binomial distribution, with the number of trials given by the herd size (*HS*) and the probability that an individual cow's udder is contaminated given as *P(UC|HC)*. Hence the number of successes, that is the number of cows with contaminated udders, is given by:

$CHs \sim \text{binomial}(HS, P(UC|HC))$

To calculate the number of cows that are not contaminated the following equation is used:

$UCHs = HS - CHs$

Bacterial numbers and concentration in milk produced by contaminated cattle

It is assumed that for each contaminated cow all the bacterial cells present that may be transferred to the milk are transferred to the milk. This is a simplification, as there may be some correlation between the degree of contamination and the proportion of cells contaminating the raw milk, but the relationship, if any, is unknown. The number of bacteria present in the milk from the contaminated portion of the herd is determined by multiplying the contamination from each cow by the number of cows contaminated within the herd, given by:

$CHb = UCL * CHs$

Chemical contamination of cattle udders

Similarly to bacterial numbers, it is assumed that all chemical contaminants present on or within the cattle's udder are transferred to the milk. Rather than using *CHb*, *CCL* is used instead, thus:

$CCL = UCL * CHs$

Herd Milk production

The volume of milk produced by each herd is determined using the Central Limit Theorem (Vose, 2000). Each cow produces on average μ_d litres of milk per day, with a variance of σ_d^2, and the daily milk production for the herd is given by the equation:

$HM \sim \text{normal}(HS * \mu_d, \text{sqrt}(HS) * \sigma_d)$

Growth of pathogenic bacteria in the farm milk vat:

The temperature range in a farm milk vat is expressed as a Triangular distribution, with minimum, most likely and maximum expressed as degrees Celsius, and based on the opinion of dairy factory quality control officers. The generation time (GT) for each

pathogen is determined from a lookup table in the Excel spreadsheet. The lookup table values were generated for temperatures ranging from 0°C to 38°C, from models developed and used by the University of Tasmania School of Agricultural Science Microbiology group for *Escherichia coli*, *Listeria monocytogenes* and *Staphylococcus aureus*. For *Yersinia enterocolitica*, and *Bacillus cereus* generation time estimates were taken from USDA's Pathogen Modelling Program (PMP) as described in section 2.2.1. A generic exponential growth rate model was used for *Salmonella* spp. and Campylobacter spp.

The time that the milk spends in the farm milk vat was described using a triangular distribution, with minimum, most likely and maximum values derived from dairy production manager's and quality control officer's opinions for the total age of milk prior to it being pasteurised.

Growth is assumed only to occur in farm vats that have milk contaminated with a bacterial pathogen. The growth of spoilage organisms is not considered at this time. The number of generations of growth is calculated from the following equation:

$$\text{Generations} = GT * t_{FV}$$

The number of bacteria present in the milk vat, determined for each pathogen, is given by the equation

$$\text{Total Bacteria Present} = N_0 * 2\text{^}(GT * t_{FV})$$

Where N_0 is the initial number of bacteria present.

Outputs:

There are two main outputs from this part of the model; the milk produced daily from each farm, and the concentration of hazards present in the milk.

The above steps are used to simulate a population of farms each with a herd of dairy cows. These cows produce a quantity of milk daily, with the concentration of contaminating hazard known for each farm with growth of bacterial hazards taken into account.

2.5.2 Milk Collection and Transport Module

Objective:

To model the collection of farm milk by tankers, and to monitor the dilution effect for chemical hazards and potential growth of bacterial hazards during transport.

Inputs:

Variable Description	Identifier
Tanker volume	MT_{vol}
Farm milk volume (for the *i*th farm)	F_{vi}
Concentration of hazards in farm milk (for the *i*th farm)	$[Hazard_{FMi}]$
Maximum pickup temperature for milk	MaxT
Temperature of milk in tanker	T_{MT}
Time milk spends in transport from farm to factory	T_{Trans}

Assumptions made within this section of the model:

- There is no time lapse between the first milk collection and the last, therefore, no bacterial growth is possible until the tanker is full
- Hazards present in the tanker are distributed evenly throughout the entire volume of milk.
- All hazards present in farm milk vats are transferred, without loss, to the milk tanker upon collection by the tanker.
- There is a constant temperature throughout the volume of milk in the farm milk vat prior to collection.
- The milk is at a constant temperature during transportation between the last farm collection and delivery at the factory.

Farm Number:

Each simulated farm is given a reference number. This has no relation to where the farm is in any particular state/region, however the farm number is a relative spatial scale, farms with their farm number close together are spatially close together, i.e. Farm3 and Farm5 are close together, whereas Farm1 and Farm60 are more distant. Each tanker collects sequentially from the farm list, with the first farm being selected randomly from the entire population of farms. This implies that within the model any given tanker collects from farms within a similar region, or collects from farms that are close together.

Tanker Number, Size and Filling

Similarly, each simulated tanker is given a number to distinguish it from the other tankers in the model. Three tanker sizes are modelled: small, medium and large. The only difference between the tanker sizes is the volume of milk they are able to transport. Based on the size of the first farm visited by each tanker, the respective size of that tanker is determined. Once the first farm for collection has been selected a logical test is performed to determine if the tanker has sufficient capacity to take the milk. That is, a

medium farm is only visited by medium and large tankers, small farms by all tanker sizes, and large farms only by large tankers

The first farm visited by the tanker is randomly selected from a distribution covering the entire population of farms using the following function:

First Pickup ~Duniform (1,N)

Where N is the total number of farms in the population of farms.

For each tanker, there may be more than one farm that is visited before the tanker has been filled. Large tankers collect from a single farm only, small tanker collect from several farms until full, however, medium sized tankers may either collect from a single farm or until full. A simple test is performed to determine if a tanker is collecting from only one farm, as given by:

Direct ~Binomial(1, 0.8)

If the return value, Direct, equals 1, then the tanker visits a single farm on that day. If the return value equals zero, the tanker visits additional farms until it is filled.

Milk Collection

For small tankers and medium tankers that are not "Direct", several farms are visited prior to the commencement of transportation of the milk to the factory. Given that the volume of milk in the tanker cannot exceed MT_{vol}, the sum of Fvi (where i ranges from 1 to n, and n is the number of farms visited by that tanker) gives the total volume of milk within the tanker. Collection continues until the following condition is met:

$$MTvol - \sum_{i=1}^{n} Fvi \geq 0$$

Hazard Contamination Level

The concentration of any given hazard present in farm milk vats is estimated as explained in the farm level module. As each tanker collects from each farm, the amount of hazard present in the raw milk from that farm is added to the amount of that hazard present in the milk tanker. The model accounts for dilution of hazard through the filling process of each tanker. The model deals with concentration of hazard; hence, a weighted mean is used to determine the final concentration of hazard in the milk contained in the tanker.

$$\text{Hazad Concentration in Tanker} = \frac{\sum_{i=1}^{n}[Hazardfm]\times Fvi}{MTvol - \sum_{i=1}^{n} Fvi}$$

Where n is the number of farms collected from.

Growth of pathogenic bacteria in milk tankers

The temperature in each milk tanker is modelled using a truncated log-logistic distribution function (Vose, 2000). Initially the parameters were derived by fitting data from the questionnaire responses to a log-logistic distribution using @Risk's data fitting function with the best RMS fit to the cumulative distribution. The distribution for the potential range of temperatures in the milk tankers was truncated to remove values less than 0 (*minT*) and greater than 17°C (*maxT*) as the former is unlikely to be reached in most farm milk vats and the latter is considered unlikely, by production managers in Australia, unless the milk is collected immediately following the completion of milking. The latter also greatly exceeds the regulatory maximum for milk temperature at farm collection.

Similarly to section 2.5.1, the potential growth of bacteria in the tanker was calculated.

Outputs

There are two outputs from this part of the model; the volume of milk within each tanker, and the concentration of hazards in the milk in each tanker.

The above steps are used to create a set of milk tankers that independently collect milk from the population of farms. The concentration of hazards present is monitored and potential growth of bacterial hazards estimated, to give a final concentration of hazards present in the milk tanker's volume of milk at the point of delivery at the factory.

2.5.3 Factory Collection

Objective:

To model the collection of milk from tankers by factories and to monitor the concentration of both bacterial and chemical hazards present in that pooled milk.

Inputs

Variable Description	Identifier
Factory Silo volume	FS_v
Milk tanker volume	MT_V
Concentration of hazard in tanker milk	$[Hazard_{MTv}]$

Assumptions made with this section of the model:

- There is no time lapse between the first tanker delivering milk to the factory and the last, that is, there is no microbiological growth occurring during silo filling.
- Hazards present in the silo are distributed evenly throughout the entire volume
- All hazards present in the raw milk in the milk tankers are transferred into the factory milk silo.
- There is insufficient time for growth of bacterial cells in the silo.

Potential growth has been accounted for in the two previous growth phases, time spent in farm milk vat and transport. These two phases account for the entire age of the milk as derived from the results of the questionnaire. For the purposes of modelling, the time spent in the farm milk vat and in transport also includes the time the milk is held in the factory silo. This approach was used because of the limitations of the data obtained from the questionnaire. Consequently, potential growth in the silo is not modelled discretely but is incorporated in potential growth during the two previous stages.

For each product that is modelled three factories are simulated. That is for liquid milk there is a 'large', 'medium' and 'small' factory simulated, similarly for cheese and powdered milk.

Factory Size

For each product being modelled there are three factory sizes used: 'small', 'medium' and 'large'. The volume of milk that each factory can collect daily is determined by a Triangular (min, most likely, max) distribution. The factory sizes differ only in their capacity to process milk. There was no difference in risk expected between factories of different sizes. However, given knowledge of factory size specific risks, the model is capable of incorporating that new knowledge without needing restructuring.

Milk Collection

Given that the volume of milk in the tanker cannot exceed the volume of milk the factory silo may contain: if $Tv_{min} > FS_v$, (where Tv_{min} is the minimum volume of milk contained in the tankers) is true then no collection occurs on that day for that factory, if this is false then milk is simulated to be collected in a manner similar to that described in section 2.5.2.

Hazard Contamination Level

The concentration of any given hazard present in factory milk silo is determined in a manner similar to that for each tanker. As each tanker delivers milk to the factory, the

amount of hazard present in the raw milk from that tanker is added to the amount of that hazard present in the factory silo. The model deals with concentration of hazard; hence, a weighted mean is used to determine the final concentration of hazard in the milk contained in the silo.

$$HazardConcentration = \frac{\sum_{i=1}^{n} [Hazardtm] \times Tvi}{FSvol}$$

where n is the number of tankers collected from.

Outputs

There are two outputs from this section of the model: the volume of milk in the each silo and the concentration of hazard present in the silo.

This part of the model simulates the delivery of milk to the factory by the tankers simulated in the previous section. The volume of milk entering the silo, daily, is monitored also the concentration of both chemical and microbiological hazards.

2.5.4 Pasteurisation

Objective

To model the effect of pasteurisation on the hazard concentration of milk in the factory silo.

Inputs

Variable Description	Identifier
Pasteurisation temperature	PsTemp
Pasteurisation time	Pst
Log-linear thermal reduction parameters	a, b

Assumptions made with this section of the model:

- Log-linear thermal inactivation of vegetative bacterial cells present
- Chemical hazards present are not affected by pasteurisation conditions
- Entire volume of milk is subjected to the same temperature and time
- *Bacillus cereus* - all vegetative cells are assumed to have sporulated prior to pasteurisation.

For each product simulated, the pasteurisation conditions can be changed to suit the process for that particular food item.

The concentration of hazards present in the factory silo is calculated from calculations described in section 2.5.3.

Effect of Pasteurisation on Hazards present in Milk

The concentration of bacteria present in the milk after it has been pasteurised is calculated from the initial concentration, the log-reduction from thermal pasteurisation (D value is the time in seconds to reduce the population of bacterial cells by one log cycle) and the pasteurisation conditions. The log-linear thermal death equation (Huang and Juneja, 2001) for bacterial pathogens is of the form

$$\text{Log}_{10}(D) = (-a * PsTemp) + b$$

Therefore

$$D = 10^{((-a * PsTemp) + b)}$$

Where a and b are regression parameters for the log-linear line of best fit, and D is time, in seconds, to reduce the bacterial population by one log, or 90%.

Hence, the total log reduction (TLR) during the time that milk is pasteurised is given as:

$$TLR = Pst/(10^{((-a * PsTemp) + b)}) = Pst/D$$

The concentration of pathogenic bacteria present in the milk after pasteurisation is calculated as:

Remaining bacterial concentration = Initial Concentration/ TLR

Outputs

There is one output from this section of the model, the concentration of bacterial pathogens in the product after pasteurisation. For products other than liquid milk, the pasteurisation step occurs prior to further processing steps. Hence the concentration of pathogens present after pasteurisation is that in the milk used for further processing.

2.6 Model Implementation and Execution

The model was developed on a Microsoft Windows based computer running Excel 2000 (Microsoft Corporation) and @Risk v4.05 and later @Risk v4.5 (Palisade Corporation). The model was designed to be as flexible as possible without compromising the logic steps within, that is, allowing the ability to update the model to incorporate new data. As a consequence of this a standard template was designed to enable manipulation of the input distributions without changing the structure of the model. The inputs and outputs of each part in the model are clearly marked within the

spreadsheet. The model itself comprises a series of linked Excel spreadsheets, with each sheet describing part of the farm-to-factory pathway as discussed above. A stochastic approach was used to run simulations of the model. For each simulation 30 000 iterations were run using latin hypercube sampling (Vose, 1996).

3. Results

3.1 Hazard Identification

The hazards that may be present in dairy products were identified in the literature review (section 1.7)

3.2 Hazard Characterisation

The characteristics of adverse health effects associated with the identified hazards are detailed in the literature review (Section 1.8), which includes the dose response relationship for the high priority bacterial pathogens and some information regarding the Australian regulatory maximum allowable limits for antibiotics and herbicides.

3.3 Thermal death kinetics of pathogenic microorganisms

A description of the log-linear thermal inactivation for each of the bacterial pathogens examined follows. Graphs showing the thermal inactivation data for each organism are Log D (seconds) against temperature (°C). Data sources, together with the raw data for all examined pathogens are listed in Appendix C.

Escherichia coli

The thermal inactivation kinetics of *E. coli* has been described in many papers. A single paper described the thermal inactivation of *E. coli* in milk (D'Aoust et al, 1998) with the majority of the published accounts describing inactivation in meat products or in liquid media. The plot for $\log_{10}(D)$ vs. temperature for *E. coli* is given (Fig 3.1) showing the pooled data from all the papers examined. The log-linear line of best fit is also shown including the regression parameters. The majority of papers describe the heat inactivation of *E. coli* O157. Because this organism is the most important of the EHEC group it was assumed to be representative of the kinetics of all EHEC organisms.

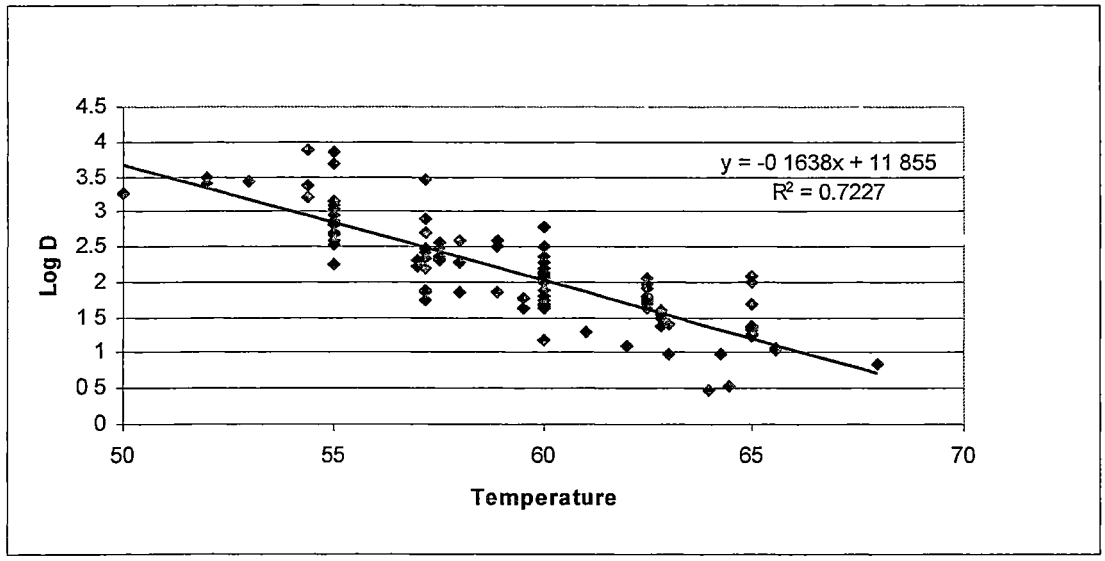

Figure 3.1 Pooled thermal inactivation data for *Escherichia coli*

Listeria monocytogenes

The thermal inactivation kinetics of *Listeria monocytogenes* has been examined in several media including milk, meats, vegetables and laboratory media. A plot of the pooled data including the log-linear regression line, gathered from the published literature, is shown (Fig 3.2) and a subset of that data related to liquid milk thermal inactivation studies only shown in Fig 3.3.

