MEAT FOOD SAFETY SCHEME

PERIODIC REVIEW OF THE RISK ASSESSMENT

NSW GOVERNMENT Food Authority

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Contents

List of tables

Glossary

ABARES	Australian Bureau of Agricultural and Resource Economics and Sciences
ABS	Australian Bureau of Statistics
ACMF	Australian Chicken Meat Federation Inc.
AMR	antimicrobial resistance
ANU	Australian National University
APVMA	Australian Pesticides and Veterinary Medicines Authority
ASTAG	Australian Strategic and Technical Advisory Group on AMR
ATDS	Australian Total Diet Study
cw	carcase weight
DAWE	Department of Agriculture, Water and the Environment (Australia)
DEDJTR	Department of Economic Development, Jobs, Transport and Resources (Victoria, Australia)
DoH	Department of Health (Australia)
EFSA	European Food Safety Authority
EHEC	Enterohemorrhagic *Escherichia coli*
ESAM	*Escherichia coli* and *Salmonella* Monitoring Program
EU	European Union
EEA	European Economic Area
FAO	Food and Agriculture Organization
FRSC	Food Regulation Standing Committee (Australia)
FSA	Food Standards Agency (U.K)
FSANZ	Food Standards Australia New Zealand
FSIS	Food Safety and Inspection Service (U.S.A)
FQ	forequarter
HEV	hepatitis E
HQ	hindquarter
IFIS	Imported Food Inspection Scheme (Australia)
JEMRA	Joint FAO/WHO Meetings on Microbiological Risk Assessment
LOD	limit of detection
MDR	multidrug-resistant
MDU PHL	Microbiological Diagnostic Unit Public Health Laboratory (Victoria, Australia)
MIC	minimum inhibitory concentration
MLA	Meat and Livestock Australia

MLVA	multiple locus variable number tandem repeat analysis
MRSA	Methicillin-resistant *Staphylococcus aureus*
NATA	National Association of Testing Authorities (Australia)
NCMMP	National Carcase Microbiological Monitoring program
NRS	National Residue Survey
NSW	New South Wales
NZ	New Zealand
PCR	polymerase chain reaction
PFGE	pulsed-field gel electrophoresis
PPP	primary production and processing
pSTEC	pathogenic Shiga toxin-producing *Escherichia coli*
QLD	Queensland
QMRA	quantitative microbial risk assessment
qRT-PCR	quantitative real-time polymerase chain reaction
RNA	ribonucleic acid
RT	ribotype
RTE	ready-to-eat
SARDI	South Australian Research and Development Institute
SNV	single-nucleotide variant
SO2	sulphur dioxide
SA	South Australia
SPC	standard plate count
spp.	multiple species
ST	sequence type
STEC	Shiga toxin-producing *Escherichia coli*
TAS	Tasmania
TVC	total viable count
UCFM	uncooked comminuted fermented meat
U.K	United Kingdom
UN	United Nations
U.S.A	United States of America
USDA	United States Department of Agriculture
VIC	Victoria

WA	Western Australia
WGS	whole genome sequencing
WHO	World Health Organization

Units of measurement

°C	degrees Celsius
cfu	colony-forming unit
cm	centimetre
g	gram
kg	kilogram
mg	milligram
MPN	most probable number
ng	nanogram

Executive summary

The previous risk assessment of the meat food safety scheme was published in 2014 (NSW Food Authority, 2014). The 2014 risk assessment was part of a comprehensive review of food safety schemes undertaken during the 2015 revision of the NSW Food Regulation, which is required to be revised at five-year intervals. Each five-year review is conducted on an alternate basis, as either a full risk assessment or an update.

A full risk assessment is reported here containing new or updated information identified in an environmental scan for issues related to meat and meat products that have impacted food safety since 2014. Information sources included;

- foodborne illness reports and recall data in Australia attributed to meat and meat products
- international issues arising from human illness or perceived hazards linked with meat and meat products
- border detections for meat and meat products
- risk assessments of meat and meat products
- emerging issues in the farm to consumer continuum for meat and meat products relevant to health risk
- research findings related to hazards in meat and meat product production and processing
- baseline surveys of microbiological and chemical hazards in meat and meat products
- other relevant sources if identified during the above activities

The hazard identification and main findings of the 2014 risk assessment remain essentially the same, in relation to the main, minor and wild game meat species. However, additional hazards have been identified due to the popularity of 'rare' or undercooked meat products (i.e. 'rare' steaks, pâté). In addition, as wild game meat species are not subject to any form of animal husbandry and may host a number of zoonotic parasites capable of causing foodborne disease, raw wild game meat products (i.e. uncooked comminuted fermented meat products) present a particular cause for concern due to the absence of a terminal cook step.

Data supporting the exposure assessment has been updated with the addition of a summary of the consumption data reported in the 25th Australian Total Diet Study (ATDS) (FSANZ, 2019a) of meat and poultry food groups by Australian consumers. Comparison of consumption data reported here and in the previous 2014 meat risk assessment (data taken from Australian Health Survey 2011–2012, ABS, 2014) is hampered by differences in the categorization of food groups and what has been reported. Data reported by the Australian Bureau of Agricultural and Resource Economics and Sciences (ABARES) has also been included, which shows the apparent annual consumption of the main meat species per person in Australia from 2014 - 2015 to 2017 – 2018 (ABARES, 2020). Poultry meat consumption was significantly higher than the consumption of the other main species across all years (ABARES, 2020). Consumption of poultry meat increased from 2014 - 2015 to 2017 - 2018, while consumption of beef and veal, lamb and mutton and pig meat either decreased slightly or remained unchanged (ABARES, 2020).

The following overview summarises the update of the hazard characterisation, in relation to foodborne illness in NSW from 2013 to 2018 due to meat and meat products (Communicable Diseases Branch, 2014a, 2015, 2016, 2017, 2018):

- Meat; alone or in a complex food(s), was identified as the suspected or responsible vehicle in a total of 9 outbreaks in NSW from 2013 to 2018. In 2018, no outbreaks were linked to meat or meat-related dishes. From 2013-2017, meat or meat-related dishes were identified as the suspected or responsible vehicle in 1-3 outbreaks annually. Liver dishes of chicken (*n* = 4), lamb (*n* = 1), pork (*n* = 1) and duck (*n* = 1) were the food vehicle responsible for the majority (7/9; 78%) of meat related outbreaks. The remaining two outbreaks were attributed to ham and roast beef.

- Undercooking was identified as a contributing factor in all seven outbreaks involving liver dishes and temperature abuse was considered a likely contributing factor in the outbreak involving roast beef. Undercooking and temperature abuse after cooking therefore accounted for the majority (8/9, 89%) of all meat related outbreaks in NSW from 2013 to 2018.
- *Campylobacter* was the causative agent for the majority (56%; 5/9) of outbreaks. The other four outbreaks across this time period were linked to *L. monocytogenes*, *S.* Typhimurium, hepatitis E (HEV) and an unknown agent. Of note, this was the first local hepatitis E outbreak recorded in Australia, which was linked to the consumption of pork liver pâté.
- Restaurants were the most common outbreak setting and were implicated in 67% (6/9) of all meat-related outbreaks. The other three outbreaks occurred in an aged care facility, a bakery and a community setting.