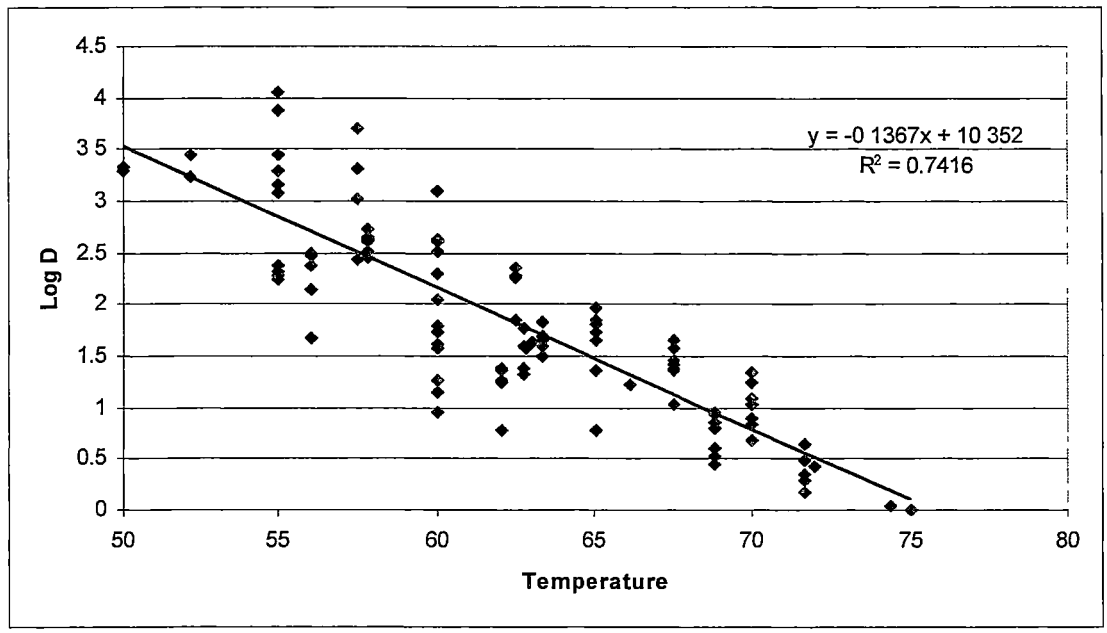

Figure 3.2 Pooled thermal inactivation data for *Listeria monocytogenes*

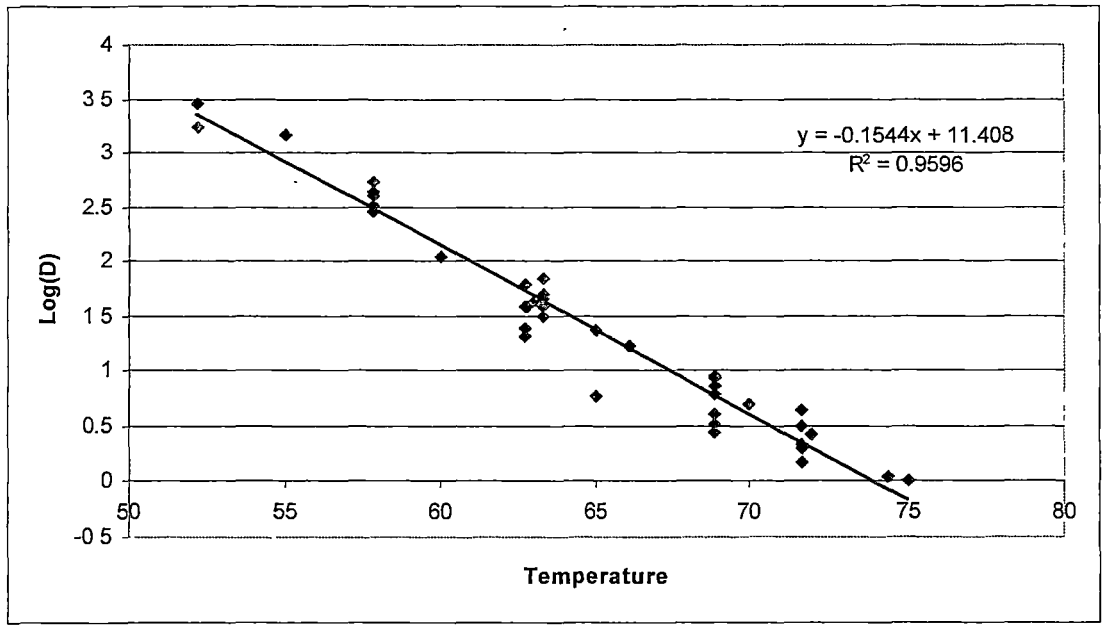

Figure 3.3 Subset of thermal inactivation data for *Listeria monocytogenes* limited to liquid milk as the medium for investigation

The subset of the pooled milk data is used as the thermal inactivation relationship for *Listeria monocytogenes* in the pasteurisation step of the model (refer to section 2.5.4)

Salmonella spp

No published literature were found that described the thermal inactivation of *Salmonella* spp in liquid milk, or other dairy products. A single paper described the thermal inactivation in eggs (Schuman and Sheldon, 1997) whereas others looked at either laboratory media or meat products (chicken, turkey, and beef). The pooled thermal inactivation data for *Salmonella* spp is shown (Fig 3.4).

There is a poor fit for the log-linear thermal inactivation model, compounded by the lack of relevant data for dairy products. In the plot of logD vs temperature there appears to be two divergent thermal inactivation curves. This is an artefact of the use of several different datasets and gives some indication of the variability in the thermal resistance of *Salmonella* spp.

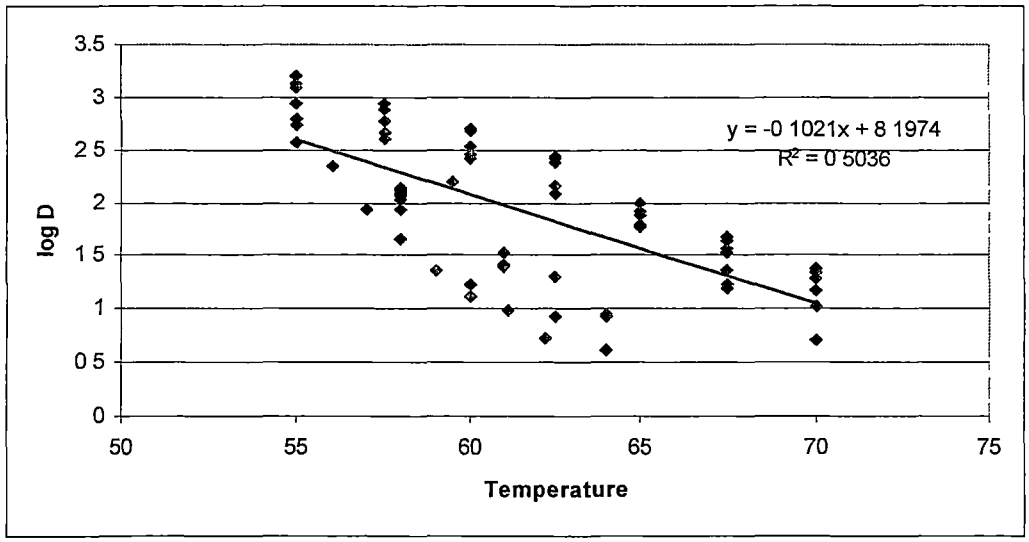

Figure 3.4 Pooled thermal inactivation data for Salmonella spp.

Campylobacter spp

There are few papers in the literature that deal with the thermal inactivation of *Campylobacter* species. Assuming that the thermal inactivation kinetics of *Campylobacter jejuni* and *C. coli* are similar, a log-linear model was constructed for these organisms (Fig 3.5). Little data exists for the thermal inactivation of *Campylobacter* spp in liquid milk

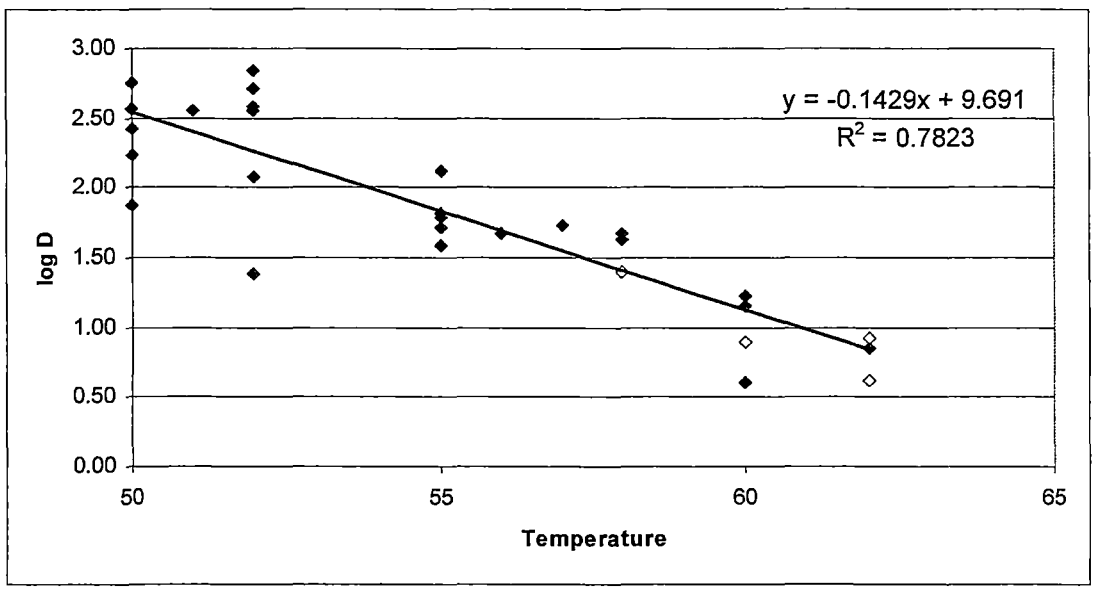

Figure 3.5 Pooled thermal inactivation data for *Campylobacter* spp. (*C. jejuni* in dark points, *C. coli* light points)

Yersinia enterocolitica

Little information exists for the thermal inactivation of *Y. enterocolitica.* Four papers were found to describe the log-linear thermal kinetics of this organism from

experimental data. Of these, two describe inactivation in milk (D'Aoust et al, 1988; Toora et al, 1991); however, there is insufficient information to construct a model from these data alone. The pooled thermal inactivation data is shown (Fig. 3.6).

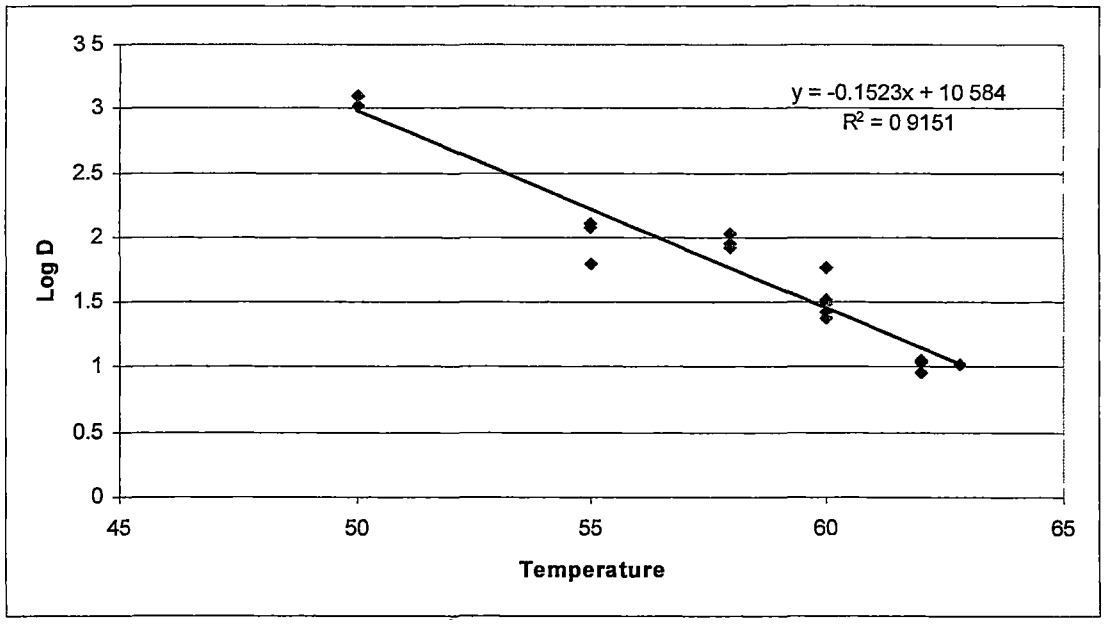

Figure 3.6 Pooled thermal inactivation data for *Yersinia enterocolitica*

Staphylococcus aureus

A description of the thermal tolerance of *Staphylococcus aureus* is found in ICMSF (1996). Several different media were used to determine this organism's thermal tolerance. The pooled data (Fig 3.7) shows a poor fit to the simple log-linear thermal inactivation model. However, if a subset of that data is taken such that only the observation specific for milk are taken the fit improves (Fig 3.8)

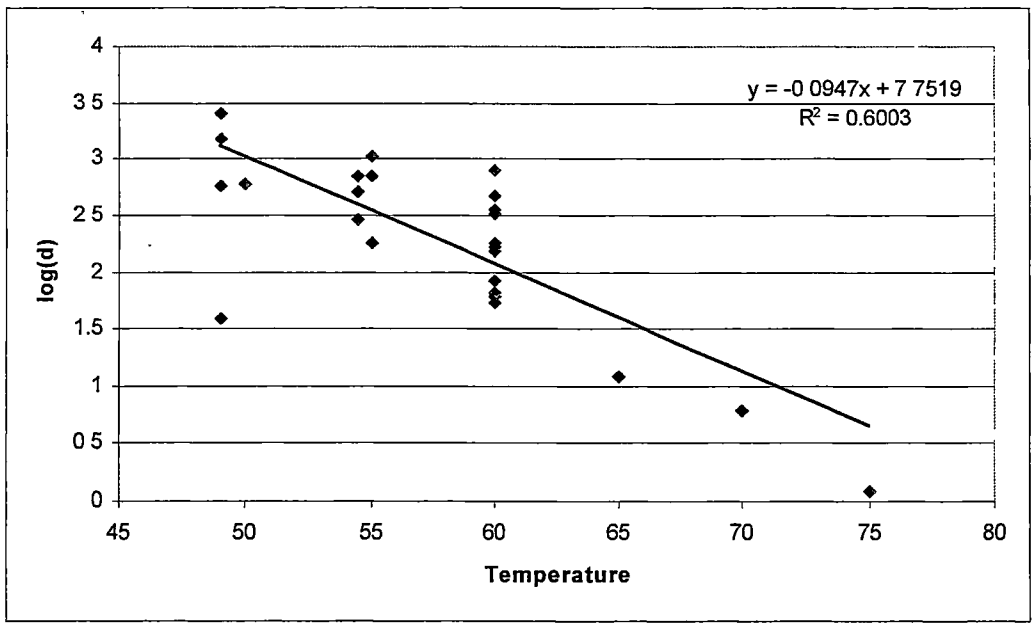

Figure 3.7 Pooled thermal inactivation data for *Staphylococcus aureus*

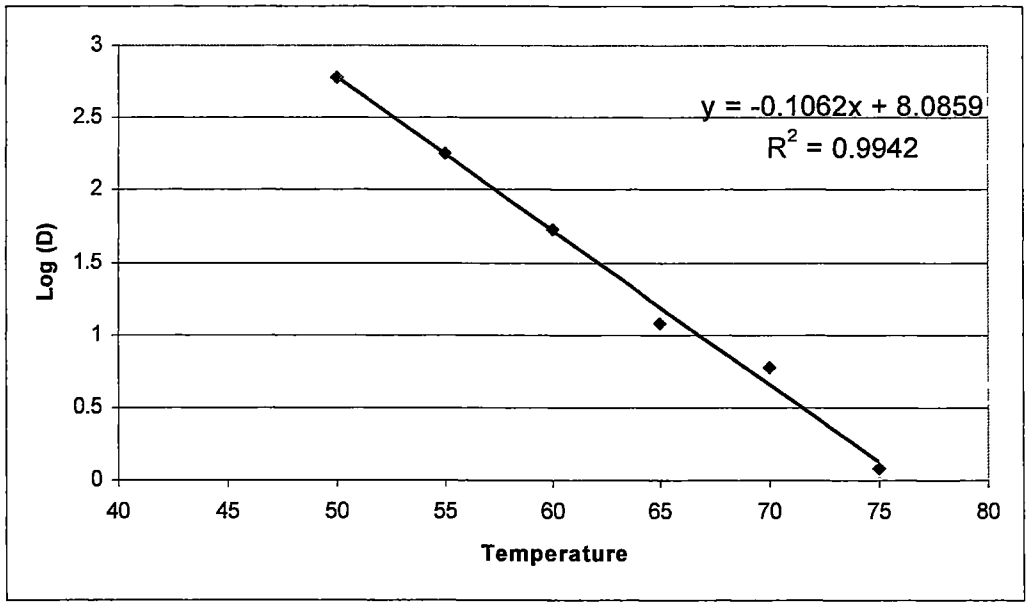

Figure 3.8 Single dataset for thermal inactivation for *Staphylococcus aureus*, liquid milk

Bacillus spp

No published thermal inactivation studies for vegetative cells of *Bacillus cereus* were found. The papers examined describe the inactivation for the spores of this species and other *Bacillus* species. Normal pasteurisation temperatures are insufficient to inactivate spores from this organism (Leontidis et al, 1999). The thermal inactivation plot for *Bacillus* spores is shown in Fig 3.9.