The following provides a brief summary of the update of the hazard characterisation, in relation to various recent domestic reports of the prevalence and level of microbiological contamination of livestock at the farm (faecal samples), in slaughter and processing establishments (carcase, lymph node and various tissue samples) and at retail (meat and offal samples):

- Meat and Livestock Australia (MLA) (2017a) commissioned a survey of beef and veal carcases from Australian export meat processing establishments, which demonstrated a low prevalence of *Salmonella*.
- Mellor et al. (2016) undertook a national survey of pathogenic (possess *stx* and *eae*) Shiga toxin-producing *E. coli* (STEC) serotypes in Australian beef cattle faeces and reported that of the samples surveyed 6.7% (100/1,500) contained pathogenic STEC O157, 1% (15/1,500) contained pathogenic STEC O26 and 0.3% (4/1,500) contained pathogenic STEC O111. Pathogenic STEC of serotypes O45, O103, O121, and O145 were not isolated from any sample.
- Bailey et al. (2017) conducted a survey of the microbiological status of lymph nodes from Australian cattle at the time of slaughter and reported an overall prevalence of *Salmonella* of 0.48%, indicating that lymph nodes are unlikely to add significantly to the *Salmonella* burden of ground beef produced from Australian manufactured beef.
- MLA (2019) funded a national survey of sheep faeces at slaughter, which indicated that Australian sheep are a potential reservoir for STEC serotypes O157 and O26. STEC serotypes O157 and O26 were present in 3.4% and 0.3% of samples, respectively.
- Dawson et al. (2020) undertook a survey of *T. gondii* contamination in 79 lamb mincemeat parcels and the probability of *T. gondii* contamination of the meat product was conservatively estimated at 43%. This study did not include an assessment of viability.
- Weaver et al. (2017) reported persistent, high levels of *Salmonella* Typhimurium 1,4,[5],12:i:- PT193 shedding in five independent pig herd production systems. Monophasic variants of *S.* Typhimurium with the serotype 1,4,[5],12:i:- have risen to international prominence due to their increasing implication in human disease and the high rate of antimicrobial resistance associated with this serovar.
- Hodgson et al. (2017) undertook a study in which the prevalence of *T. gondii* in sow hearts was estimated to be 8.3%. The study did not include an assessment of viability.
- Al-Habsi, Jordan, et al. (2018) reported a high faecal carriage rate for *Salmonella* of 26.5% amongst Australian rangeland goats at slaughter, which aligns with previous comparable studies.
- Al-Habsi, Yang, et al. (2018) reported a faecal carriage rate of 8% for *Campylobacter* spp. amongst rangeland goats at slaughter.

- Data collected over the last four years in the NSW Food Authority poultry verification surveys has revealed a reduction in the prevalence of *Salmonella* at both processing plants and retail, while the prevalence of *Campylobacter* remains high for samples collected from both processing plants and retail. The concentration of *Salmonella* and *Campylobacter* in retail portions (for positive samples) remained low but at levels higher than found in the baseline studies conducted prior to the introduction of Standard 4.2.2: Primary production and processing standard for poultry meat. However, the proportion of portions samples with concentrations of *Salmonella* and *Campylobacter* above the limit of detection was low. This may indicate that the overall concentration of *Campylobacter* on poultry meat is decreasing.
- Abraham et al. (2019) reported that *Salmonella* spp. was recovered from 26.5% of pooled caecal samples from surveyed poultry abattoir plants. Twelve serotypes were isolated, the most frequent serovar was Sofia (34.0%), followed by Abortusovis (15.1%), Adelaide (15.1%) and Typhimurium (7.6%).
- Walker et al. (2019) reported that *Campylobacter* were detected in 90% of chicken meat and 73% of chicken offal products (giblet and liver). The level of contamination was generally low, with 98% of chicken meat samples reported to have on average <10,000 cfu *Campylobacter* per carcase.
- The NSW Food Authority (NSW Food Authority, 2018) conducted a survey of poultry livers from supermarkets and butchers. A total of 96% of the individual livers tested positive for *Campylobacter* (*Campylobacter* was detected both externally and internally in 88% of samples). *Campylobacter* was detected at the level of greater than 10^3 cfu/ml in 12.3% of the surface of chicken livers tested and in 1.6% of the inside chicken livers tested.

National recalls and failures of imported food at border control:

- From January 2014 to August 2020, eleven imported meat products failed inspection and testing requirements (DAWE, 2020a). The majority of failures (7/11, 64%) were due to *L. monocytogenes* contamination of ham originating from Spain (*n* = 6) or Italy (*n* = 1), followed by *L. monocytogenes* contamination of prosciutto (2/11, 18%) originating from Italy.
- Between the 17/10/2015 and 15/10/2020, fourteen recalls were due to microbial contamination and six recalls were due to the presence of foreign material, such as plastic (*n* = 2), metal (*n* = 2), rubber (*n* = 1) and bone fragments (*n* = 1). Recalls involving microbial contamination of meat were mainly due to *L. monocytogenes* (*n* = 9), with contamination occurring in German sausages (*n* = 3), ham (*n* = 2), frozen meals (*n* = 2), silverside (*n* = 1) and chicken liver pâté (*n* = 1).

The risk characterisation largely aligns with the previous risk assessment (NSW Food Authority, 2014) and regulations are still applicable to manage risk. Within the poultry industry, further improvements may be driven by the future adoption of poultry process hygiene criteria and national performance reporting. While the continuing trend of outbreaks linked to undercooked animal liver dishes, warrants further promotion of guidance material already prepared by the NSW Food Authority (NSW Food Authority, 2020a) and Food Standards Australia New Zealand (FSANZ) (FSANZ, 2017). Other novel strategies could also be explored, to ensure that educational material and training reaches those within the food service setting responsible for the safe preparation of these dishes. Australia also recently experienced its first recorded local HEV outbreak, which was linked to consumption of pork liver pâté. Consumption of raw or undercooked pork products (e.g. pâté, sausages, salami) has been identified as a risk factor for HEV infection in developed countries (EFSA Panel on Biological Hazards et al., 2017). Presently, the only efficient control option for HEV infection from consumption of meat, liver and products derived from animal reservoirs is sufficient heat treatment (EFSA Panel on Biological Hazards et al., 2017). A useful initiative would be the implementation of education campaigns, especially for the meat industry and butcheries and for consumers within risk groups, to help prevent the most serious HEV infections. This risk assessment also identified knowledge gaps due to the scarcity of studies on the presence of pathogens, including parasites and viruses, in domestic game meat animals

and to what extent this may result in contamination of meat cuts. While contributing only a small part of the overall meat and food supply in Australia, surveys and targeted research to generate the missing information would provide data necessary to inform future risk assessments concerning game meats.

1. Introduction

1.1 NSW Food Regulation 2015

The Food Regulation 2015 underpins the NSW Food Authority's food regulatory work, which aims to reduce the incidence of foodborne illness linked to certain food sectors in NSW [for a review see (NSW Food Authority, 2020c)]. It is important to the food industry as it sets minimum food safety requirements for food industry sectors that have been identified as higher risk, including the meat sector.

These businesses are subject to Food Safety Schemes because of the priority classification. Under each scheme there are licence categories that specify the types of activities each business is licensed to perform.