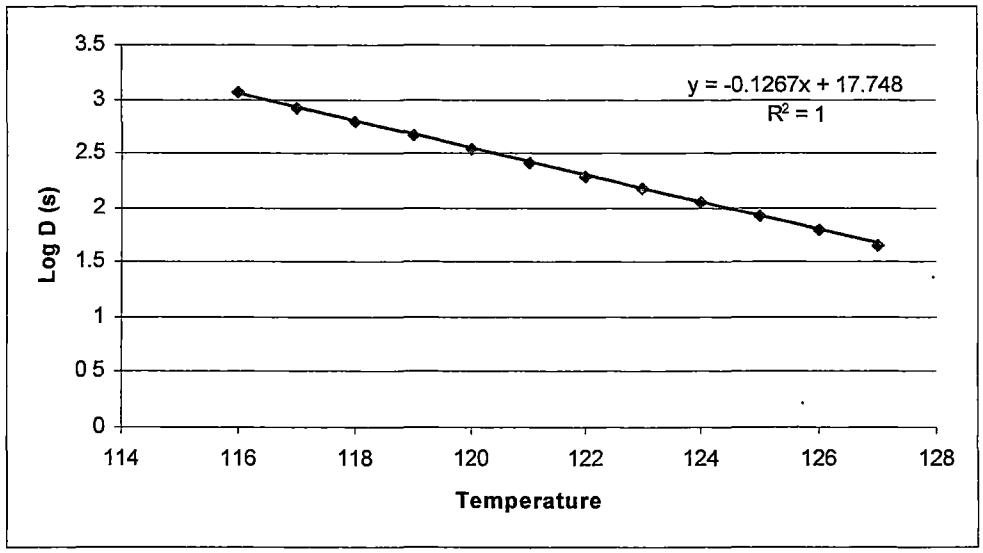

Figure 3.9 Thermal inactivation dataset for *Bacillus* spores (Leontidis et al, 1999)

A summary of the parameters for the log-linear thermal inactivation kinetics for each organism is presented in Table 3.1.

Table 3.1 Thermal inactivation parameters derived from pooled data

Organism	a	b	R^2 [b]
E. coli	0.1638	11.855	0.723
Listeria monocytogenes (all data)	0.1367	10.352	0.742
(liquid milk data)	0.1544	11.408	0.960
Salmonella	0.1021	8.1974	0.503
Campylobacter spp	0.1429	9.691	0.782
Yersinia enterocolitica	0.1523	10.584	0.915
Staphylococcus aureus (all data)	0.0947	7.752	0.994
(liquid milk data)	0.1062	8.086	0.994
Bacillus spp (spores)	0.1267	17.748	1[a]

[a] based on model predictions for *B. stearothermophilus* (Leontidis et al, 1999)

[b] R^2 is the linear regression coefficient

3.4 Consumption patterns of dairy products in Australia

The Australian dairy industry produced 10.17 billion litres of raw milk in the 1999/2000 financial year. This is an increase in production from 8206 million litres in 1994/95. Approximately 20 - 25% of the raw milk produced in Australia is used as drinking milk; the remainder is used for the manufacture of other dairy products.

Estimates by the Australian Dairy Corporation (ADC) on consumption of liquid milks in Australia, show a slight change from ~105 litres consumed per person annually to ~102 litres, in the same period. A detailed look at consumption patterns of dairy products in Australia follows with comparisons between estimates provided by the ADC and the figures presented in a survey conducted by the Australian Bureau of Statistics (ABS, 1997).

Product Groups

To characterise more accurately the risk associated with dairy products, it is important to know the total volume of products consumed, the type of product and the form in which it is consumed, the frequency of consumption, the volume consumed per person and, if possible, differences in consumption among different sub-groups in the Australian population based on age, gender and health status. The National Nutrition Survey (NNS), conducted by the Australian Bureau of Statistics (ABS) in 1995, provides a detailed examination of the consumption patterns of all foods groups, including dairy, by the Australian population (ABS, 1997). The information presented in the NNS is split into broad food group and within each category there are individual product types or groups. The dairy product groups are shown (Table 3.2a).

Table 3.2a Categories for Milk products and dishes in the National Nutrition Survey

	NSS Group	Products Included
1	Dairy Milk	Drinking milk, including full fat, fat increased, low fat, condensed, evaporated and powdered
2	Yoghurt	Natural, flavoured, low fat, buttermilk, yoghurt drinks
3	Cream	Thickened, sour, reduced fat, artificial
4	Cheese	Natural, reduced fat, cottage, cream, processed, camembert, brie and cheese dishes
5	Frozen milk products	Ice creams (all types), frozen yoghurts, thick shakes, frozen dairy desserts
6	Other dishes where milk or a milk product is a major component	Custards, sweet sauces, dairy desserts, cheese-, milk- and cream-based desserts
7	Milk substitutes	Soy beverages and ice confection, and non-dairy cheese substitutes
8	Flavoured Milks	Flavoured full fat, low fat and unspecified fat level

The NNS food groups were chosen to reduce statistical uncertainty, however, these food groups span different product groups from the ADC and DRDC production figures, which leads in some cases to apparent difference in consumption estimates. To accommodate this difference the ABS survey groups have been used and, where possible, the ADC production figures correlated with the ABS product groups.

Consumption Data

Australia's population of ~19.5 million consume ~4.3 million litres of milk per day, with ~400 000 litres being flavoured milks, around 252 tonnes of cheese and ~250 tonnes of yoghurt. This equates to approximately 400g of dairy products per person per day, or 2 million tonnes of dairy products consumed annually throughout the nation.

The consumption data is divided into three forms. Firstly the total annual consumption of Australian dairy products, secondly the consumption patterns for specific age groups, split between males, females and persons as presented in the ABS survey, and thirdly by state and territory. Consumption data by state and territory has been compiled for those persons aged 19 and over. This accounts for ~68% of the total daily consumption or ~75% of the population. It is important to note that when using the state and territory consumption figures that a large part (~25%) of the consumption for that state has not been included, i.e. consumption attributable to those people aged less than 19 years of age. Consumption estimates from the DRDC and ADC have used supermarket sales as an indication of consumption. This assumes that the population consumes all dairy products sold through supermarkets. The loss of products due to spoilage, poor handling, and feeding to pets is not known; hence, these consumption figures may overestimate the true consumption pattern of dairy products in Australia (see Table 3.2). Conversely, the proportion of sales direct to door and through small retail outlets is ignored.

The annual consumption of dairy products in Australia was calculated using the daily consumption figures for each age group (ABS, 1997), based on the estimated population for each age group (see Appendix B), added together and multiplied by 365 (days in the year) as presented in Table 3.2. A comparison of the DRDC and ADC production and consumption statistics for the 1995/96 financial year has also been included. This table summarises the consumption for each NNS product group and where possible, the ADC production and consumption data has been entered as a comparison. Table 3.2 shows that there are gaps in the information that is currently available.

Estimates of annual consumption from the ABS survey indicate that drinking milk, flavoured and plain, is the most frequently consumed dairy product in Australia with an annual consumption of 1.6 billion litres. This correlates well with the ADC production figure of 1.9 billion litres and the ADC consumption estimate of 1.6 billion litres. A similar pattern can be seen for yoghurt, cheese, and frozen milk products, the next most commonly consumed dairy products. The remainder of the product groups lack key data to enable this comparison to be performed.

The bulk of the information presented in the NNS survey (ABS, 1997) is condensed in the following tables and figures. The mean daily intake of dairy products,

by fine age group (shown in Figure 3.10), indicates a gradual decrease in the daily consumed volume with increasing age, with consumption ranging from ~500 grams per day in young children down to ~250g in the elderly population. Table 3.4 shows the breakdown by product category for mean daily consumption by fine age group. The mean consumption of dairy products by state and territory for persons aged 19 and over is between 250 and 350 grams per day (Figure 3.11.). Table 3.5 provides a detailed summary of the daily consumption by state and territory for persons aged 19 and over.

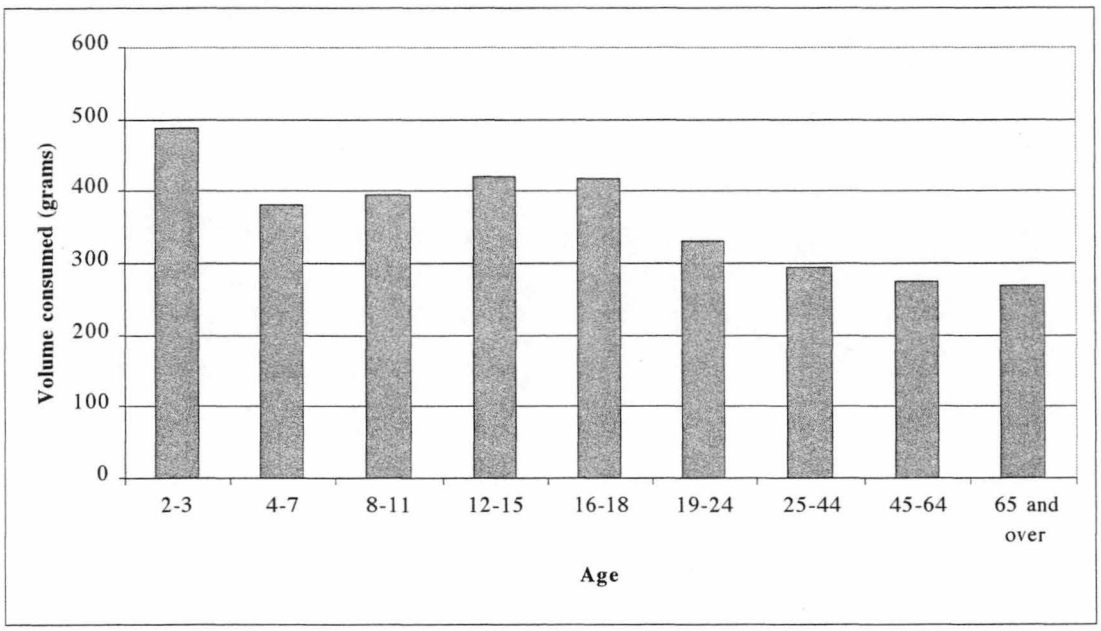

Figure 3.10: Mean daily consumption of dairy products per person by fine age group (after ABS, 1997)

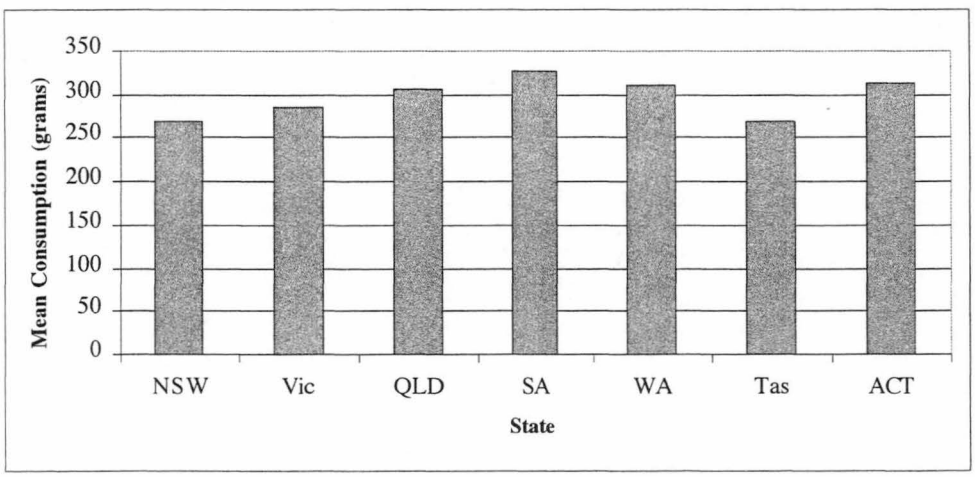

Figure 3.11: Mean daily consumption of dairy products per person by state and territory (after ABS 1997)

Table 3.2b – Total annual consumption of Australian dairy products

	Dairy Milk[b]	Yoghurt[a]	Cream	Cheese[a]	Frozen Milk Products	Other Dishes where milk or a milk product is a major component	Milk Substitutes	Flavoured Milks[b]
All Ages ABS stats (95/96) based on population of 17564932	1.45E+09	9.06E+07	1.55E+07	9.20E+07	1.52E+08	8.30E+07	3.09E+07	1.32E+08
Production Figures from ADC (95/96)	1.89E+09	9.32E+07	ND	2.41E+08[c]	2.03E+08[d]	ND	ND	ND
Consumption Figures from ADC (95/96)	1.75E+09	7.97E+07	2.10E+08[d]	9.38E+07[e]	2.00E+08[d]	3.02E+07	ND	1.43E+08
Export Volume[g]	6.6E+07	2.0E+06	ND	1.11E+08	ND	ND	ND	ND
Volume Unaccounted for[h]	7.60E+07	1.15E+07	-	3.58E+07	2.30E+06	-	-	-
Percentage of Production Remaining[i]	4.0%	12.3%	-	14.9%	1.1%	-	-	-

a – values in kg
b – values in litres
c – includes all cheese types
d – data has been taken from 1993/94 financial year due to discontinuation of series in 1995/96.
e – only includes Australian produced cheeses, imports have been excluded
f – NNS survey includes buttermilk. No data for buttermilk production in the ADC statistics.
g – Export volume based on ADC figures
h – Calculates the volume of product remaining from the ADC production figures after consumption and export have been subtracted
i – gives the percentage of production volume unused
ND – indicates no specific data

Table 3.4 - Daily consumption of dairy products in Australia by fine age group (ABS, 1997)

	Mean Total Intake[a]	Population size Estimate	Total Consumption of Dairy Products[c]	Dairy Milk[b]	Yoghurt[c]	Cream[c]	Cheese[c]	Frozen Milk Products[c]	Other Dishes where milk or a milk product is a major component[c]	Milk Substitutes[c]	Flavoured Milks[b]
2-3	*487.9*	517536	2.53E+05	2.01E+05	9.57E+03	2.59E+02	5.59E+03	8.75E+03	1.27E+04	8.54E+03	6.31E+03
4-7	*381.3*	1031614	3.93E+05	2.86E+05	1.46E+04	4.13E+02	1.13E+04	3.33E+04	2.31E+04	3.82E+03	2.02E+04
8-11	*394.1*	1032682	4.07E+05	2.93E+05	1.23E+04	1.03E+03	1.29E+04	4.96E+04	1.41E+04	4.44E+03	2.01E+04
12-15	*421.4*	1019896	4.30E+05	2.99E+05	1.55E+04	1.33E+03	1.48E+04	6.00E+04	1.17E+04	1.53E+03	2.59E+04
16-18	*417.5*	757948	3.16E+05	2.19E+05	1.37E+04	1.59E+03	1.42E+04	3.19E+04	6.06E+03	0.00E+00	2.95E+04
19-24	*332*	1699348	5.64E+05	3.75E+05	1.63E+04	4.59E+03	2.72E+04	3.99E+04	1.72E+04	7.31E+03	7.65E+04
25-44	*294.2*	5592190	1.65E+06	1.13E+06	8.00E+04	1.68E+04	9.17E+04	1.06E+05	5.31E+04	2.63E+04	1.43E+05
45-64	*275.1*	3752980	1.03E+06	7.57E+05	5.52E+04	1.01E+04	5.29E+04	6.00E+04	4.28E+04	1.91E+04	3.57E+04
65 and over	*267.8*	2160738	5.79E+05	4.27E+05	3.09E+04	6.48E+03	2.14E+04	2.66E+04	4.67E+04	1.36E+04	5.83E+03
Total Dairy Products Consumed Daily	**3271.3**	**17564932**	**5.62E+06**	**3.99E+06**	**2.48E+05**	**4.26E+04**	**2.52E+05**	**4.16E+05**	**2.28E+05**	**8.47E+04**	**3.63E+05**

a – Values in grams
b – Values in litres
c – Values in kg

Table 3.5 - Daily consumption of dairy products in Australia by state and territory for persons aged 19 and over(ABS, 1997)

	Mean Total Intake[a]	Population size Estimate	Total Consumption of Dairy Products	Dairy Milk[b]	Yoghurt[c]	Cream[c]	Cheese[c]	Frozen Milk Products[c]	Other Dishes where milk or a milk product is a major component[c]	Milk Substitutes[c]	Flavoured Milks[b]
NSW	*268.4*	4541092	1.22E+06	8.75E+05	5.45E+04	1.09E+04	6.04E+04	7.36E+04	5.31E+04	2.45E+04	6.63E+04
Vic	*285.3*	3325795	9.49E+05	6.86E+05	5.06E+04	1.16E+04	5.15E+04	5.55E+04	3.53E+04	1.70E+04	4.09E+04
QLD	*306.1*	2407414	7.37E+05	5.27E+05	3.44E+04	5.30E+03	3.39E+04	5.06E+04	3.39E+04	8.67E+03	4.31E+04
SA	*326.1*	1062165	3.46E+05	2.18E+05	1.27E+04	4.14E+03	1.86E+04	1.91E+04	1.27E+04	4.04E+03	5.70E+04
WA	*311.2*	1226002	3.82E+05	2.49E+05	2.17E+04	3.80E+03	1.84E+04	2.10E+04	1.78E+04	9.69E+03	4.08E+04
Tas	*269.1*	336449	9.05E+04	6.59E+04	5.05E+02	1.58E+03	4.51E+03	6.16E+03	4.37E+03	7.74E+02	3.33E+03
NT[d]	-	105305	-	-	-	-	-	-	-	-	-
ACT	*312.4*	201035	6.28E+04	4.37E+04	3.82E+03	6.03E+02	3.76E+03	4.58E+03	1.65E+03	1.07E+03	3.56E+03
Total Dairy Products Consumed	**2078.6**	**13205257**	**3.79E+06**	**2.67E+06**	**1.78E+05**	**3.80E+04**	**1.91E+05**	**2.30E+05**	**1.59E+05**	**6.57E+04**	**2.55E+05**

a – Values in grams
b – Values in litres
c – Values in kg
d – data for Northern Territory is included in Australian totals in NNS survey

3.5 Model Inputs

The inputs parameters used in the model are detailed in this section. The majority of the values listed derive from the survey data (Appendix D). A few of the derived values are from published reports on the prevalence of pathogens in dairy herds (Rohrbach et al, 1992; Coia et al, 2001; Jayarao and Henning, 2001). The inputs used for the farm level module are presented in Table 3.6, indicating both the parameter values and the distribution sampled from for each iteration, similarly for the milk collection and transport module (Table 3.7), and the Factory module (3.8).