Meat food businesses need to meet food safety and labelling requirements, which vary depending on the business type:

- retail meat premises (butchers)
- meat vans
- poultry product transport
- meat and poultry processing plants
- game meat harvester vehicles and game meat field depots/chillers
- game meat processing plants
- red meat abattoirs (domestic and export)
- poultry and non-red meat abattoirs
- poultry live transport
- poultry meat producers (farms)
- animal food vans
- animal food processors
- knackeries and rendering plants
- Uncooked Comminuted Fermented Meat (UCFM) manufacturers

The NSW Food Authority has prepared the NSW Food Safety Schemes Manual to specify testing requirements for the Food Safety Schemes under the Food Regulation 2015 (NSW Food Authority, 2020b). The requirements referred to in the Manual are mandatory. The Meat Food Safety Scheme details requirements for sampling and analysis for meat business licensees.

1.2 Meat and meat products facilities in NSW

NSW is the largest producer of poultry meat in Australia, producing around a third of the national total [for a review see (NSW Food Authority, 2020d)]. NSW is also the second largest beef producer, accounting for around 20% of Australia’s total.

The NSW Food Authority currently licenses approximately 8,000 businesses in the meat sector, including about 60 abattoirs, 350 meat processing plants and 1,800 retail premises (butchers), as well as cold stores and more than 4,500 food transport vehicles.

1.3 Legislation and Standards applicable to meat food businesses

The Australia and New Zealand food regulatory system involves the Australian Government, New Zealand and Australian states and territories. In this system food standards are developed under the Australia New Zealand Food Standards Code (FSANZ, 2019b), which is administered by FSANZ and enforced by state and territory governments. The standards in the Australia New Zealand Food Standards Code are legislative instruments under the Legislation Act 2003. The NSW Food Authority enforces the Food Act 2003 (NSW) and associated regulations within NSW in respect of all food for sale.

Depending on the type of meat food business (NSW Food Authority, 2020d), the following Standards may apply:

Chapter 1, Part 1.2 - Labelling and other Information Requirements

Standard 1.3.1: Food Additives

Standard 3.2.2: Food safety practices and general requirements (apply in Australia only)

Standard 3.2.3: Food premises and equipment (apply in Australia only)

Standard 4.2.2: Primary production and processing standard for poultry meat (apply in Australia only)

Standard 4.2.3: Primary production and processing standard for meat (apply in Australia only)

Primary Production and Processing (PPP) standards aim to strengthen food safety and traceability throughout the food supply chain from paddock to plate.

Standard 4.2.2: Primary production and processing standard for poultry meat, commenced on 20 May 2012 (FSANZ, 2019c). In Standard 4.2.2, poultry means chicken, turkey, duck, squab (pigeons), geese, pheasants, quail, guinea fowl, muttonbirds and other avian species (except ratites).

Standard 4.2.3: Primary Production and Processing standard for meat, came into effect on July the 31st 2015 (FSANZ, 2019d). In Standard 4.2.3, animal means an animal of one of the following species: Bovine, Caprine, Ovine, Porcine, Bubaline, Camelidae, Cervidae, Crocodylidae, Lagomorph, Ratite or Soliped. However, a reference to an animal does not include an animal of a species within this list if that animal was slaughtered in the wild.

Standard 4.2.3: Primary Production and Processing standard for meat, specifies the Australian Standards which cover the slaughter and processing of animals for human consumption, including of animals in the wild, and the preparation, packing, transportation or storage of meat or meat products. Persons involved in such activities must comply with the relevant Australian Standards:

AS 4464:2007 - Hygienic Production of Wild Game Meat for Human Consumption

AS 4466:1998 - Hygienic Production of Rabbit Meat for Human Consumption

AS 4467:1998 - Hygienic Production of Crocodile Meat for Human Consumption

AS 4696: 2007 - Hygienic Production and Transportation of Meat and Meat Products for Human Consumption

AS 5008: 2007 - Hygienic rendering of animal products

AS 5010: 2001 - Hygienic Production of Ratite Meat for Human Consumption

AS 5011: 2011 - Hygienic productions of natural casings for human consumption

Additional legislative requirements apply to meat businesses as follows –

Prevention of Cruelty to Animals Act 1979 and Prevention of Cruelty to Animals Regulation 2012:

- retail meat premises (butchers)
- red meat abattoirs
- poultry and non-red meat abattoirs
- live poultry transport
- poultry meat producers (farms)

National Residue Survey (DAWE, 2020b):

- red meat abattoirs
- poultry and non-red meat abattoirs

Industry Animal Welfare Standards for Livestock Processing Establishments preparing meat for human consumption (Edge, 2009):

- red meat abattoirs

National Farm Biosecurity Manual for Poultry Production (DAWE, 2009):

live poultry transport

Australian Standard for the Hygienic Production of Pet Meat AS 4841:2006: PISC Technical Report 88 8 – Amended 2009:

- animal food vans
- animal food processors
- knackeries

New South Wales Standard for Construction and Hygienic Operation of Retail Meat Premises (NSW Food Authority, 2015):

- retail meat premises (butchers)

1.4 Updating the 2014 Risk Assessment

This Risk Assessment was produced following a literature review for issues related to meat and meat products that have impacted meat food safety since 2014. Information sources included published reports on the following:

- foodborne illness reports and recall data in Australia attributed to meat and meat products
- international issues arising from human illness or perceived hazards linked with meat and meat products
- border detections for meat and meat products
- risk assessments of meat and meat products
- emerging issues in the farm to consumer continuum for meat and meat products relevant to health risk
- research findings related to hazards in meat and meat product production and processing
- baseline surveys of microbiological and chemical hazards in meat and meat products
- other relevant sources if identified during the above activities

The current Risk Assessment includes discussion of meat and meat products identified from the literature review conducted as detailed above.

2. Risk assessment

2.1 Hazard identification

2.1.1 Meat

2.1.1.1 Biological hazards

In the previous Risk Assessment (NSW Food Authority, 2014), work conducted by FSANZ (FSANZ, 2013a) was referenced in regard to the principal microbial hazards associated with the four main meat species (cattle, sheep, goats and pigs). This table is reproduced below (Table 1). A range of pathogenic microorganisms including pathogenic *E. coli*, *Salmonella* spp., *Campylobacter* spp., *Yersinia* and *Toxoplasma* have been associated with the major meat producing animals. The principal microbiological hazards identified in the on-farm phase of meat production and after slaughtering operations include pathogenic *E. coli* and *Salmonella* spp., although there is some variation between meat species (FSANZ, 2013a). FSANZ (2013) derived this information from industry data, microbiological analyses and published scientific data. It is important to note that FSANZ (2013) did not attempt to document the severity of illness presented by these hazards, or determine the likelihood of their occurrence in the final meat product or characterise the risk they may present (FSANZ, 2013a).

Additional hazards have been identified in the current risk assessment, due to the popularity of undercooked or 'rare' meat. Eating undercooked meat increases the risk of foodborne illness and the opportunity for exposure to unfamiliar risks, such as foodborne parasites and viruses. A 2014 Australian Department of Health-funded report identified toxoplasmosis as one of the foodborne pathogens that continues to cause deaths in Australia (Kirk, Glass, Ford, Brown, & Hall, 2014). The significance of *T. gondii* as a public health hazard in Australian sheep meat has been the focus of a couple of recent reports (Dawson et al., 2020; MLA, 2017b). Lamb is typically marketed without freezing and is often served 'rare', which may lead to viable cysts being present in the meat at the point of consumption (Dawson et al., 2020). Therefore, *T. gondii* has been included as an additional hazard of concern in this meat species. Similarly, the consumption of raw or undercooked pork products (e.g. pâté, sausages, salami) has been identified as a high risk factor for HEV infection in developed countries (EFSA Panel on Biological Hazards et al., 2017). As Australia recently experienced its first recorded local HEV outbreak, linked to consumption of pork liver pâté, HEV is included as an additional hazard of concern in this meat species.

Table 1: Principal microbiological hazards associated with the four main animal species (FSANZ, 2013)

Animal	Principal microbiological hazard
Cattle	Pathogenic *Escherichia coli*, *Salmonella* spp., *Campylobacter jejuni* and *C. coli*
Sheep	Pathogenic *E. coli* and *Salmonella* spp.
Goats	Pathogenic *E. coli* and *Salmonella* spp.
Pigs	*Salmonella* spp., *Yersinia enterocolitica* and *Y. pseudotuberculosis*, *Toxoplasma gondii*, *C. jejuni* and *C. coli*

The work of FSANZ (FSANZ, 2013b) in assessing the microbiological hazards associated with the minor and wild game meat species (including buffalo, camels, alpacas, llamas, deer, horses, donkeys, rabbits, crocodiles, ostrich and emu) was also referenced in the previous Risk Assessment (NSW Food Authority, 2014). While acknowledging that data was limited, the assessment did not identify any substantial differences in the microbiological hazards associated with the major and minor and wild game meat species or potential human exposure through the consumption of meat (FSANZ, 2013b). Since this time, PrimeSafe (a Statutory Authority in Victoria) requested a review of diseases and pathogens of Australian invasive animals that may present food safety and human health risks (DEDJTR, 2016). The

review covers diseases and pathogens of both introduced species (pigs, goats, rabbits, hares, horses and deer) and native species (kangaroos and wallabies). The report discussed a wide range of pathogenic bacteria, viruses, parasitic helminths and protozoa that are carried by invasive species in Australia. While microbial hazards were identified in the report that are additional to those identified in the FSANZ hazard assessment (FSANZ, 2013b), there is limited or no evidence for the importance of these in Australia. The authors of the report concluded that further research is required to improve our understanding and knowledge of the diseases circulating in invasive species, the risks posed to food safety and human health, and mitigating procedures or steps required to reduce these risks. However, several microbiological hazards identified in the report (DEDJTR, 2016) may be of particular concern in food products where meat is consumed raw (e.g. UCFM) or where cooking times are reduced to achieve a rare product. Further discussion on these hazards in regard to UCFM products, can be found in Section 2.3.9.1.

Campylobacter and *Salmonella* are the principal pathogens of concern found on poultry meat. Standard 4.2.2: Primary Production and Processing Standard for Poultry Meat is intended to specifically reduce contamination of poultry, poultry carcases and poultry meat by pathogenic *Campylobacter* and *Salmonella*.

Aside from work conducted domestically to identify and rank microbial hazards associated with meat, a number of international studies have recently been conducted and are summarised in Section 2.1.1.1.1. *Clostridium difficile* and antimicrobial resistant microorganisms were addressed as a specific hazard in the 2014 Meat Risk Assessment (NSW Food Authority, 2014). Since this time, there have been a number of surveys conducted which have reported a high prevalence of *C. difficile* in Australian neonatal veal calves (Knight, Putsathit, Elliott, & Riley, 2016) and neonatal pigs (Knight, Squire, & Riley, 2015). These recent findings are briefly discussed in Section 2.1.1.1.2. In their Annual Report on Emerging and Ongoing Issues, FSANZ recognise antimicrobial resistance as an ongoing food safety issue (FSANZ, 2019e). Antimicrobial resistant microorganisms are discussed in Section 2.1.1.1.3.

2.1.1.1.1 International studies to identify and rank microbial hazards associated with meat

In France, a quantitative assessment was undertaken to determine the main microbiological hazards when consuming red meat (De Oliveira Mota, Guillou, Pierre, & Membré, 2020). de Oliviera Mota et al. (2020) aggregated data available in the literature to identify and characterise the main microbiological hazards in muscle and offal from beef, pork and other small ruminants from France. Subsequently, a risk assessment model was built to estimate the associated number of foodborne illnesses and deaths. de Oliviera Mota et al. (2020) determined that the major contributor of foodborne illness cases attributable to red meat consumption was *Campylobacter* spp. (30%), of which 55% of cases were attributable to beef meat. The pathogen responsible for the second highest number of cases was *C. perfringens* (22%), followed by *Salmonella enterica* (17%) and hepatitis E (11%). The pathogen that induced the highest mortality was *S. enterica*, with cases mostly related to pork consumption. Hepatitis E was the main contributor to the number of years in good health lost from red meat consumption in France, with this effect mainly due to pork liver consumption.

In the U.S.A, data was used to model and estimate the annual likelihood of illness per kilogram, and per serving, of food consumed for *Salmonella* and STEC O157 in beef, lamb, pork and poultry (Hsi, Ebel, Williams, Golden, & Schlosser, 2015). For STEC O157, beef has the highest per unit risk, followed by lamb, pork and poultry. When the risk of illness per serving for each commodity was determined for STEC O157, the rankings remained the same, except that beef and lamb were not significantly different. For *Salmonella*, poultry has the highest per unit risk followed by pork, beef and lamb. While Hsi et al. (2015) reported that there were differences between the per unit and per serving risk rankings determined for *Salmonella*, it was concluded that the risk of *Salmonella* illness per serving is similar among the four meat commodities considered.

In Switzerland, a risk ranking was undertaken of antimicrobial-resistant hazards found in meat (Collineau et al., 2018). A semi-quantitative risk assessment model from slaughter to consumption was developed following the Codex Alimentarius guidelines for risk analysis of foodborne antimicrobial resistance (AMR). Collineau et al. (2018) used data from the Swiss AMR monitoring program, which consisted of 208 combinations of animal

species/bacteria/antimicrobial classes identified as relevant hazards. Exposure assessment and hazard characterisation scores were developed and combined using multicriteria decision analysis. In their analysis, poultry-associated combinations presented the top ten risk characterisation rankings out of all combinations of animal species/bacteria/antimicrobial classes. In particular, contamination with extended-spectrum β-lactamase/plasmidic AmpC-producing *E. coli* in poultry meat ranked high for both exposure and hazard characterisation. Tetracycline- or macrolide-resistant *Enterococcus* spp., as well as fluoroquinolone- or macrolide-resistant *Campylobacter jejuni*, ranked among combinations with the highest risk.

It should be noted that regional variation in factors influencing microbial contamination of foods and food safety (such as environmental, socioeconomic, enforcement of food safety standards etc.) and the method of risk ranking employed in each analysis (i.e. variation in modelling approaches), make it difficult to draw direct comparisons between countries and/or studies. While these studies provide an indication of the pathogen/commodity pairs of most concern within the country in which the study took place, the knowledge is not necessarily directly transferrable to the Australian situation.