The input parameters for the thermal inactivation model used for the pasteurisation section of the model are presented in Table 3.1. The pasteurisation conditions for the two products that have been modelled are 15-30s 75-78°C for liquid milk production and 15-25s at 73-78°C for cheese production. Pasteurisation conditions do not differ widely between different product lines in Australia. In terms of the model, the milk that is received at each of the factories is assumed to be pasteurised by that factory. Any further processing occurs after the point of pasteurisation.

Table 3.6 Input Parameters: distributions and values for the farm level module

Input	Distribution	Parameter value(s)	Units	Source
P(LF) Prob. Large farm	Beta ($\alpha1$, $\alpha2$)	$\alpha1 - 40$ $\alpha2 - 519$	-	NSW survey data
P(MF) Prob. medium farm	Beta ($\alpha1$, $\alpha2$)	$\alpha1 - 367$ $\alpha2 - 192$	-	NSW survey data
Herd Size LF	Normal (μ, σ)	$\mu - 390$ $\sigma - 75$	Cows	NSW survey data
Herd size MF	Normal (μ, σ)	$\mu - 174$ $\sigma - 30$	Cows	These inputs are rounded to whole number values
Herd Size SF	Normal (μ, σ)	$\mu - 70$ $\sigma - 15$	Cows	
P(HC) *E. coli* Prob. Herd contaminated	Beta ($\alpha1$, $\alpha2$)	$\alpha1 - 21$ $\alpha2 - 1832$	-	Coia et al, 2001; Steele et al, 1997; Rohrbach et al, 1992; Jayarao and Henning, 2001
P(HC) *Listeria*	Beta (α 1, $\alpha2$)	$\alpha1 - 66$ $\alpha2 - 2079$	-	
P(HC) *Salmonella*	Beta ($\alpha1$, $\alpha2$)	$\alpha1 - 38$ $\alpha2 - 2107$	-	
P(HC) *Yersinia*	Beta ($\alpha1$, $\alpha2$)	$\alpha1 - 53$ $\alpha2 - 372$	-	
P(HC) *Campylobacter*	Beta ($\alpha1$, $\alpha2$)	$\alpha1 - 57$ $\alpha2 - 2088$	-	
P(HC) *Bacillus*	Triang (min, most-likely, max)	Min – 0 ML – 0.5 Max – 0.6	-	Estimated value
P(HC) *S. aureus*	Triang (min, most likely, max)	Min – 0 ML – 0.5 Max – 0.6	-	Estimated value
P(ChemHaz) Antibiotic	Gamma (α, β)	$\alpha - 195$ $\beta - 7.98 \times 10^{-6}$	-	AMRA, 2001
P(ChemHaz) Pesticide	Beta ($\alpha1$, $\alpha2$)	$\alpha1 - 1$ $\alpha2 - 83$	-	AMRA, 2001
P(UC|HC)	Uniform (min, max)	Min – 0.1 Max – 0.2	-	Assumed value
Chb (all pathogens)	Fixed value	100	Cells	Assumed value
CCL (all chemical hazards)	Fixed value	0.1	Grams	Estimated value
Milk production per cow	Normal (μ, σ)	$\mu - 20$ $\sigma - 5$	Litres	Expert opinion
T_{FV} Temperature in farm vat	Triang (min, most likely, max)	Min – 1 ML – 4 Max – 6	°C	NSW Survey data
t_{FV} time spent in farm vat	Triang (min, most likely, max)	Min – 1 ML – 16 Max – 72	Hours	NSW Survey data
P(> compliance temperature)	Beta ($\alpha1$, $\alpha2$)	$\alpha1 - 40$ $\alpha2 - 262$	-	NSW Survey data

Table 3.7 Input Parameters: distributions and values for the milk collection and transport module

Input	Distribution	Parameter value(s)	Units	Source
Tanker volume	Fixed value	Small 10000 Medium 20000 Large 40000	Litres	Expert opinion
MaxT Max. temperature in tanker	Fixed value	17	°C	NSW survey data
T_{MT} Temperature in milk tanker	Log-Logistic (γ, β, α)	γ – 1.1499 β – 2.7994 α – 2.6358	°C	NSW survey data
T_{Trans} Time spent in milk tanker	Triangular (min, mostlikely, max)	Min – 1 ML – 4 Max – 18	Hours	Expert opinion

Table 3.8 Input Parameters: distributions and values for the factory module

Input	Distribution	Parameter value(s)	Units	Source
Factory silo volume Small	Pert (min, most likely, max)	Min – 1 000 ML – 5 000 Max – 10 000	L	NSW Survey data
Medium		Min – 10 000 ML – 40 000 Max – 600 000	L	
Large		Min – 500 000 ML - 1 000 000 Max - 2 000 000	L	

3.6 Farm Level Module

In the final draft of the model 1000 farms were modelled. In a simulation with 30000 iterations, the mean number of farms in each class (small, medium and large) was 72, 609 and 319 respectively. The mean milk production from these farms was estimated to be 3 126 000 (5^{th} percentile 2 987 000, 95^{th} percentile 3 270 000) litres per day, being produced from a mean total herd size of 156 000 (5^{th} 149 000, 95^{th} 164 000) cows. There were 268 000 cows in NSW in 2000, including both cows "in milk" and "dry", ~60% of the dairy herd is "in milk". These cows produced around 3.5 million litres of raw milk per day. Thus from the 1000 farms (86% of total farms) that are modelled, 87% of the daily milk production is accounted for from ~57% of the total herd size in NSW. The initial, estimated mean contamination of raw milk with

microbiological and chemical hazards, with associated confidence intervals, is presented in table 3.9.

Table 3.9 Estimated mean concentration of hazards in raw milk.

Hazard	Mean	5% Percentile	95% Percentile	Units
E. coli	8.51×10^{-3}	3.50×10^{-3}	1.52×10^{-2}	Cells/L
Salmonella spp	1.33×10^{-2}	6.60×10^{-3}.	2.19×10^{-2}	Cells/L
L. monocytogenes	2.31×10^{-2}	1.33×10^{-2}	3.54×10^{-2}	Cells/L
Y. enterocolitica	9.36×10^{-2}	5.94×10^{-2}	0.134	Cells/L
C. jejuni	1.99×10^{-2}	1.11×10^{-2}	3.11×10^{-2}	Cells/L
B. cereus	0.275	8.71×10^{-2}	0.467	Cells/L
S. aureus	0.275	8.61×10^{-2}	0.466	Cells/L
Antibiotic	1.17×10^{-6}	0.00	3.06×10^{-6}	Grams/L
Pesticide	8.93×10^{-6}	0.00	2.76×10^{-5}	Grams/L

The concentration of microbiological hazards in the raw milk is affected by the storage conditions in the farm milk vat in the event that these conditions permit the growth of the organisms present. Table 3.10 shows the estimated mean concentration of microbiological hazards after storage in the farm milk vat.

Table 3.10 Concentration of microbiological hazards present in the farm milk vat after storage

Hazard	Mean	5% Percentile	95% Percentile	Units
E. coli	3.13×10^{-2}	4.18×10^{-3}	0.111	Cells/L
Salmonella spp	5.29×10^{-2}	8.89×10^{-3}	0.162	Cells/L
L. monocytogenes	0.752	3.32×10^{-2}	2.93	Cells/L
Y. enterocolitica	94.3	5.24	299	Cells/L
C. jejuni	1.99×10^{-2}	1.11×10^{-2}	3.10	Cells/L
B. cereus	4.88	1.04	9.95	Cells/L
S. aureus	0.275	8.64×10^{-2}	0.467	Cells/L

By varying the udder contamination level (UCL, CCL), the concentration of the hazards present in the farm milk vat changes in proportion to the change in the contamination level. That is, if 10 000 cells enter the milk through each contaminated cow, the concentration of bacteria in the farm milk vat prior to the growth phase is 100 times greater than with the initial contamination level of 100 cells per cow.

The change in concentration of the hazards present in the farm milk vat varied from none, for antibiotics, pesticides, *C. jejuni* and *S. aureus*, up to 10^3 for *Y.*

enterocolitica. Table 3.11 shows the $\log_{10}$ change in the mean concentration of all hazards in ascending order.

Table 3.11 Mean increase in hazard concentration between the farm milk vat and up to prior to collection by the milk tanker

Hazard	Mean Log_{10} Increase
Campylobacter jejuni	0
Staphylococcus aureus	0
Antibiotic	0
Pesticide	0
Escherichia coli	0.566
Salmonella spp	0.600
Bacillus cereus	1.25
Listeria monocytogenes	1.51
Yersinia enterocolitica	3.00

For each organism the estimated increase due to growth can be attributed to the ability of that organism to grow, or not, in low temperature environments, and the probability that each farm's milk vat will exceed the regulatory temperature limit and allow growth of non-psychrotrophic organisms. Growth shifts the estimated cumulative distribution of the concentration of hazard to the right.

3.7 Milk Collection and Transport Module

In the final draft of the model 50 tankers were modelled. In a simulation with 30000 iterations, the mean volume of milk collected by these tankers was estimated to be 681 000 litres per day. The estimated mean contamination of raw milk with hazard in the milk tankers, with associated confidence intervals, is presented in table 3.12.

Table 3.12 Estimated mean concentration of hazards in raw milk present in the milk tanker

Hazard	Mean	5% Percentile	95% Percentile	Units
E. coli	3.21×10^{-2}	0.00	0.112	Cells/L
Salmonella spp	5.11×10^{-2}	5.31×10^{-4}	0.189	Cells/L
L. monocytogenes	0.767	5.32×10^{-3}	2.96	Cells/L
Y. enterocolitica	86.5	0.129	393	Cells/L
C. jejuni	2.00×10^{-2}	2.39×10^{-3}	4.99×10^{-2}	Cells/L
B. cereus	0.275	8.04×10^{-2}	0.481	Cells/L
S. aureus	5.64×10^{-2}	2.09×10^{-3}	0.190	Cells/L
Antibiotic	1.64×10^{-6}	0.00	5.93×10^{-6}	Grams/L
Pesticide	8.89×10^{-6}	0.00	3.63×10^{-5}	Grams/L

The concentration of the microbiological hazards present in the raw milk is affected by the storage conditions in the milk tanker as it transports the milk from the farms to the factory. Table 3.13 shows the estimated mean concentration of these hazards after the transportation.

Table 3.13 Concentration of microbiological hazards present in the milk tanker after transportation

Hazard	Mean	5% Percentile	95% Percentile	Units
E. coli	3.68×10^{-2}	0.00	0.117	Cells/L
Salmonella spp	5.76×10^{-2}	0.00	0.205	Cells/L
L. monocytogenes	1.01	4.34×10^{-3}	3.24	Cells/L
Y. enterocolitica	158	0.138	565	Cells/L
C. jejuni	2.00×10^{-2}	1.63×10^{-3}	5.37×10^{-2}	Cells/L
B. cereus	0.357	9.46×10^{-2}	0.659	Cells/L
S. aureus	5.83×10^{-2}	1.58×10^{-3}	0.192	Cells/L

During transportation the model predicts that there will be bacterial growth, however, the amount of growth is not estimated to be as great as within the farm milk vat. This is due to the smaller amount of time available for growth to occur. Table 3.14 shows the $\log_{10}$ change in the concentration of the microbiological hazards present in the tanker from the point of collection at the farm to just prior to delivery at the factory.

Table 3.14 Change in mean hazard concentration in the milk tanker between farm pickup and factory delivery

Hazard	Mean Log_{10} Increase
Antibiotic	0.00
Pesticide	0.00
Campylobacter jejuni	0.00
Staphylococcus aureus	0.014
Salmonella spp	0.052
Escherichia coli	0.061
Bacillus cereus	0.113
Listeria monocytogenes	0.120
Yersinia enterocolitica	0.262

All microbiological hazards are predicted to increase during transportation. There is an increase in the spread of the distribution of the mean concentration for each hazard. This means that there is an increased, though small, probability of encountering an increased number of pathogens. Corresponding to this is the reduced, though still large, probability of encountering a small number of pathogens. For example, the estimated probability of encountering less than 20 cell/L of *Yersinia enterocolitica* in the farm

milk vat just prior to collection by the tanker and in the tanker after transportation is 0.65 and 0.64 respectively, whereas the probability of encountering greater than 1000 cells per litre is 0.015 and 0.028.

3.8 Factory Level Module

In the final draft of the model 3 factories were modelled for each product, those products being; liquid milk, cheese, and milk powder. The mean total daily milk collection for all factories was estimated to be 2 020 000 litres. This is greater than both the daily milk production at the farm level and the daily milk collection by the tankers. However, for a single product the factory collection (i.e. 3 factories) is ~500 000 litres per day. The model does not differentiate between tankers that have delivered milk and those that have not. Thus on a single iteration a single tanker may deliver milk to both the "large milk powder factory" and the "small cheese factory".

The estimated concentration of all hazards modelled after the daily collection of milk at the factory is shown in table 3.15.

Table 3.15 Estimated mean concentration of hazards in raw milk present in the factory silo

Hazard	Mean	5% Percentile	95% Percentile	Units
E. coli	2.94×10^{-2}	0.00	9.81×10^{-2}	Cells/L
Salmonella spp	4.82×10^{-2}	0.00	0.156	Cells/L
L. monocytogenes	0.801	3.82×10^{-3}	2.76	Cells/L
Y. enterocolitica	140	0.103	426	Cells/L
C. jejuni	1.69×10^{-2}	1.42×10^{-3}	6.45×10^{-2}	Cells/L
B. cereus	0.3046	6.05×10^{-2}	0.732	Cells/L
S. aureus	4.37×10^{-2}	0.00	0.159	Cells/L
Antibiotic	1.01×10^{-6}	0.00	4.14×10^{-6}	Grams/L
Pesticide	7.56×10^{-6}	0.00	9.94×10^{-5}	Grams/L

The mean concentration of the antibiotic and pesticide modelled are below the regulatory limit. However, the distribution about the mean for these concentrations spans several orders of magnitude, with the maximum concentration, for the antibiotic and pesticide respectively, of 2.35×10^{-4} g/L (0.24 mg/L) and 4.92×10^{-4} g/L (0.49 mg/L). The most commonly used antibiotic in the Australian dairy industry is neomycin; its MRL is 0.5 mg/kg (DFSV, 2001). It was not detected in 476 samples taken in a recent survey for antimicrobial residues, i.e. the observed probability of detection is less than 2.1×10^{-3} (ADASC, 2001). The estimated mean concentration of

antibiotic residues in the factory silo of 1.01 x 10^{-3} mg/L is around 4500 times smaller than the MRL for this antibiotic. The modal value was zero. Detections of antibiotic residues in factory silos have occurred in about 0.04% of samples taken. The model did not predict that these substances would exceed the MRL. With the exception of *L. monocytogenes* and *Y. enterocolitica*, the microbiological hazards may be present at an average concentration of less than one cell per litre.

3.9 Pasteurisation Module

The estimated likely contamination of pasteurised milk with the microbiological hazards modelled, is negligible, effectively zero (Table 3.16). There was no data available to validate these estimates. The simulation output of predicted mean concentration for *Salmonella* spp. and *B. cereus* in pasteurised milk is shown in Figures 3.12 and 3.13.