2.1.1.1.2 *Clostridium difficile*

Clostridium difficile infection was once considered a primarily nosocomial concern. Globally, community-associated *C. difficile* infection cases that occur without any recent contact with the hospital environment are increasing. In some regions of the world, including Australia, community-associated *C. difficile* infection now accounts for up to 25% of all cases (Bloomfield & Riley, 2016; Slimings et al., 2014). Increasing rates of *C. difficile* infection in the community suggest exposure to *C. difficile* reservoirs outside the hospital, including animals, the environment, or food. *C. difficile* is ubiquitous in the environment and has a wide host range [for a review see (Moono et al., 2016; Weese, 2020)]. The clinical presentation of *C. difficile* infection in humans and livestock varies from asymptomatic/subclinical carriage to mild diarrhea, severe diarrhea, and sometimes, life-threatening pseudomembranous colitis in humans.

C. difficile colonizes the gastrointestinal tracts of animals during the neonatal period, multiplies, and is excreted, but cannot/does not compete well when other bacterial species start to colonize (Knight & Riley, 2019). *C. difficile* is displaced as the microflora matures. The exact timing of this change is not clear, but it is probably linked to changes in diet, for example during weaning of young animals (Knight & Riley, 2019). *C. difficile* is commonly isolated from food production animals, although prevalence is species- and age-dependent (Squire, Knight, & Riley, 2015). *C. difficile* is particularly prevalent in production animals such as piglets and calves both in Australia (Knight et al., 2016; Knight et al., 2015) and other countries (Hensgens et al., 2012). To date, *C. difficile* has not been recovered from retail meat in Australia although only limited surveys have been undertaken mainly on meat from adult animals (Knight & Riley, 2019). Outside of Australia, a number of international surveys have reported on the presence of *C. difficile* on retail meats, especially beef, pork and poultry (Bouttier et al., 2010; de Boer, Zwartkruis-Nahuis, Heuvelink, Harmanus, & Kuijper, 2011; Limbago et al., 2012; Rodriguez-Palacios, Staempfli, Duffield, & Weese, 2007; Visser et al., 2012). Contamination of meat is thought to result from gut content spillage during evisceration or by accumulation of spores within the abattoir environment (Knight & Riley, 2019).

There have been two recent national surveys undertaken within Australia to investigate *C. difficile* in neonatal veal calves (Knight et al., 2016) and neonatal pigs (Knight et al., 2015). Knight et al. (2016) reported that of those neonatal veal calves sampled at three abattoirs in Australia in 2013, *C. difficile* was present on 25.3% (76/300) of carcases and in 60.0% (18/30) of faecal samples. *C. difficile* produces two toxins (TcdA and TcdB) as its main virulence factors (Moono et al., 2016). The majority of strains isolated from animals produce an additional binary toxin (*C. difficile* transferase) that is associated with increased virulence (Moono et al., 2016). Knight et al. (2016) reported that multiple polymerase chain reaction (PCR) ribotypes (RT) were detected in their survey, with four binary toxin-positive RTs accounting for 70.3% (71/101) of isolates; RT127 (32.7%), RT288 (28.7%), RT033 (6.9%) and RT126 (2.0%). These findings confirm that Australian neonatal veal calf carcases may be contaminated with potentially significant strains of *C. difficile* at slaughter. In another survey, Knight et al. (2015) investigated the prevalence and nature of

gastrointestinal carriage of *C. difficile* in Australian neonatal pigs by culture of rectal swabs and characterisation of the isolates. Rectal swabs (*n* = 229) were collected from piglets aged <7 days from 21 farms across Australia. *C. difficile* was isolated from 67% (154/229) of samples by enrichment culture. The majority (87%; 130/154) of isolates were toxigenic. Typing revealed 23 different RTs, several of which are known to cause disease in humans, including RT014, which was isolated most commonly (23%; 36/154). RT014 accounts for ~25% of *C. difficile* cases in Australia (Knight, Squire, Collins, & Riley, 2017). Knight et al.'s (2015) study revealed that colonisation of Australian neonatal piglets with *C. difficile* was widespread in the herds sampled. Furthermore, the isolation of multiple strains of *C. difficile* known to cause disease in humans suggests that neonatal pigs are a source/reservoir for *C. difficile* infection in humans.

The Australian practice of slaughtering neonatal animals for human consumption has been identified as potentially presenting a significant risk for community-associated *C. difficile* infection (Knight et al., 2017). There remains a consumer demand for neonatal veal products and these are traditionally supplied from the dairy industry (Knight et al., 2017). However, as suckling age piglets are not slaughtered for meat on a large scale, Knight et al. (2017) predict that they are unlikely to contribute to a persistent or substantial community reservoir.

To date, there has been no incontrovertible proof of foodborne or environmental transmission of *C. difficile* (Lim, Knight, & Riley, 2020). As outlined by Lim et al. (2020), such proof remains elusive given (a) not all individuals exposed to *C. difficile* will develop symptoms (depending on the vulnerability of their gastrointestinal tract microbiota), (b) the ubiquitous nature of *C. difficile*, and (c) the ability of *C. difficile* to form spores that remain dormant until the environment is suitable for growth, making it difficult to perform contact tracing. However, as reviewed by Lim et al. (2020), recent advances in whole genome sequencing (WGS) technologies have shown that many *C. difficile* strains from humans, animals, food and the environment are genetically closely related and, in some cases, indistinguishable (Janezic, Mlakar, & Rupnik, 2018; Knetsch et al., 2014; Knight et al., 2017; Rodriguez et al., 2014). This suggests possible zoonotic and/or anthroponotic transmission between animals and humans with contaminated food and environment acting as the conduit between the two. For example, in a study of 40 contemporaneous Australian RT014 isolates of human and porcine origin, 42% of human strains showed a clonal relationship [separated by ≤2 single-nucleotide variants (SNVs) in their core genome] with one or more porcine strains, consistent with recent inter-host transmission (Knight et al., 2017). Clones were spread over a vast geographic area with 50% of the human cases occurring without recent healthcare exposure. The authors concluded that these findings suggest a persistent community reservoir with long-range dissemination, potentially due to agricultural recycling of piggery effluent.

As noted in the previous meat risk assessment (NSW Food Authority, 2014), the NSW Food Authority has been monitoring the emergence of this organism for some time and will continue to do so. At this time there is no obvious specific intervention for *C. difficile* and good hygienic practice in meat processing and in the kitchen, which are already enforced or promoted by the NSW Food Authority, would seem to be applicable (NSW Food Authority, 2014).

2.1.1.1.3 Antimicrobial resistant organisms

The development of AMR and emergence of multidrug resistant pathogens are global concerns for both public health agencies and the agri-food industry. Antimicrobial resistant pathogens increase the risk of an infected individual suffering an adverse health effect, such as reduced treatment efficacy, and increased disease severity, hospitalization and mortality. Australia has strict regulations regarding antimicrobial use in livestock. Fluoroquinolones, colistin and 4th generation cephalosporins have never been registered for use in Australian food-producing animals, gentamycin use is banned and 3rd generation cephalosporin usage remains restricted (APVMA, 2017).

In their Annual Report on Emerging and Ongoing Issues, FSANZ (2019) recognised AMR as an ongoing food safety issue which has been identified for management through other processes (FSANZ, 2019e). FSANZ is a member of the Australian Strategic and Technical Advisory Group on AMR (ASTAG) and continues to be engaged in activities consistent with and complementary to the overall Australian Government effort to contain AMR (DoH, 2020a). The

2020 Strategy (DoH, 2020a) builds on the original 2015 strategy, broadening its ambit to encompass food, the environment and other classes of antimicrobials such as antifungals and antivirals.

The Australian government recently published a review of published and grey literature[1] on AMR in food (DoH, 2018). The aim of this study was to review published and grey literature on the presence and extent of AMR in food in Australia and New Zealand for the period 1999 to early 2018. The report provided an overview of available evidence for AMR presence in the food production, processing and retail sectors of red meat, pork, poultry meat, dairy, egg, seafood and horticultural products. In regard to Australian red meat (particularly beef), pork and chicken meat, the available AMR literature and data were assessed and designated as substantial. It was concluded that for these Australian food sectors, AMR prevalence data for animal pathogen, sentinel indicator and zoonotic foodborne pathogen bacteria are largely available. A number of knowledge gaps were also identified in the report (DoH, 2018). Amongst those identified knowledge gaps, given the size of the sheep meat industry, was the absence of AMR information on ovine sentinel bacteria. The literature review also revealed that a comprehensive AMR knowledge of *Salmonella* spp. from poultry meat was lacking, with AMR investigations of *Salmonella* spp. limited to a 2007-2008 pilot survey of AMR in foods in which 100 isolates were randomly tested.

Outside of the 1999 to early 2018 period covered in the literature review of the report by the Department of Health (DoH, 2018), there have been a number of AMR studies relating to Australian food production animals and their meat. These studies are briefly described below and generally demonstrate low levels of resistance to compounds of critical clinical importance, amongst chickens, beef cattle, sheep, pigs, goats and their meat. Of note, amongst those studies reviewed, was the first report of fluoroquinolone-resistant *Campylobacter* in Australian poultry (Abraham et al., 2020).

While Australia has one of the most conservative approaches in the world to the use of antimicrobials in food producing animals (DoH & DAWE, 2020), industry and government need to continue to proactively monitor AMR and antimicrobial stewardship practices to ensure the long-term protection of both animal and human health. It should be noted, that while the use of WGS to predict AMR is still in its infancy (Jennison, 2017), the first longitudinal genomic study of over 600 *Campylobacter* isolates from meat at the retail level was recently undertaken in Australia (Wallace et al., 2020). As computational tools and bioinformatics approaches mature to enable the rapid prediction of antibiotic resistance genes and their targets in newly sequenced genomes, enhanced knowledge will be gained on the prevalence of AMR genetic markers, the genetic relatedness of isolates from different animal sources and, our ability to identify new or emergent AMR pathogens within the Australian food supply. The NSW Government plays an established role in antimicrobial stewardship and resistance in accordance with the National Antimicrobial Resistance Strategy. Within scope of the Department of Primary Industries and Local Land Services is antimicrobial stewardship and antimicrobial resistance in terrestrial livestock, bees, aquatic animals, companion animals, pet shops and wildlife (NSW Government, 2018). As mentioned in the 2014 meat risk assessment (NSW Food Authority, 2014), there is no current role for the NSW Food Authority beyond its existing role in promoting good hygienic practices to combat the foodborne transmission of bacteria with AMR.

2.1.1.1.3.1 AMR in chickens

Recently, three reports were published that were part of an Australia-wide study of AMR in chicken meat (Abraham et al., 2019; Abraham et al., 2020; O'Dea et al., 2019). A total of 200 pooled caecal samples (five caecal samples in each pool) were collected between June and November 2016, from twenty poultry abattoir plants owned by seven commercial companies that process approximately 11 million chickens per week, representing 95% of Australian chicken meat production (Abraham et al., 2019; Abraham et al., 2020; O'Dea et al., 2019).

[1] Grey literature is research that has not been published commercially and is therefore not necessarily searchable via the standard databases and search engines. Examples of grey literature include, but are not limited to, government reports, conference proceedings, research reports and policy statements.

As part of the Australia-wide study of AMR in chicken meat, Abraham et al. (2019) assessed the frequency of AMR among *E. coli* and *Salmonella* isolated from meat chickens (Abraham et al., 2019). The survey involved the characterisation of the AMR phenotype of *E. coli* (*n* = 206) and *Salmonella* (*n* = 53) from caecal samples of chickens at slaughter (*n* = 200). A large proportion of *E. coli* isolates (63.1%) were found to be susceptible to all tested antimicrobials. Antimicrobial resistance was observed for trimethoprim/sulfamethoxazole (8.7%), streptomycin (9.7%), ampicillin (14.1%), tetracycline (19.4%) and cefoxitin (0.5%). With regard to resistance to critically important antimicrobials, only two *E. coli* isolates demonstrated resistance to fluoroquinolones, attributed to mutations in the quinolone resistance-determining regions of *gyrA*. All *Salmonella* isolates were susceptible to ceftiofur, chloramphenicol, ciprofloxacin, colistin, florfenicol, gentamicin and tetracycline. A low frequency of *Salmonella* isolates exhibited resistance to streptomycin (1.9%), ampicillin (3.8%), and cefoxitin (11.3%). AMR was only observed among *Salmonella* Sofia serovars. None of the *Salmonella* isolates exhibited a multi-class-resistant phenotype. Abraham et al. (2019) concluded that their results provide strong evidence that resistance to the highest priority critically important antimicrobials is absent in commensal *E. coli* and *Salmonella* isolated from Australian meat chickens, and demonstrates low levels of resistance to compounds with less critical ratings such as cefoxitin, trimethoprim/sulfamethoxazole, and tetracycline.

Also part of the Australia-wide study of AMR in chicken meat, Abraham et al. (2020) investigated AMR and the genomic characteristics of *Campylobacter jejuni* (*n* = 108) and *C. coli* (*n* = 96) from caecal samples of chickens at slaughter (*n* = 200) (Abraham et al., 2020). The majority of the *C. jejuni* (63%) and *C. coli* (86.5%) samples were susceptible to all antimicrobials. Fluoroquinolone resistance was detected among both *C. jejuni* (14.8%) and *C. coli* (5.2%), although this only included three sequence types (STs) and one ST, respectively. This is the first study to describe the detection of fluoroquinolone-resistant *Campylobacter* in Australian poultry. Multidrug resistance among strains of *C. jejuni* (0.9%) and *C. coli* (4.1%) was rare, and fluoroquinolone resistance, when present, was never accompanied by resistance to any other agent. Comparative genome analysis demonstrated that Australian isolates were found dispersed on different branches/clusters within the international collection. The major fluoroquinolone resistant STs of *C. jejuni* (ST7323, ST2083, and ST2343) and *C. coli* (ST860) present in Australian chickens were similar to those of international isolates and have been reported previously in humans and animals overseas. The authors of the study stated that the detection of a subpopulation of *Campylobacter* isolates exclusively resistant to fluoroquinolone was unexpected, as fluoroquinolones are excluded from use in Australian livestock. Genetic characterisation of these isolates suggests that they may have evolved outside the Australian poultry sector and were introduced into poultry by humans, pest species, or wild birds. Although human illness is typically self-limiting, a minority of cases do require antimicrobial therapy. Ensuring that *Campylobacter* originating from meat chickens does not acquire resistance to fluoroquinolones is therefore a valuable outcome for public health (Abraham et al., 2020).