Table 3.16 Mean estimated concentration of microbiological hazards in milk immediately after pasteurisation (assuming no further contamination) and the mean volume of milk required to encounter 1 cell

Hazard	Mean Concentration (cells/L)	Equivalent Volume (litres)
E. coli	$<10^{-14}$	$>10^{10}$
Salmonella spp	10^{-9}	10^{9}
L. monocytogenes	$<10^{-14}$	$>10^{10}$
Y. enterocolitica	$<10^{-14}$	$>10^{10}$
C. jejuni	$<10^{-14}$	$>10^{10}$
B. cereus	2	0.5
S. aureus	$<10^{-14}$	$>10^{10}$

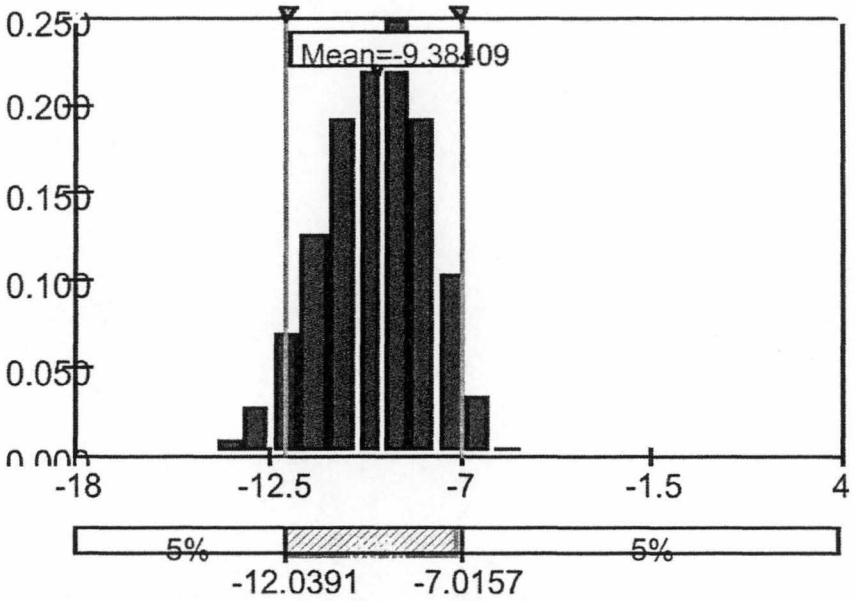

Figure 3.12: Mean estimated concentration of *Salmonella* spp. in pasteurised liquid milk. (X-axis values are in $\log_{10}$ scale. Vertical delimiters demote the 5th and 95th percentiles)

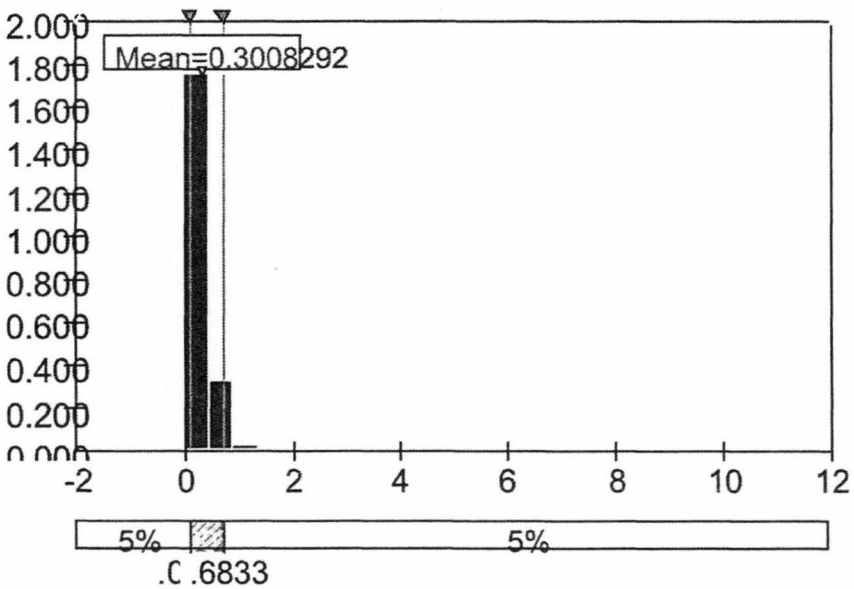

Figure 3.13: Mean estimated concentration of *Bacillus cereus* in pasteurised liquid milk. (X-axis values are in $\log_{10}$ scale. Vertical delimiters demote the 5th and 95th percentiles)

4. Discussion

4.1 Assumptions and Methods

There are two types of assumptions listed in the description of the model (section 2.5), critical and non-critical. A critical assumption is one that affects the estimates of hazard concentration and/or frequency sufficiently to have a bearing on the final interpretation. Conversely, a non-critical assumption is one that affects neither the estimated concentration, nor frequency, of hazards present in milk, or perhaps does but only in a trivial sense. That is, the criticality of each assumptions listed are based on the effect they have on estimated food safety risks. Assumptions are used to simplify the modelling of a complex system. 'Parsimony' is considered of importance in modelling, the fewer the assumptions used in a model the greater the parsimony.

Farm level Module

The assumption that there is no seasonal variation in milk production is incorrect. However, this assumption is non-critical because it does not relate to annual food safety risks, only to milk production. If it were demonstrated that seasonal milk production affected the likelihood and severity of hazard contamination, the model would need to be updated to account for seasonal variation. Related to this is the assumption that all cows produce the same mean volume of milk per day. This assumption has three parts; that the daily milk production is not related to status with respect to the occurrence of pathogen, the breed of the cows, nor related to herd size. These are again non-critical assumptions, and are not related to estimation of food safety risks. The final non-critical assumption listed for this section of the model is the spatial distribution of hazards in the farm milk vat. It is assumed that they are evenly distributed, that is, there is no clumping of bacterial cells and there are no "hot spots" for chemical hazards.

Three farm sizes were used as inputs in the model. These three class sizes were chosen on an arbitrary basis as the range of farm sizes in NSW scaled from 10 to over 20000 cows. A simple method was required to cover most of this range, and produce as similar proportion of farms in each of the appropriate classes. Hence a distribution for the actual farm sizes was not used, as this produced too many 'large' farms and too few 'medium' farms. An alternative method was considered using a Uniform distribution between 0 and 1. If the value sampled from that distribution was within any particular range (accounted for by the 'large', 'medium' and 'small' classes), then the number of cows on that farm would follow the distribution for cow umber as used in the model. Regardless, the approach used allows the user to quickly gauge the number of farms in each class (using a sum function in Excel).

The potential growth of pathogenic bacteria in the farm milk vat would be affected by the assumptions regarding the constant temperature of the farm milk vat, the lack of a lag phase for contaminating organisms and similar growth phase for the contaminating bacteria. The constant temperature in each farm milk vat is considered as the average temperature of the milk in that vat prior to collection by the milk tanker. Growth predictions from this mean temperature are similar to those obtained through the integration of all time temperature intervals provided that the temperature does not fluctuate greater than ~5°C (Ross, 1999). Assuming lack of a lag phase for the contaminating pathogenic bacteria simplifies the module. It has been observed that the lag is inversely proportional to the maximum specific growth rate, at a given temperature; however, these effects have not been modelled (Smith, 1985; Mackey and Kerridge, 1988; Baranyi and Roberts, 1994). Similarly, by taking all cells present for each pathogen as being in the same growth phase, the complexity of the module is reduced (Baranyi and Roberts, 1994). These assumptions are critical, and investigation into their effects on the risk estimate is warranted. Investigation into the time taken to resolve the lag phase in several bacteria including; *Listeria monocytogenes*, *E. coli*, *S. aureus*, *Salmonella* spp., *C. perfringens* and *B. stearothermophilus*, has been undertaken (Ross, 1999). The two remaining assumptions listed for this module are simplifications of the potential contamination events and the magnitude of those events: critical assumptions, for which no published information to assess their validity are available. Any cow will have some degree of contamination on the udder even with sanitation and washing of the udder. It is not possible, however, to determine precisely the distribution for the possible numbers of contaminating bacteria from the published literature (most likely because this quantity would be difficult to measure). It is possible to interpolate the likely contaminants of raw milk from farm microbiological test results, but a better solution would be to conduct research to determine the type of bacteria present as udder contaminants, the extent of contamination within the herd and on individual udders and the magnitude of that contamination. A prelude to such research would be to determine if suitable measurement systems exist for procuring the desired data.

The constant value used to estimate the degree of contamination of raw milk from the udders of contaminated cattle is an assumption that is subject to error. For example: a cow may be infected with a high level of *Salmonellae*. This could induce a high rate of voiding of soft faeces, which may lead to an increase in the numbers of *Salmonellae* present on the cow's udder. Due to a higher amount of bacterial contamination of the udder more *Salmonella* could enter the milk. Also, *Listeria monocytogenes* is recognised as a cause of mastitis in cows (Varnam and Evans, 1991), and could lead to an increase in the level of this organism being shed into the milk though the udder. There may be other influences on the probability of the udder being contaminated, including: environmental conditions, the geography surrounding the farm and the region,

the health status of the cow, the time of year etc. There is no published information about the relationship between these factors. Including them into the model increases the complexity of the model without necessarily improving the accuracy of the predictions.

Milk Collection and Transport Module

The assumptions in this module are all related to hazards, and hence they are potentially 'critical'. One example is the assumption that no time elapsed between the first milk collection and the last. This removes the complicating factor of having different populations of bacterial pathogens in different growth phases within each tanker. That is, the average time and temperature is used to determine the growth in the farm milk vat and the tankers. By taking into account travelling times of bulk milk tankers between farms, the model reflects reality but a layer of complexity is added to the model. In the end this complexity was judged unnecessary because, although it may be a reason why bacterial counts could increase, the amount of time usually involved is quite small (range about 0.5 to 3 hours) and unlikely to be sufficient to result in growth. Further consideration of inclusion of this factor in the model would require evidence from a study evaluating the importance of bacterial growth in bulk milk tankers in the 'between pick up interval'. This assumption is linked to another assumption, that of the milk in the tanker being at a constant temperature despite several intakes from different farm vats and the inevitable variation induced by the performance of refrigeration systems. Milk collected from each farm would realistically be at different temperatures, however, it is assumed that the dilution effect from multiple farm milks entering the tanker evens out the temperature to a constant, thus simplifying the integration of potential growth from multiple temperatures (Ross, 1999).

It is assumed that all hazards present in the farm milk vat are transferred to the milk tanker without loss. That is, there are no residual hazards present in the farm milk vat before the next day (iteration). Milk vats are not cleaned on a daily basis, and the actual mechanisms for hazard transfer between the milk vat and the milk tanker are not properly understood. There is likely to be a residual level of hazard in the farm milk vat after collection, but this residual amount is an unknown value. The assumption that the milk in the farm milk vat is at a constant temperature throughout the entire volume is a simplification of the minor temperature variations between different regions within the milk vat (Alavi et al, 2001). These temperature variations may or may not be significant to the growth of the bacteria present in the vat.

Until the point in the model when the tankers deliver milk to the processing factory and the milk is mixed further, each tanker is considered separately. The importance of this is that it allows us to make predictions about the potential bacteria growth in each tanker. There may be tankers that do not have any pathogens in them and others with large amounts.

Factory Module

The three assumptions used in this module are similar to three of those in the above module, i.e. no time lapse between the first milk delivering milk to the factory and the last, hence precluding the possibility of microbial growth. The average time and temperature between the farm and factory is used to calculate growth potential of microbial hazards that may be present. The hazards present in the raw milk entering the factory silo are distributed evenly throughout the volume of milk in the silo. All hazards are transferred from the milk tanker to the silo without loss; hence there are no hazards present in the tankers between days (iterations).

Pasteurisation Module

It is assumed that vegetative bacterial cells present in the milk as it is pasteurised are inactivated according to log-linear thermal kinetics. This assumption is a simplification of the true thermal inactivation kinetics, and will be discussed more fully later (section 4.3). Chemical hazards are assumed to be unaffected by the time or temperature of pasteurisation, hence, only dilution is considered in the model. At this stage there are no concentration steps considered during processing. Minor fluctuations in the time and temperature of each litre pasteurised are not accounted for in the model. It is simply assumed that for each given pasteuriser the time and temperature is constant for that day (iteration), however, between different pasteurisers and between pasteurisation runs different time/temperature combinations are modelled. There is a lack of published information regarding the thermal inactivation of vegetative cells of *Bacillus cereus*. Hence it is assumed that prior to pasteurisation, the vegetative cells have sporulated and are unlikely to be inactivated by pasteurisation.

4.2 Hazard identification

The ranking of hazards into the 4 groups (see table 1.10) is arbitrary. Those hazards listed are a subset of the potential hazards that may be found in liquid milk (van Gerwen, 2000) including chemical hazards. Some of the hazards (Aflatoxins, *Enterococci* and mycotoxins) that were highlighted for investigation were considered of importance by the dairy industry representatives simply because there is a lack of data concerning them. The nature of the work undertaken did not generate new data about these poorly understood hazards rather it involved a systematic synthesis of the existing published information about the hazards listed, where that information that was available, to produce the risk assessment model. That is not to say that these hazards should be excluded from investigation, but that the published information about these hazards was insufficient to include them into the risk assessment model. Further investigation into the following hazards would be of benefit in determining their food safety risk for the

dairy industry: antibiotic resistant *Enterococci*, aflatoxins, *Cryptosporidium* spp, mycotoxins, *Toxoplasmosis gondii*, *Clostridium* spp, and viral hazards. The required information for these hazards includes the frequency and severity of contamination of milk at the farm level, growth potential, the effect of pasteurisation on these hazards and potential adverse health effects from the ingestion of these hazards through dairy products.

4.3 Thermal inactivation of bacterial pathogens

It is assumed that the thermal inactivation of bacterial pathogens present in raw milk follows log-linear kinetics. For several organisms, e.g. *E. coli* O157:H7, *Yersinia enterocolitica*, and *Salmonella* Enteritidis this has been shown to be invalid in at least some situations (Toora et al, 1992; Humpheson et al, 1997; Juneja et al, 1998; Huang and Juneja, 2001). The conditions used to simulate pasteurisation conditions in the model are a temperature range between 74°C and 78°C for a duration of 15 to 20 seconds. The experimental conditions for which the non-log-linear thermal inactivation kinetics have been reported were 55 to 63°C for 60 to 4500 seconds. Firstly, the temperatures used to demonstrate non-log-linear thermal kinetics are lower than those used in pasteurisation. Secondly, the time of exposure to the elevated temperature is between 3 and 300 times longer than those used in HTST (high temperature short time) pasteurisation. Examination of the experimental data shows that for the initial 20 seconds log-linear inactivation kinetics are displayed, regardless of temperature (Toora et al, 1992; Humpheson et al, 1997). This indicates that for HTST pasteurisation, the assumption of log-linear inactivation kinetics appears to be valid. However, if a lower temperature and longer time were used to pasteurise milk, as with batch pasteurisation, biphasic inactivation (initial rapid reduction in cell numbers followed by a more gradual decrease) might be observed (Toora et al, 1992; Humpheson et al, 1997; Juneja et al, 1998). The model developed in this risk assessment assumes that HTST pasteurisation is used. Milder heat treatments that demonstrate non-log-linear thermal inactivation are unlikely to be used in the processing of raw milk (Geeraerd et al, 2000; Chandler pers comm., 2002).

With the exception of *Bacillus stearothermophilus* and *B. cereus* spores (Fernandez et al, 1999; Leontidis et al, 1999), published reports on thermal inactivation kinetics have dealt with temperatures below 70°C. The model describes pasteurisation temperatures exceeding 70°C, thus it has been assumed that log-linear thermal inactivation kinetics holds up to 78°C. The difference between the experimental temperatures used and those used in the model can be reconciled. At 60°C the D value, in seconds, for *Salmonella* Enteritidis PT4 is 13.2. This is the maximum temperature

within the limits of the data set (Humpheson et al, 1998). From the model the upper confidence interval of the mean estimated concentration of *Salmonella* spp. is 0.156 cells/L (1.56 x 10^{-4} cfu/ml), hence even if pasteurisation were at the lower, 60°C, temperature, survival would be negligible: in the order of 1 cell per 10 000 litres of milk.

The method to estimate the parameters of the log-linear thermal inactivation models used surrogate data in some cases as a source of data for the bacterial pathogen being modelled. In some cases there was no specific data for inactivation in liquid milk. For these organisms the pooled data from thermal inactivation studies were used (section 3.3). Most notable are the variations in thermal tolerance in strains of *Salmonella* spp (Humpheson et al, 1998; Veeramuthu et al, 1998; Smith et al, 2001). There appears to be two different inactivation curves (Fig 3.1.2.4), giving a poor fit to the single log-linear regression line. However, re-examination of the data did not show that the data set was derived from two distinct groups of data and that *S. senftenberg* was not included in the dataset, *S. senftenberg* has a higher thermal tolerance than other Salmonella spp (Murphy et al, 1999). The situation is reversed for *Listeria* spp, with statistically non-significant differences in the thermal inactivation in milk between three species (*L. ivanovii*, *L. seeligeri* and *L. welshimeri*) and three strains of *L. monocytogenes* (Bradshaw et al, 1991). Differences in the thermal kinetics are also evident upon examination of data derived from different food types or laboratory media (Mackey and Bratchell, 1989; Juneja et al, 1997). Estimates using broth systems with a similar pH and water activity to milk provide an adequate means to describe the thermal inactivation kinetics of some bacteria; however, in plant measurements or those with milk as the medium for investigation are by far the best means to estimate the true thermal inactivation kinetics (D'Aoust et al, 1988).

4.4 Consumption patterns

Australians consume between 250 and 500 grams of dairy products daily with the major components being liquid milk, yoghurt and cheese. There is good agreement between the consumption figures for both the Australian Bureau of Statistics (ABS) survey data and the Australian Dairy Corporation (ADC) and Dairy Research and Development Corporation (DRDC) consumption data, however, there are some critical data gaps in the production figures collected from the ADC. The consumption data presented from the ABS survey matches closely the production and consumption figures from the DRDC and ADC for the 1995/96 financial year, however, as the annual raw milk production in Australia has increased from 8206 million litres to 10179 million litres in the past 5 years it is necessary to extrapolate the consumption figures to reflect the change in production volumes. Similarly the Australian population has risen from ~17million to ~19million, with a difference in age structure, i.e. a greater number of

people aged 65 and over. When calculating the exposure to hazard of an individual it is necessary to take the changes in age structure of the population into account. For the majority of dairy products there are more recent production figures, moreover it is possible to reduce the uncertainty of extrapolating from this data through the acquisition of further ABS nutritional survey data and further collection of Australian dairy production statistics.

4.5 Model implementation and estimates

The farm level module is potentially critical in determining the food safety risk associated with dairy production. This is because many different contamination events and types of hazard occur at this module. Hence accurately modelling this aspect of the production process is pivotal in determining the food safety risks associated with dairy products. Some of the estimated input parameter distributions do not accurately reflect the true contamination at the farm level, as can been seen with the modelled and observed contamination of milk by antibiotics (see section 3.8).

The level of contamination with microbiological hazards from individual cows was set as a constant (see section 3.5). It is not know if there is a variable magnitude in contamination or not, however, it seems likely that this is the case. *Listeria monocytogenes* is recognised as a cause of mastitis in cattle (Varnam and Evans, 1991). Sub clinically infected cows are likely to shed this organism into the milk at higher concentrations than those that are not infected, thus an increased load in milk of this organism may be expected from a herd with infected cattle. The USDA/FDA (2001) risk assessment for *Listeria monocytogenes* in ready to eat foods revealed that this organism's presence in pasteurised milk ranked it as the second highest source of exposure. The large volumes of milk consumed in the USA and the relatively low exposure per volume gives a small risk of infection per serving. However, in the event of a pasteurisation failure, the widespread consumption of this product poses a far greater risk of infection and illness from *Listeria monocytogenes*. In Australia, where milk production practices are comparable, the situation is likely to be similar. Therefore it is important to elucidate the magnitude of contamination of raw milk at the farm level with *L. monocytogenes* to determine the risk from this organism through the consumption of dairy products, however, post-pasteurisation contamination is of more concern.

Potentially *Y. enterocolitica* is an organism that may be of concern for the dairy industry. The growth model used for this organism allowed growth at low temperatures. However this is not necessarily an indication of this organism's potential threat to health. There are no dose response models developed for this organism, and its incidence in Australia is less than 8 cases per million people annually, with no reported foodborne infections between 1980 and 1995 (CDN, 2000). It is readily inactivated

through pasteurisation, although it may survive if present in high concentrations (10^8 cfu/ml) before pasteurisation (Toora et al, 1991). There is little emphasis laid upon this organism in Australia's dairy industry, however this is not surprising given its low status as a disease causing organism in this country (CDN, 2000). The model estimates indicate that *Campylobacter* is an organism that has little impact in the dairy environment. It lacks the necessary ability to grow at low temperatures for it to be of major concern, however it is recognised as having significant disease causing potential in other products, such as poultry (Altekruse et al, 1999).

The mean growth rate was used to model potential increases of pathogenic organisms in milk. However, using the upper confidence interval for growth rate estimates did not dramatically increase the likelihood of pathogen surviving pasteurisation (data not shown). Even using an unrealistic increase in growth rate (100times faster) would not impact on the survival of pathogen post-pasteurisation, however, it would be of importance if adherence to regulatory guidelines for pasteurisation conditions were not met. However, this would be the case even with lower than average growth rates, thus pasteurisation is of vital importance for milk prior to consumption .

In terms of trade, antibiotic and pesticide residues are an important issue. The model does not predict any failures to meet Australian regulatory standards for the MRL. However, recent surveys conducted by dairy authorities in Australia (ADASC, 2001; DFSV, 2001) show that there are some antimicrobial residues detected in factory silos (0.04% positive). The model estimate for antibiotic concentration in the factory silo and the percentage of tests positive for the presence of antibiotics found in the survey are not in agreement with these observations. There are a number of possible explanations or causes for this discrepancy: no particular antibiotic is specified in the survey, hence the MRL is also unknown, the concentration of the positive samples from the survey is not specified, in the model the level of contamination arising from each contaminated cow in the farm module is an estimate as the actual contamination level is unknown. There is a lack of information regarding the magnitude of contamination per cow at the farm level for antibiotics and pesticides. This is an important issue and further investigation is warranted. The rationale behind the inclusion of chemical contaminants in the risk assessment was two-fold. Firstly, to complete the assessment as much as possible by including further food safety hazards. Second, to highlight the ability of the modelling approach to accurately model the effects of the addition of these types of hazards in the assessment.

4.6 Further Avenues for Research

Construction of the model revealed several new aspects of the dairy industry that could be further investigated to improve predictions of risk. Each of the required areas is discussed.

Pasteurisation was another important issue in the overall development and implementation of the model. A key aspect of the outputs from the model is the importance of the widespread use of pasteurisation as a means to reduce microbial hazards to low levels. Current regulatory practice in Australia provides a safety margin of greater than 1000 fold; however, it was not possible with the data available to determine the frequency or occurrence of pasteurisation failure. Data concerning this would provide an interesting avenue of research into the importance of pasteurisation. Coupled with the use of an appropriate stochastic model the effects of pasteurisation failure on the risk from microbial pathogens in liquid milk could be determined. Also the level at which microbial pathogens become a concern may also be elucidated, thus giving insight as to the necessity of pasteurisation for these hazards.

The single largest gap in data that prevents the successful completion of the risk assessment model is the effects of post pasteurisation contamination on the hazard concentration in the milk. It is known that pasteurisation is an effective means of reducing microbiological hazards that may be present in milk to undetectable levels (Toora et al, 1991). It is also known, from the NSW survey, that routine tests for microbiological hazards in dairy products at the factory show presence of some of those hazards. This implies that between the time that the milk is pasteurised and the finished product comes off the production line, there has been further contamination of that product. What is required is an evaluation of the frequency of this contamination, the magnitude of that contamination, and which hazards are introduced. It is possible to model this aspect without further data collection in a limited way. From this basis it is possible to determine the frequency of contamination and the magnitude of that contamination from the product microbiological test results. The main obstacle in determining the likely frequency and magnitude of contamination with microbiological hazards, is that few of the potential pathogens are tested for directly and that surrogate organisms are used as presumptive tests for the pathogens of concern (Ingham et al, 2000).

The time temperature conditions to which the finished product is exposed once it leaves the production line is another gap in the information required to assess risks in the dairy products and processes. The conditions of storage, transport, and retail and domestic handling are important in terms of shelf life and microbiological hazard concentration. The range of temperatures that the product is exposed to once it leaves the production factory is not fully known, especially during transport, however there are

some reports available on the temperature distribution for domestic and retail refrigeration (Audits International, 2000; Ross, 2002). To fully characterise the potential impact of these steps in the farm-to-fork continuum further research is needed. Time temperature data loggers provide a means to determine the storage conditions of the finished product once it leaves the factory.

The final step in the formal risk assessment process is to elucidate the risk of contracting illness from the hazards that may be present in the product being consumed. An estimate of the likely concentration of microbiological hazard in the finished product at the point of consumption has not been completed because of a lack of data concerning post-pasteurisation contamination and storage conditions between the factory and the consumer. There are suitable dose response models in the published literature for a study of this kind, together with the consumption pattern estimates by age and state, it is possible to construct a framework for the completion of this stage in the model. There are several considerations for the successful completion of the risk estimate. Both age and health status should be accounted for in determining the likelihood and severity of adverse effects to ingested hazards. Of the dose response models examined (section 1.8) few looked at the difference in the probability of illness as a function of health status. Hence selection or development of appropriate dose response models is of importance.

Some other areas for further investigation and data generation include: the validity and estimation of the inputs to the farm level module; the effects of seasonal variation on the concentration of hazards that may be present in milk; expansion of the model to cover the entire Australian dairy industry, or validation of extrapolation of the current model; the inclusion of non-log-linear thermal inactivation models to predict the effect of pasteurisation on microbiological hazards that may be present in milk, or validation of the models currently used to test their applicability to the Australian dairy industry. Other areas that could be examined include: a detailed examination of the effect of 'between pick up' times and temperatures in the bulk milk tankers on the growth of microorganisms in the milk (see section 4.1); examination of the potential for growth of bacterial hazards in the farm milk vat prior to collection by the tanker. A clearer picture of the presence or absence of antibiotic residues could be gained from further study.

5. Conclusions

The model estimates the concentration of seven hazards that may be present in raw milk arising from contamination of cows at the farm level and estimates the changes in concentration through collection by milk tankers (accounting for dilution and bacterial growth) to delivery at processing factories. The effect of pasteurisation on microbiological hazards that may be present is also estimated and is estimated separately for different production lines and pasteurisation conditions (e.g. liquid milk, cheese). The model can also been used as a scenarios analysis tool. By changing the inputs and/or distribution parameters it is possible to estimate the effect of contamination events at the farm level on the concentration of hazard that may be present in the factory silo. In this way it is also possible to model the efficacy of pasteurisation. With a model of this size and complexity there are problems that could not be tackled effectively in the time given or with the resources available. These have been highlighted in section 4.9. Primarily the areas that need the most attention for the successful completion of the risk assessment model are post-pasteurisation contamination and time-temperature conditions between the end of production (at the factory) and the consumption of dairy products (consumer).

Notes on Modelling

There are several points to consider regarding the attempt to model a complex system such as the production of dairy products in Australia. With a model of this size there comes a point where adding more detail becomes an onerous and difficult task. This extra detail may add to the "apparent reality" of the model, however the outputs become increasingly difficult to interpret.

The size of the model is a stumbling bock for computing power at the present time. Although at the time of writing the computers used to run the model are mid-to-high end consumer level machines, there are constraints, in terms of processing power and memory. That is, the time taken to perform a 'run' of the model increases almost exponentially with the addition of new inputs and outputs. The size of the simulation files produced by @Risk also increases, thus requiring a greater amount of physical memory (RAM) in the computer, this is also related to the complexity and stability of the program used to simulate the model. A further consideration is the ability of the modelling software to cope with the complexity of the system being modelled. The approach used for the dairy model was such that the software was being pushed to its limits.

The model has been designed for flexibility. It is with this in mind that there is a lack of detail in some aspects of the model, among which include: contamination events

at the farm level and post-pasteurisation, growth rate estimates for bacterial pathogens, thermal death equations, seasonal variation. The latter two aspects have been highlighted for the following reasons:

- Thermal death equations – as has been mentioned previously, the thermal death kinetics of bacterial pathogens present in the milk is considered to be log-linear. This has been shown to be a poor approximation of the true kinetics for some organisms (Humpheson et al, 1998). This is a particularly important aspect. Assuming log linear kinetics there is an infinitely small probability, effectively zero, that bacterial pathogens survive pasteurisation, thus all contamination is due to post-pasteurisation contamination. If on the other hand non-log-linear thermal death kinetics were modelled, there may be an increased chance of pathogens surviving pasteurisation. For a simpler overall risk assessment model, log-linear thermal death kinetics was chosen as the most suitable as they hold well over a broad temperature range.
- The DRDC and industry partners in the project had stated from the beginning that they would appreciate the inclusion of seasonal variation within the model. It was considered that this was an additional complication on an already complicated model and was omitted from the initial draft of the model. Subsequently it was realised that it was unnecessary to include this aspect in the model simply because the required estimates from Summer/Spring or Winter/Autumn could be generated simply by altering the appropriate inputs and computing two separate 'runs' of the model. The effect of seasonal variation on the concentration and likely frequency of contamination is unknown and warrants further investigation.

Risk assessment – A modeller's view.

Food safety risk assessment is primarily concerned with quantifying the risk associated with a particular hazard being present in food and or causing illness. There are different ways to assess the risk of a certain event happening. The assessment may be either qualitative or quantitative. Moreover a quantitative assessment may be stochastic or deterministic, that is, the assessment may take into account variability in the system being modelled or it may not.

Variability is an inherent aspect of risk assessment. There is, for example, a varying degree of susceptibility among humans to infection from any particular pathogen, the number of the organism of concern varies; the prevalence of pathogen or toxigenic organism is variable, and cooking procedures vary widely. To estimate the risk of a certain event happening it must fall between two extremes; it will never happen; or it will always happen. Furthermore, the chance that it will always and never happen changes depending on who is observing. This introduces two concepts: uncertainty and

risk perception. Simply by measuring an entity there are problems involved when trying to define exactly that measurement, the instrument may not be calibrated correctly, for example. Two different people looking at the same event may consider its likelihood of occurrence to be different. Physicists call this the Heisenburg uncertainty principle, which applies to measurements of the energy or position of an electron. This situation is analogous to two risk assessors arriving at different interpretations of the results of an assessment. It is not to say that either or both are wrong, but that they have arrived at different conclusions after considering the same event and its associated data. Despite these complicating factors, it is possible to produce an assessment based on the four key aspects of a risk assessment: the hazard - the organism or chemical of concern in the particular food; the exposure - the probability and magnitude of contact with the hazard; the dose-response - how many infectious or toxic particles are required to produce symptoms of disease and to what severity; and risk characterisation - integration of the above to produce a risk statement describing the severity and extent of disease with included uncertainty (Buchanan et al, 1998). These steps should be designed to be as objective and unambiguous as possible.

Furthermore a model's effectiveness is highlighted when it fails to produce predicted values that are similar to known, observed values. This could be due to one of two causes; the inputs for the model are wrong, or the theory behind the model is not a true reflection of reality. An old saying goes: garbage in garbage out, and is especially applicable to modelling. What this means is, if the inputs for a model do not reflect the real or observed range of values, then the model will produce a worthless or meaningless output. For this reason a large part of producing a model is to elucidate the range of possible values for each variable prior to construction of the model itself. That is, modelling is not a substitute for research that involves the collection of data, but should be complementary. A risk assessment is the culmination of a long series of collected data put into a structured form to produce meaningful results and interpolations to correct that data within a conceptual model.

The question arises "Why model?" The short answer, simply, is to predict, but this is not the sole purpose. Baird-Parker and Kilsby (1987) recognised that being able to describe microbial systems in unambiguous equations is a true sign of predictive modelling. With knowledge of a few key parameters it should be possible to predict what will happen to a microbial community over time. With an even greater understanding it is possible for risk assessment as a science to develop into something that is reliable and wholly inclusive; a state, which at the present time, it has not reached. The assessment process is capable of identifying the research needs for the situation being considered and useful for defining the current state of knowledge about that situation.

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Appendices

Computer specifications used for running the model

Primary system:

- Gateway Select 700
- Athlon 700 Mhz
- 15 Gb HD
- 128 Mb RAM

Secondary portable system

- Dell Latitude
- Pentium 4 1.6Ghz
- 18.5 Gb HD
- 512 Mb RAM

Appendix A. NSW Dairy Industry Survey

SafeFood NSW / Dairy Research and Development Corporation

NSW Dairy Industry Risk Assessment

SafeFood NSW is undertaking a risk assessment project covering the entire NSW dairy industry, .In order to better target the risks associated with dairy products produced within the state. This project will ensure efficient risk minimisation strategies can be developed, and is occurring as part of a much larger National Dairy Industry Risk Assessment Project being funded by the Dairy Research and Development Corporation.

Attached is a proforma consisting of 6 sections, which has been sent out to every milk processing and dairy product manufacturing factory within the state. The completion of this form will assist SafeFood NSW in gaining the necessary data to properly conduct the risk assessment. Your cooperation is greatly appreciated with providing this information, which will lead to a much more scientifically robust assessment.

The proforma has been designed so that it is simple to complete and will take up very little of your time. However, if you are able to provide more detailed information, such as individual herd sizes, milk transport logistics, it would enhance the accuracy of the project.

This data provided by industry will be used to form the most comprehensive risk assessment of the Australian Dairy industry to date. The first draft of the NSW project report is due in October, with the final report on the NSW element of the risk assessment due to be completed by the end of the year.

All results will be treated in the strictest confidence.

All returns are to be completed by 30th July and returned in the prepaid envelope to
Attention: David Miles
SafeFood NSW
PO Box A2613
Sydney South 1235

Thank you for your co-operation

Terry Outtrim
Executive Director – Dairy

SafeFood NSW / DRDC Dairy Industry Risk Assessment

(Please complete the sections applicable to your business)

Section 1 MILK AND DAIRY PRODUCTS

What products does your factory produce, and approximately what is the annual production volume?

- ❑ Pasteurised Liquid Milk Products.....volume:.....L
- ❑ Cheese.....volume:.....kg
- ❑ Cheese with moisture >40%, pH>5.0.....volume:.....kg
- ❑ Yoghurt and cultured dairy products.....volume:.....kg
- ❑ Milk powder.....volume:.....tonnes
- ❑ Cream .....volume:.....kg
- ❑ Refrigerated Ice Cream Mixes (eg soft serve) .....volume:.....L
- ❑ Frozen Ice Cream and related products .....volume:.....L
- ❑ Dairy Desserts/ Dips.....volume:.....kg
- ❑ Sweetened Condensed Milk.....volume:.....L
- ❑ Butter.....volume:.....kg
- ❑ Kashta.....volume:.....kg

Other (please specify).....

Section 2 FARM MILK PICKUP

What is the number of farms supplying milk to your factory?

❑ Milk supplied from another factory (go to Section 3)

- ❑ 1-20
- ❑ 20-40
- ❑ 40-60
- ❑ 60-80
- ❑ 80-100
- ❑ >100

What is the average herd size of the farms supplying your factory?