The Australia-wide study of AMR in chicken meat evaluated the AMR of enterococcal species isolated from Australian meat chickens (O'Dea et al., 2019). A particular focus of this study was vancomycin resistance, as questions have been raised about whether Australian meat chickens are responsible for the high rate of vancomycin resistance in *E. faecium* isolates obtained from Australian hospitals. Overall, 205 individual isolates were obtained, consisting of five different species. *E. faecium* was the most frequently isolated species (37.6%), followed by *E. durans* (29.7%), *E. faecalis* (20%), *E. hirae* (12.2%), and *E. gallinarum* (0.5%). All isolates were susceptible to vancomycin and gentamicin. One isolate was linezolid resistant, however no *cfr* or *optrA* genes were identified, indicating resistance may be due to chromosomal mutations. The results of this study provide strong evidence that Australian chicken *E. faecium* isolates are unlikely to be precursor strains to the currently circulating vancomycin-resistant strains being isolated in Australian hospitals.

2.1.1.1.3.2 AMR in beef

While the results are not publicly available at the time of writing, a survey of AMR in the faecal bacteria of healthy beef cattle at the time of slaughter was conducted through MLA in 2019 (Barlow et al., 2019). The sampling design is

consistent with the design of a 2013 survey (Barlow et al., 2015, 2017), and the bacteria being isolated and AMR methods will produce comparable data. When available, the results of the 2019 survey will not only produce another point estimate of AMR prevalence in bovine commensals and pathogens against antibiotics of interest in human medicine, but it will be comparable to the results from 2013, thus allowing assessment of trends through time (Barlow et al., 2019). If antibiotic usage in the cattle industry, or other factors, is contributing to the increase in AMR prevalence, then it should become apparent by comparing the results of the two surveys (Barlow et al., 2019). Australia does not have a large and ongoing national integrated surveillance system, such as exists in some other countries, and the comparison of the two bovine surveys will help to answer the question of how often surveillance should occur and how extensive it should be (Barlow et al., 2019).

2.1.1.1.3.3 AMR in sheep

MLA funded a study into the AMR of *E. coli*, *Salmonella* and *Enterococcus* from healthy sheep at slaughter (MLA, 2019). A total of 14 Australian sheepmeat processors agreed to participate in the survey, collectively representing 65% of total Australian lamb production and 83% of total Australian mutton production. The survey comprised 800 faecal samples, collected from across three animal groups: pasture-fed lamb (*n* = 414), feedlot lamb (*n* = 163) and sheep (*n* = 223). For a summary of the findings of this survey in relation to the prevalence and concentration of key foodborne pathogens, see Section 2.3.4. A subsample of 100 *E. coli* (randomly selected), along with 76 *Enterococcus* (preferencing clinically significant species - *E. faecalis* and *E. faecium*) and all 81 *Salmonella* isolates were tested for antimicrobial susceptibility. The minimum inhibitory concentration (MIC) is the lowest concentration of an antibiotic that inhibits the growth of a given strain of bacteria. Epidemiologic breakpoints are measures of a drug MIC distribution that separate bacterial populations into those strains representative of a wild type population, and those strains with acquired or mutational resistance to the drug. A bacterial strain with a drug MIC that is greater than the epidemiologic breakpoint is likely to have an acquired form of resistance, whereas a bacterial strain with a drug MIC lower than or equal to the epidemiologic breakpoint is likely from the wild type distribution of the bacterium for a particular drug. The epidemiologic breakpoint is not the same as a clinical breakpoint. A clinical breakpoint is the concentration of antibiotic that defines whether an infection by a particular bacterial strain/isolate is likely to be treatable in a patient. The authors of the MLA (2019) study report that resistance to clinically significant antimicrobials was generally low across all isolate groups. Of the 100 *E. coli* tested, 97% were considered pan-susceptible regardless of whether epidemiological or clinical breakpoints were used, 2% were non-wild for tetracycline (i.e. a microorganism with acquired and/or mutational resistance mechanisms to a certain drug) and 1% were considered clinically resistant to sulfisoxazole. When epidemiological breakpoints were considered, 100% of *E. faecalis* (*n* = 34) and 83% of *E. faecium* (35 of 42 isolates) were considered wild type. Of the remaining *E. faecium*, 6 (14.2%) were considered non-wild for ciprofloxacin and 1 (2.4%) for streptomycin. Of the 81 *Salmonella* tested, 80 (99%) were considered pan-susceptible, with just a single isolate confirmed as non-wild type for ampicillin, streptomycin and tetracycline. The authors of the report concluded that the rate of detection of AMR in isolates from sheep was low, suggesting that sheep production practices are likely to have minimal impact on the development of resistance to antimicrobials considered highest priority and critically important to human medicine.

2.1.1.1.3.4 AMR in pigs

Sahibzada et al. (2020) investigated the prevalence and AMR of methicillin-resistant forms of *Staphylococcus aureus* (MRSA) in an intensive pig production system in Australia, which was experiencing an ongoing MRSA outbreak amongst its human workforce (Sahibzada et al., 2020). While zoonotic transmission of MRSA to farmworkers is an established risk, the presence of MRSA in food animals raises the question of whether transmission of MRSA by contaminated food could occur. However, staphylococcal food poisoning with MRSA has rarely been reported (Jones, Kellum, Porter, Bell, & Schaffner, 2002; Kluytmans et al., 1995). Overall, Sahibzada et al. (2020) reported that MRSA was isolated from 490 out of 658 samples from pigs and the environment. In pigs, a prevalence of 75.2% was found. None of the 490 MRSA isolates were resistant to ciprofloxacin, gentamicin, linezolid, mupirocin, rifampicin,

trimethoprim/sulfamethoxazole, teicoplanin or vancomycin. Ciprofloxacin (a fluoroquinolone) and vancomycin (a glycopeptide) are both classified as critically important for use in humans (WHO, 2017). Vancomycin is particularly important in the treatment of staphylococcal disease in humans because it is the last line of defence. A low frequency of resistance was identified to neomycin (9.1%) and quinupristin–dalfopristin (9.3%). Two-thirds of the MRSA isolates were resistant to amoxicillin–clavulanate (63.8%) and tetracycline (63.8%). Chloramphenicol resistance was observed in 80.9% of the isolates. Most of the MRSA isolates were resistant to ceftiofur (93.6%), erythromycin (96.5%), clindamycin (97.7%) and penicillin (100%). The majority of MRSA isolates collected in this study were observed to exhibit multidrug-resistance. A total of 11 (2.4%) isolates were resistant to one or two non-beta-lactam antimicrobials, 267 (54.5%) to three, 128 (26.1%) to four and 79 (16.1%) to five, and four isolates (0.8%) were resistant to six of the non-beta-lactam drugs in the test panel.

2.1.1.1.3.5 AMR in goats

Al-Habsi et al. (2018) undertook a study to investigate AMR in *Salmonella* isolates from Australian rangeland goats (Al-Habsi, Jordan, et al., 2018). Faecal samples (*n* = 400) were collected at slaughter from four consignments of goats (100 samples per consignment), each from one of four localities in Western Australia. For information on the rate of carriage of *Salmonella* spp. and the dominant serovars present, see Section 2.3.6.1.1. The majority of isolates (89/106; 84.0%) remained phenotypically susceptible to all thirteen antimicrobials in the study (cefoxitin, azithromycin, chloramphenicol, tetracycline, ceftriaxone, amoxicillin-clavulanic acid, ciprofloxacin, gentamicin, ceftiofur, trimethoprim-sulfamethoxazole, ampicillin, nalidixic acid and streptomycin). Isolates with AMR to one (3/106; 2.9%), two (10/106; 9.4%) and three (4/106; 3.7%) antimicrobials drugs were identified, with the four isolates clinically resistant to three classes (β–lactamase, Macrolides and Tetracylines) of the antimicrobial agents classified as multi-drug resistant (MDR). Resistance was most frequently detected to azithromycin (14.2%), followed by tetracycline (10.5%), ampicillin (5.7%), amoxicillin–clavulanate and cefoxitin (3.8%), trimethoprim/sulfamethoxazole (1.9%), gentamicin (0.9%) and streptomycin (0.9%). No isolate was resistant to four or more antimicrobials, or to critically important antimicrobials such as fluoroquinolones and extended spectrum cephalosporins. Al-Habsi et al. (2018) concluded that the rate of detection of AMR was very low, with some resistance to low-importance drugs present in the *Salmonella* population, despite the absence of active selection pressure.