- ❑ 1-40
- ❑ 100-250
- ❑ 500-800
- ❑ 40-100
- ❑ 250-500
- ❑ >800

What is the compliance rate for farm milk temperature? (ie less than 4°C at pickup)

- ❑ 95-100%
- ❑ 80-90%
- ❑ 90-95%
- ❑ less than 80%

What is the maximum temperature that milk is regularly picked up at.....°C

Section 3 MILK INTAKE

What is the annual milk intake for your factory (in litres)?.....L

What is the storage temperature when delivered to the factory?

Minimum.....°C Maximum.....°C Average.....°C

What is the age of the milk when it is pasteurised?

Minimum.....hrs.. Maximum.....hrs. Average.....hrs.

❑ pasteurised milk delivered - Go to Section 5

Section 4 PASTEURISATION

How may pasteurisers do you operate within your factory?

Batch..... HTST.....

For each pasteuriser, please complete the following table. Where a pasteuriser is used for several different products, please list each set of time/temp conditions

Pasteuriser	Normal operating temperature (°C)	Diversion valve set temperature (°C)	Holding time (secs)
1			
2			
3			
4			

Section 5 TRANSFER OF MILK

Do you also send milk / cream / skim / concentrate to other factories?

❑ NO - Go to Section 6 ❑ YES

If Yes, which products and what annual volume?

❑ Raw milk.....L ❑ Pasteurised milk.....L

❑ Raw cream.....L ❑ Pasteurised Cream.....L

❑ Other (eg skim concentrate).....

.....

How many factories do you send product to?.....

Do you send product interstate? Where?.....

Section 6 MICROBIOLOGICAL TESTING

End product testing

What type of end product testing program do you have in place?

.....

.....

.....

.....

List the number of final product failures that have occurred in the last 2 years

Date (month/year)	Product	Reason	Volume involved

Environmental sampling

Do you conduct a regular environmental microbiological sampling plan?

❑ NO ❑ YES

If Yes, how often do you detect high levels of bacteria from environmental swabbing?

.....

.....

.....

.....

From what environment do you most often detect high levels of bacteria?

.....

.....

Appendix B Profile of the Australian population's health

A report submitted to the Dairy Research and Development Corporation as part of contractual obligations for the completion of the project "Food Safety Risk Assessment for the Australian Dairy Industry".

Written by Dr. Tom Ross (2001)

Australian Susceptible Populations

Some food-borne diseases are more likely to affect members of the population with specific medical conditions, or of certain ages. The probability of acquiring infectious disease in particular is affected by immune system function. For example, epidemiological data infers that susceptibility to listeriosis varies enormously, with those with the most compromised immune systems, e.g. AIDS patients, transplants recipients or other on immuno-suppressive therapy, much more likely to become ill. Similarly, very young infants do not have fully developed immune responses, and immune function in human adults decreases with age. Also, the developing foetus is at increased risk from a range of chemical contaminants. In this section is described the age structure and health status of the Australian population to better characterise risks of food-borne disease, in particular the risks to groups of known increased susceptibility.

Age and Gender Structure

The age structure of the Australian population is described by data from the Australian Bureau of Statistics (ABS, 2001) and Australian Institute of Health and Welfare (AIHW, 2001) and is shown in Figure 1 below. Since the turn of the century the population at all ages has grown significantly, but it has also aged as a whole. Australians have been having smaller families, so there has been a fall in the proportion of children. In particular, the proportion of the population aged 65 and over has increased markedly and in 1998 had reached 12%. The very young, at increased risk of a range of infectious diseases, comprise about 5% of the population.

Numerical estimates of the percentage of the population in various age and gender groups.1999 are shown in Table 1.

Table 1. Age/gender structure of the Australian population as at 30 June 1999 (*after* AIHW, 2001).

Range (years)	males % of total population	females % of total population
0–4	3.44	3.27
5–14	7.16	6.81
15–24	7.27	6.94
25–34	7.63	7.61
35–44	7.70	7.73
45–54	6.74	6.62
55–64	4.46	4.38
65–74	3.28	3.56
75–84	1.71	2.43
85+	0.39	0.88

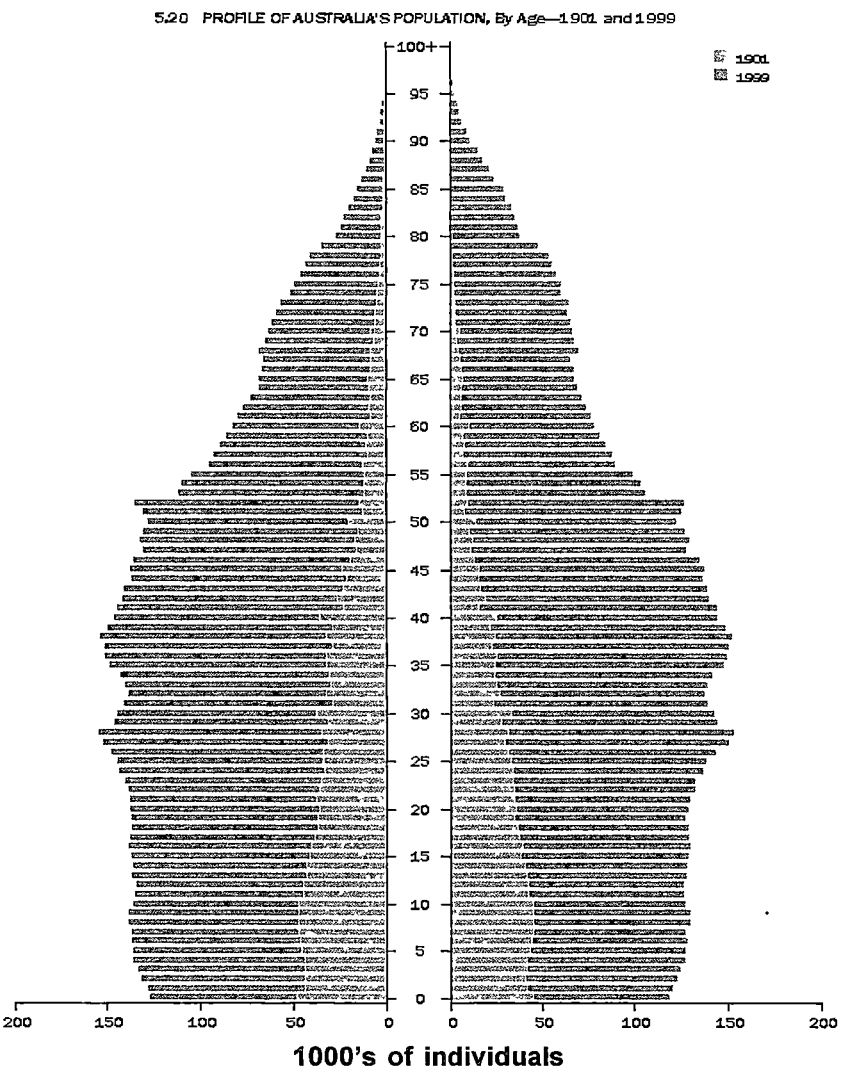

Figure 1. Comparison of then age-gender structure of the Australian population by age and gender in 1901 & 1998 (ABS, 2000).

Health Status

The prevalence among the Australian population of a number of diseases follows the pattern seen in Figure 2. Included are cancer, diabetes, chronic obstructive pulmonary disease, acute respiratory disease and osteoporosis and osteoarthritis. Some of these conditions predispose to other illness. In addition, for some disease there is an age based peak of prevalence among the very young that declines rapidly with the first few years of life. Hence , the very young, and older adults (from about age 55), are recognised as being at increased risk of food-borne infectious disease.

Conditions known to affect immune status include HIV/AIDS, cancers and organ-transplants (due to the use of immunosuppressive drugs and therapies and to immnosuppression caused by the cancerous cells directly), those with liver and kidney disease, alcoholism, diabetes and pregnancy. In addition, some toxins, e.g. methyl mercury, benzimidazole used in antihelminthics, are known to pose a greater hazard to developing foetuses. Some data are available that describe the levels of these diseases and conditions among members of the Australian population.

Organ Transplant Recipients

Functional renal transplant recipients are reported to be 25 per 100,000 Australian population (AIHW, 2000) with the number rising at the rate of an additional 1 person per 100,000 per year. The increase in the number of people with functional transplants is due mainly to marked improvement in the survival of kidney transplants. Of people who had a cadaveric kidney transplant in 1983, 58% had a functioning transplant 5 years later, increasing to 73% of those who had a transplant in 1993 (Disney *et al.,* 1998b, 1999). There are approximately 500 transplants performed per year. Consequently, the rate for functioning kidney transplants has increased, from 9 per 100,000 in 1979 to 25 per 100,000 in 1998. There were 517 kidney transplant operations in 1998. In Australia in 1997/8 in public hospitals there were 139 liver transplants (11% died, 85% went home); 79 lung transplants (11% died, 87% went home); 23 multiple organ transplants (4% died, 91% went home); 73 heart transplants (4% died, 92% went home) (TR: GET REF).. We have not yet found survival data for these other transplants. If we assume the same relationship between annual rates of transplants and survivors in the community, we estimate an additional 2600 organ transplants recipients in Australia.

HIV/AIDS

At the end of 1998, there were around 11,800 people living with HIV. By then, the cumulative number of HIV infections in Australia was estimated to be about 17,600. A total of 2,430 persons were estimated to be living with AIDS in 1998 (NCHECR, 1999). The majority of cases are males aged between 30 and 44 years (AIHW, 2000).

Cancers (excluding non-melanoma)

Cancerous cells may suppress or damage the immune system. Each year, approximately 345,000 new cancer cases are diagnosed in Australia. A large proportion of these, approximately 270,000, are non-melanocytic skin cancers (NMSC) which, if treated early, are far less life-threatening than most other cancers. Discounting these leaves 75,000 new cancer cases per year. Mortality data is also available but prevalence data, required to assess the number of Australians more susceptible to food-borne illnesses, is less readily available, as commented on by SACR (1999).

SACR (1999) surveyed South Australians for the prevalence of different types of cancers, and presented gender and age-separated prevalence data. The probability of diagnosis of cancer increases markedly with age (see Figure 2, below). Crude estimates (i.e. across all cancers and ages) were 1475 and 1369 (age-standardised) cases per 100,000 population for males and females respectively.

The mean prevalence per 100,000 males and females of cancer cases diagnosed within 10 years varied by index day and age, is shown in Table 2, below:

Table 2. Prevalence of Cancer by Age (SACR, 1999)

Age Group	0-9	10-19	20-29	30-39	40-49	50-59	60-69	70-79	80+
Cases/100000	63.2	106.6	262.3	657 1	1494.2	2933.2	5950.3	9565.8	12127.2

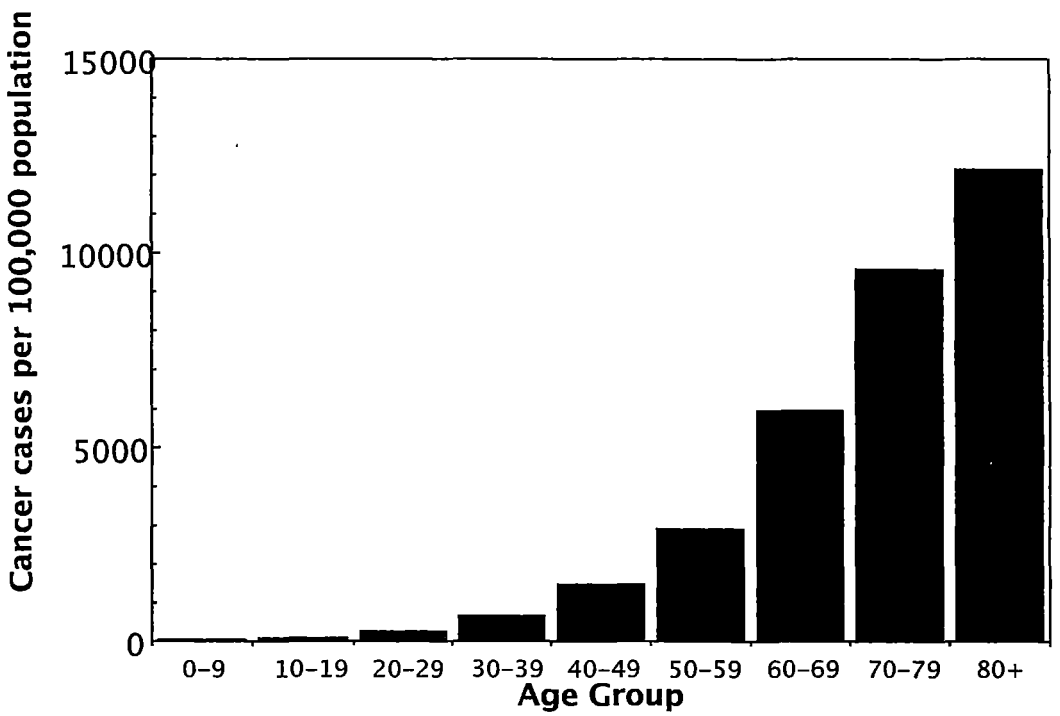

Figure 2. Cases of cancer (non-melanoma) per 100,000 Australians by Age

We have been unable to locate equivalent Australia-wide data, nor the proportion of those cases undergoing active treatment that would reduce immunity.

Kidney Disease, Dialysis and Liver Disease

About 28 per 100,000 Australians require dialysis (AIHW, 2000) with the number rising at the rate of an additional 1 person per 100,000 per year. The increase in the number of people on dialysis is mainly due to older patients being accepted on the program. In 1998, 38% of new patients were aged 65 years and over compared with 7% in 1979 (Disney et al., 1999). Stagnancy in the availability of new donor or cadaver kidneys during the 1990s has also contributed to the increase in dialysis patients (Disney *et al.*, 1999).

The prevalence of cirrhosis and other chronic liver disease was estimated at about 70 per 100,000 males and 50 per 100,000 females (Mathers *et al.*, 1999). Cases are concentrated among those aged 35 years and over.

Diabetes

Diabetes is a long-term (chronic) condition in which blood glucose levels remain high because the body produces little or no insulin or cannot use insulin properly. Diabetes also contributes to many pregnancy-related complications for the mother and the unborn child.

There are no consistent national estimates of the prevalence of diabetes. According to the 1995 National Health Survey (ABS, 1997), over 430,700 Australians (2.4%) reported that they had been diagnosed with diabetes at some point in their lives. Of those, 82% reported that they currently have diabetes (ABS 1997). The true prevalence of diabetes is considered to be higher than the figures given above suggest because a large proportion of diabetes, especially Type 2 diabetes, remains undiagnosed in the community. It has been estimated that for every person in the population diagnosed with diabetes, there is one undiagnosed person (DHAC, 1999). It is therefore estimated that there were about 700,000 people with diabetes in Australia in 1995 (Amos *et al.*, 1997).

The prevalence of diabetes increases with age, from 0.1% among people aged less than 15 years to 8.9% among those aged 75 years and over (ABS, 1997).

Alcohol Dependency

There are no data available that directly indicate the incidence of alcohol-related physical health debilitation in the Australian community (Grant and Petrie, 2001). Nonetheless, some data are available which enable crude estimates to be made. "Hospital separations" data describe the conclusion of a stay in hospital by a single patient[1]. and can be used to gauge the level of morbidity due to a particular condition in the community (AIHW, 2000). Hospital stays where alcohol dependence was the primary reason were approximately 9900 for men and 4700 for women in 1997-98 in Australia. Of those hospital stays, there was a strong age-dependence with prevalence

peaking in people of age 45 –54. Similarly, a single day survey of clients at alcohol and drug dependency treatment services (which achieved 92% coverage across Australia) reported that 2570 Australians were treated. In the National Drug Strategy Household Survey 1% of (~5,000) males reported attending an alcohol treatment program, though whether this was for physical health reasons is not disclosed. Based on these data we estimate the level of Australians to be severely debilitated through alcohol dependency to be of the order of 0.1%.

Pregnancy

ABS (2001) reports 249300 births in Australia in 1998, in a population then of 18871800[2]. In 2001, the population is expected to be closer to 19300000. Accordingly, but ignoring the slowly declining birth rate, 257600 births would be expected. Further, ignoring multiple births, and because each pregnancy only lasts 9 months, the number of Australian women pregnant at any one time is expected to be ~ 193,200 (or 0.99% of the total population) in 2001.

Thus, the proportion of Australian *women* that are pregnant at any given time is ~ 2%. This is consistent with the figure of 1.7% for USA presented in CAST (1994).

Conclusions

From the data presented in above it is evident that the likelihood of an individual being in many of the susceptibility classes increases with age. As noted by Hitchins (1996) it is highly likely that the inclusion of both age persons and those with cancer or diabetes would lead to 'double-counting' of the prevalence of susceptible populations within the Australian community. Conversely, even without underlying disease such as cancer or diabetes, elderly Australian are still more susceptible to infectious disease because their immune system 'weakens' with age.

Table 3 below summarises the data for the percentage of the population in various categories of increased susceptibility to food-borne illness.

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[1] If the same patient re-enters the hospital that is considered a separate case. It is possible, thus, that some separations involve the same patient many times.

[2] We note that from Figure 1 can be inferred that there are ~245,000 births per annum.

Table 3. Estimate of the proportion of the Australian population at increased risk of food-borne illness.

Predisposing Condition	Percentage of Australian Population Affected
Age > 65 years	10.16
Age > 60 years	13.70
Age < 30 days	0.25
Organ Transplant Recipients	
Kidney	0.03
Other	0.01
HIV	0.10
AIDS	0.01
Cancers (non-melanoma)	1.42
(Leukaemia ~ 3% of all cases)	
Pregnancy	0.99
Kidney Disease, Dialysis	0.03
Cirrhosis, Chronic Liver Disease	0.12
Diabetes	1.97
Alcohol Dependency	0.10
TOTAL (including age >60 years)	18.7
TOTAL (including age >65 years)	15.2

The data shown in Table 3 are generally consistent with estimates made for other nations, e.g. G. Paoli (*pers. comm.*, 1999) estimated the susceptible population to be 17% using North American data. Lindqvist and Westoo (2001) derived an estimate of 20.1% for Sweden (including the population > 65 years old) while Buchanan *et al.* (1997) and CAST (1994) estimated the affected USA population at 20%. Hitchins (1996) estimated ..... (TR to complete)

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Appendix C Complete data set for bacterial thermal inactivation

Bacterium	Strain(s)	Medium	Initial Cell Count	Temp	Time (s)	Survivors	D value (s)	Z-value	Reference
E. coli	10	raw milk	1.00E+05	>64.5	16.2	0			D'aoust et al, 1988
			1.97E+05	60	16.2	1.68E+04	15.15		
	5 from ground beef	ground beef		54.4			7434.00		Clavero et al, 1998
				58.9			312.60		
		grwoth medium		58.9			388.20		
		MSMA or		62.8			34.20		
		MEMB		62.8			37.20		
				65.6			10.80		
				65.6			12.00		
	5 from faeces	ground beef		54.4			1565.40		
				62.8			31.80		
				62.8			39.60		
				65.6			10.80		
				65.6			11.40		
	P204	ground turkey		55			4772.40		Veeramuthu et al, 1998
		Petrifilm coliform		60			328.20		
				65			101.40		
		Phenol red sorbitol		55			7131.00		
				60			598.20		
				65			123.60		
	E30138	TSB		62.5			62		Blackburn et al, 1997
	E30228	3.5% NaCl		62.5			112		
	E30480	pH5.1		62.5			80		
	E32511			62.5			59		
		pH6.8		64.5			3.5		
		pH7.0		59.5			42		
		pH6.8		59.5			60		
	ATCC 43894	beef		53			2766	5.59	Orta-Ramirez et al, 1997

		58	386		
		63	26		
		68	7		
ATCC 43894	ground beef	63	10	3.79	Smith et al, 2001
		61	19		
		58	73		
		55	1204.80		
	beef gravy	60	114.00		Juneja et al, 1998
	ground turkey	52	3066.00	4.47	Kotrola et al, 1997
	3% fat	55	462.00		
		57	204.00		
		60	42.00		
	turkey meat				Kotrola and Conner, 1997
		52	2538.00		
	3% fat	55	750.00		
		57	168.00		
		60	54.00		
4 strains	ground beef	55	1278.00		Juneja et al, 1997
		57.5	297.00		
		60	190.20		
		62.5	55.80		
		65	23.40		
	ground chicken	55	709.80		
		57.5	227.40		
		60	97.80		
		62.5	49.20		
		65	21.60		
4 strains	ground turkey				Juneja and Marmer, 1999
		55	690.60		
		57.5	215.40		
		60	113.40		
		62.5	48.60		
		65	17.40		
	ground lamb	55	714.60		
		57.5	220.20		

				60	115.80		
				62.5	51.00		
				65	22.80		
			ground pork	55	688.80		
				57.5	204.00		
				60	120.60		
				62.5	43.20		
				65	18.00		
	4 strains	BHI broth		55	1071.60		Huang and Juneja, 2001
				55	1108.80		
				57.5	372.60		
				57.5	372.60		
				60	131.40		
				60	232.20		
				62.5	91.20		
				62.5	114.00		
				65	49.20		
				65	47.40		
Salmonella	5	raw liquid egg yolk		60	16.8	4.33	Schuman and Sheldon, 1997
		ph6.3		61.1	9.6		
				62.2	5.22		
		liquid egg white		55.1	479.4	3.54	
		pH8.2		56.7	177.6		
				58.3	60		
	PT4	Nutrient Broth	varies	60	13.2	3.32	Humpheson et al, 1998
				59	22.8		
				58	46.2		
				57	88.2		
				56	217.2		
				55	376.8		
	phage type 4 (P167807)	TSB	pH7.3	62.5	8.4		Blackburn et al, 1997
			pH6.9	62.5	20		
			pH6.8	59.5	160		

	6 species	ground chiken		67.5	17.16	Murphey et al, 1999
				70	10.56	
		peptone-agar		67.5	15.66	
				70	5.1	
	S.typhimurium DT104-10127	ground beef low fat		64	9	5.07 Smith et al, 2001
				61	34.2	
				58	135.6	
				55	543	
	DT104-10601			64	4.2	4.13
				61	24.6	
				58	129	
				55	633	
	DT104-01071			64	8.4	4.77
				61	25.8	
				58	123.6	
				55	616.2	
	S.typhimurium DT104 8 strains	chicken broth		58	117	Juneja and Eblen, 2000
				58	130.2	
				58	129.6	
				58	141	
				58	87	
				58	116.4	
				58	137.4	
				58	106.8	
Listeria monocytogenes		milk		60	110	7.3 Mackey and Bratchell, 1989
		slug flow heat exchanger		63	43	
				65	23	
				70	4.9	
				72	2.7	
				75	1	
	BS-9	raw milk	1.00E+05	57.8	435.6	5.8 Bradshaw et al, 1991
			1.00E+05	63.3	38.7	
			1.00E+05	68.9	3.3	
			1.00E+05	71.7	2.2	

Scott A		1.00E+05	57.8	330	6.2	
		1.00E+05	63.3	31		
		1.00E+05	68.9	4		
		1.00E+05	71.7	2		
SE-31		1.00E+05	57.8	528.6	5.3	
		1.00E+05	63.3	46.1		
		1.00E+05	68.9	2.8		
		1.00E+05	71.7	1.5		
BS-9	Sterile Milk	1.00E+05	52.2	2848.3	6.7	
		1.00E+05	57.8	409		
		1.00E+05	63.3	68		
		1.00E+05	68.9	9.1		
Scott A		1.00E+05	52.2	1704.8	7	
		1.00E+05	57.8	290.2		
		1.00E+05	63.3	50.6		
		1.00E+05	68.9	7.3		
SE-31		1.00E+05	57.8	440.5	6.8	
		1.00E+05	63.3	49.6		
		1.00E+05	68.9	6.2		
		1.00E+05	71.7	4.4		
F5069	Sterile Milk	3.63E+06	57.8	331	7	Bunning et al, 1988
		6.77E+07	62.8	38.3		
		1.95E+06	66.1	16.9		
		1.90E+06	68.9	8.6	7.3	
		1.97E+06	71.7	3.1		
		2.63E+06	74.4	1.1		
3 serotypes	vegetables		56	48	6.7	Mazzotta, 2001
	onions		60	13.8		
			62	6		
	broccoli		56	138	7.8	
			60	37.2		
			62	23.4		
	peppers		56	234	5.5	
			60	55.2		

			62			18.6		
	mushrooms		56			300	4.9	
			60			41.4		
			62			18		
	peas		56			312	5.5	
			60			62.4		
			62			24.6		
4 strains	whole milk							Donnelly and Briggs, 1986
F5207			62.7			24		
19111			62.7			21		
F5069			62.7			39		
			55			1440	4.3	
			62.7			60		
			65			6		
serotype 4b (NCTC 11994)	minced beef		50			1962	4.2	Bolton et al, 2000
			50			2166		
			55			204		
			55			192		
			60			18.6		
			60			9		
serotype 4b	different media used	pH7.2	55			176.4		McMahon, 1999
		pH5.7	55			235.8		
L. innocua M1	ground chicken		67.5			23.64		Murphey et al, 1999
			70			7.98		
	peptone-agar		67.5			10.8		
			70			6.78		
Y. enterocolitica 5 human isolates	Skim milk/ whole milk	1.00E+09	71.8	18s	0			Toora et al, 1991
2 culture collection		1.47E+09	62.8	death curve		10.53		
						10.35		
15	raw milk	1.00E+05	>63	16.2	0			D'aoust et al, 1988
		3.33E+05	60	16.2	9.00E+00	3.55		
3	phys. saline	6.2	58	420		84	4.0-4.52	Sorqvist, 1989
		6.1	60	270		30.6		
		6.1	62	90		11.4		
		6	58	420		108		

			6.1	60	270		24		
			6.2	62	90		10.8		
			6.3	58	420		90		
			6.2	60	270		26.4		
			6.2	62	90		9		
	serotype 0:3	minced beef		50			1044		Bolton et al, 2000
				50			1272		
				55			117.6		
				55			63.6		
				60			58.2		
				60			33		
	GER serotype 0:3	various media		55			120		McMahon, 1999
				55			127.8		
C. jejuni	15	raw milk	1.00E+05	>63	16.2	0			D'aoust et al, 1988
			2.00E+05	60	16.2	1.97E+01	4.04		
		skim milk		55			0.74-1	5.71-8.02	Doyle and Roman, 1981
		skim milk		55		0.00E+00		-	Christopher et al, 1982
		1% peptone solution		55			38.40	4.62	Blakenship and Craven, 1982
				55			65.40	5.30	
		milk		55			66.00	5.30	Waterman, 1982
	1	phys. saline	5.01E+05	58	150		46.8	4.94	Sorqvist, 1989
			1.26E+06	60	60		14.4		
			7.94E+05	62	45		7.2		
C. coli	2	phys. saline	1.58E+06	58	240		25.2	5.07-5.6	
			1.00E+06	60	150		7.8		
			3.98E+06	62	60		4.2		
			2.00E+06	58	240		42.6		
			2.00E+06	60	150		16.8		
			2.00E+06	62	60		8.4		
B. cereus									
B. stearothermophil	spores	DDS water		116			1138.2	7.9	Leontidis et al, 1999

us

117	842.4
118	629.4
119	470.4
120	351.6
121	262.8
122	196.2
123	147
124	109.8
125	82.2
126	61.2
127	45.6

Appendix D NSW Survey Results (raw data)

	Section 1 Milk and Dairy Products											
Factory	Pasteurised liquid milk (L)	Cheese (kg)	Cheese with Moisture >40%, pH >5.0 (kg)	Yoghurt and cultured dairy products (kg)	Milk powder (tonnes)	Cream (kg)	Refrigerated Ice cream mixes (eg. Soft serve) (L)	Frozen ice cream and related products (L)	Dairy desserts/dips (kg)	Sweetened condensed milk (L)	butter (kg)	Other
A1		732,000	200,000									
A2				1,500,000								
B1	66,000,000					2,000,000				8,000,000		10,000,000
B2												
B3												76,000,000
B4	40,500,000	2,300,000			850	3,000,000		1,700,000		1,000,000		
B5	200,000,000											
B6								17,800,000				
B7				47,500					4,800			17,800
C			1,200,000									
D		13,000,000	5,000		6,200						1,000,000	
E												Flavourings
F												Fat
G	200,000											
H												2,880,000,000,000
I					NB -->>							
J			200	25,000								
L		180,000										
M								+				
N			12,500									
O		100,000			105,000							NB-->>
P								+				
Q1	170,000,000					4,900,000						

Q2										
R										8,000
S1								28,000,000		
S2	33,800,000					320,000				
T		6,300								
U		840,000								
V	300,000	115,700	510,000	450,000						
W							15,000			
X							300,000			
Y			24,000							
Z							6,400			10,000
AA										233,862
AB										25,000
AC	2,000	10,000	4,500					26,000		
AD									70,000	
AE					25					35
AF	+		+	+		+				
AG								50,000		
AH								20,000		

	Section 2 Farm MilK Pickup																
Factory	Number of Supplying farms	Exact number	Herd size of farms												Compliance farm milk temperature (<4°C)		Max Milk temp
			1 to 20	21-50	51-80	81-100	101-150	151-200	201-250	251-300	301-350	351-400	401-500	500+	Summer/ Spring	Winter/ Autumn	
A1																	
A2																	
B1	>100														95 - 100	95 - 100	15
B2	20 - 40	30		4	4	7	6	4	3			2			90 - 95	95 - 100	38
B3	60 - 80	65			5		30		20		10				95 - 100	95 - 100	10
B4	>100																20
B5	>100	300		6	30	30	40	30	20	10	5	5	3	3	80 - 90	90 - 95	8
B6	20 - 40	23															15
B7		0															
C	-																
D	>100	127			3	0	56	46	39	20	2	2	5	1	90 - 95	95 - 100	10
E																	
F																	
G	1 to 20	1						1							95 - 100	95 - 100	4
H	>100	273															
I																	
J	-																
K																	
L																	
M																	
N																	
O																	
P																	

Q1	20 - 40	30											95-100	95-100	15
Q2	80-100	86		6	40	10	20	3	6			1	95-100	95-100	6
R															
S1															
S2	60-80	68											95-100	95-100	4
T															
U	1 to 20	3											95-100	95-100	4
V															
W															
X															
Y															
Z															
AA	1 to 20	1											95-100	95-100	4
AB															
AC	1 to 20	1				1							95-100	95-100	4
AD															
AE															
AF	1 to 20	18			6		9		3				95-100	95-100	4
AG															
AH															

	Milk Intake Section 3								
Factor y	Total intake (12 months)	milk temperature at intake						age of milk at pasteurisation		
		0-2	2 to 4	4 to 6	6 to 8	8 to 10	> 10	Min	Max	Average
A1										
A2	1,350,000	15	80	5						
B1	105,000,000		98	2				24	60	30
B2	20,916,354	1	93	5			1	41	66	60
B3	76,000,000		95	4		1				
B4	200,000,000		99	1				28	72	
B5	200,000,000		80	20				8	72	48
B6	2,300,000		98	2				40	64	52
B7	60,000,000		97	3				42	72	60
C	13,000,000		100					46	96	72
D	183,000,000		5	90	5			1	48	24
E										
F										
G	200,000		100					1	48	24
H								40	64	48
I										
J	96,000	80		90						
K	144,000			90	10					
L										
M										
N	10,000									
O										
P										
Q1	185,000,000		100					24	72	55
Q2	52,000,000		98	2						
R										
S1										
S2	33,078,190		85	15				45	70	60
T										
U	5,200,000			0					72	
V	6,200,000	100						24	72	48
W	1,600	All mix received solid frozen - All units sold solid frozen				Min temp -20C				
X										
Y	2,000,000				95	5		2	4	3
Z	23,000		90	10						
AA	240,727	10	90					28	78	39
AB										
AC	40,000	50	50					2	48	12
AD	17,000	70	25	5						
	39,000									
AE										
AF			50	50				20	72	
AG	40,000									
AH	150,000									

	Section 4 Pasteurisation				
Factory	Number of Pasteurisers				
	Batch	HTST	Operating Temp	Diversion Valve temp	Holding time (s)
A1					
A2	1		90	84	360
B1		2	78	75	15
			78	75	15
B2		1	77	74	18
B3					
B4		5	74	73	15
			74	73	15
			80	78	25
			78	76	0.1
			78	76	15
B5	0	5	75 - 79	74	15
			75 - 78	74	15
			75 - 78	74	15
			74 - 78	74	15
			78 - 80	78	25
B6	0	1	84	78	20
B7			92	90	900
			92 / 82	90 / 80	900
			143	134	4
C	1		75	72	23
D		1	74	72.5	16
E					
F					
G	1		72	-	900
		1	73 - 77	72.5	20
H		1	75	72.6	17.5
I					
J					
K					
L					
M	1				
N					
O					
P	2	1	80	-	600
Q1		3	76	74	28
			76	74	26
			80	76	27
Q2					
R					
S1		1	85	79.5	26
S2		2	75-76	72.5	33
			75-78	72.5	29
T					
U		1	75	72.5	17
V	1		85		1800
		1	74	72.6	40
W					
X	2		4C - 72C		30
Y		1	78	72.5	15

Z					
AA	2		140	138	16
			140	138	16
AB					
AC	4		65		1800
			90		
			80		15
			72		15
AD					
AE					
AF		1	77-79	74	35
AG					
AH	2		85		900
			90		900

Factory	Section 5 Transfer of Milk					
	Transfer of products to other factories					Number of Factories sent to
	Raw Milk (L)	Raw Cream (L)	Past. Milk (L)	Past. Cream (L)	Other (L)	
A1		107,000				2
A2						
B1	10,000,000				5,000,000	4 to 7
B2	14,125,093		6,791,261			4
B3	76,000,000					8
B4	39,000,000	1,800,000	20,000,000	3,000,000	16,000,000	4
B5				2,000,000		2
B6	1,800,000					4
B7						
C						
D	51,000,000					8
E						
F						
G						
H	+	+			skim milk	up to 8
I						
J						
K						
L						
M						
N						
O						
P						
Q1				3,200,000	1,250,000	8
Q2	52,000,000					1
R						
S1						
S2						
T						
U						
V			300,000			2
W						
X						
Y						
Z						
AA						
AB						
AC						
AD						
AE						
AF	3,000,000				3,000,000	2
AG						
AH						

Section 6 of the data from the questionnaire has not been included as the information contained within s considered of a sensitive nature.