In a study by Wilson et al. (2019), three isolates of *S.* Typhimurium (Sal-12, Sal-43 and Sal-240) and one isolate of *S.* Infantis (Sal-576) from goat faecal samples were tested for their sensitivity to a panel of 14 antibiotics (Wilson, Fox, Fegan, & Kurtböke, 2019). All isolates (100%) were susceptible to ampicillin, streptomycin, tetracycline, florfenicol, norfloxacin, kanamycin, gentamicin, ciprofloxacin, chloramphenicol, trimethoprim-sulfamethoxazole and nalidixic acid. *S.* Typhimurium Sal-43 was resistant to sulphafurazole and Sal-576 was resistant to cefoxitin. This study was part of a larger evaluation of 19 *S.* enterica strains isolated between 2001 and 2013 from Australian food production chains. Wilson et al. (2019) concluded that the findings of their study suggest that resistance to clinically relevant antibiotics is not widespread among *Salmonella* isolated from Australian food-producing animals.

2.1.1.2 Chemical hazards

The National Residue Survey (NRS) program monitors the levels of, and associated risks from, pesticides and veterinary medicine residues and contaminants in Australian food products [for an overview see (DAWE, 2019b)]. NRS supports Australia's primary producers and food processors in producing products which meet both Australian and relevant international standards. NRS programs cover a range of commodities including the following meat products: cattle, sheep, pigs, chicken, goat, horse, kangaroo, wild boar, poultry (duck, turkey, spatchcock, quail), deer, camel, emu, buffalo and ostrich. Chemicals are tested according to the commodity to be sampled and may include anthelmintics, antibiotics, anticoccidials, contaminants, fungicides, herbicides, hormones, insecticides, metals, mycotoxins and other veterinary drugs and sedatives. NRS results, which show the full range of commodities and chemicals tested each financial year, are available on the Department of Agriculture, Water and the Environment

(DAWE) website. The results highlight a high degree of compliance with Australian standards. The average compliance rate for animal food products in 2018–19, relative to Australian standards was 99.79% (DAWE, 2019a). This result indicates that chemical hazards are well controlled at primary production under existing regulatory and non-regulatory measures.

Sulphur dioxide (SO_2) is a chemical used as a preservative in some foods, such as meat. It is strictly controlled by the Food Standards Code as some people might have a serious reaction to it. Standard 1.3.1 of the Code permits the use of SO_2 in sausage and sausage meat to a maximum of 500 mg/kg. While raw meat is not permitted to contain any SO_2. In the previous risk assessment (NSW Food Authority, 2014), screening results for SO_2 were reported for meat products sampled by the NSW Food Authority between July 2007 and December 2013. While the number of positive samples was found to be low during this period, the results led to strengthened enforcement action being undertaken. SO_2 remains a potential chemical hazard and results of SO_2 testing conducted by the NSW Food Authority are reported within in Section 2.3.10.

2.1.1.3 Physical hazards

A physical hazard can be defined as any physical material not normally found in a food that can cause illness or injury to a person consuming the product. These materials include, but are not limited to, glass, metal, rubber, plastic, wood and bones. Physical hazards in finished meat and poultry products can arise from several sources, such as contaminated raw materials, poorly designed or maintained facilities and equipment, faulty procedures during processing, and improper employee training and practices. Physical hazards are less likely than chemical or biological contaminants to affect large numbers of people and, are most likely to be reported by production or by consumer complaints. Table 10 lists all consumer level recalls of meat and meat products in Australia from 17/10/2015 to 15/10/2020, including six consumer level recalls due to the presence of physical objects of plastic (n = 2), metal (n = 2), rubber (n = 1) and bone (n = 1).

2.2 Exposure assessment

2.2.1 Consumption of meat

A summary of the consumption data reported in the 25th ATDS (FSANZ, 2019a) of meat and poultry food groups by Australian consumers (2 years and above) is provided in Table 2. The only food groups reported to be consumed by the majority of the Australian population are beef, veal and large game (63%) and poultry and game birds (58%). Offal (including pâté and liverwurst) was the food group reported to be consumed by the smallest proportion of the population (<1%). The mean food consumption amount for consumers of poultry and game birds was the highest of all food groups (76 grams per consumer per day). Comparison of consumption data reported here and in the previous 2014 meat risk assessment (data taken from Australian Health Survey 2011–2012, ABS, 2014), is hampered by differences in the categorization of food groups and what has been reported.

Table 2: Consumption data for Australian consumers (2 years and above) of meat and poultry food groups[a]

Food group	Proportion of population consuming food groups (%)	Mean food consumption amount for consumers (grams per consumer per day)
Bacon	20	18
Beef, veal and large game	63	56
Lamb, mutton, goat, kangaroo and rabbit	16	59

Food group	Proportion of population consuming food groups (%)	Mean food consumption amount for consumers (grams per consumer per day)
Meat sausages and frankfurts	17	67
Offal (including pâté and liverwurst)	<1	24
Pork (except bacon) and deli meats (except frankfurts and poultry-based)	41	35
Poultry and game birds	58	76

[a] Data reported in the 25th ATDS (FSANZ, 2019a)

The apparent consumption of the main meat species per person in Australia was reported by ABARES (ABARES, 2020) and is provided in Table 3. Across all years, chicken meat consumption was significantly higher than the consumption of the other main species. Only consumption of chicken meat increased; albeit slightly, from 2014-2015 to 2017-2018. From 2014-2015 to 2017-2018 consumption of beef and veal, lamb and mutton and pig meat, decreased slightly or remained unchanged. Australia is a relatively small producer of chicken meat in a global sense, yet Australians rate as among the highest consumers of chicken meat on a per capita basis (ACMF, 2020a). In 2019 Australia was the fifth largest consumer of chicken meat on a per capita basis; after Malaysia, Qatar, the United States and Kuwait, when calculated based on available data on total chicken meat consumption (USDA, 2020) and population estimates (UN, 2019).

Table 3: Apparent consumption per person of the main meat species in Australia[a]

Year	Apparent consumption per person (kg (cw))			
	Beef and Veal	Lamb and mutton	Pig meat	Chicken Meat
2014–15	27	9	27	46
2015–16	25	9	28	49
2016–17	25	8	28	49
2017-18	24	8	27	47

[a] Data reported by ABARES (ABARES, 2020)

2.3 Hazard characterisation

2.3.1 Overview of foodborne illness and meat and meat products in NSW from 2013 to 2018

The hazard characterisation of the previous risk assessment (NSW Food Authority, 2014) included outbreaks of foodborne illness that occurred in Australia from 2009 to 09/2012 (Data from OzFoodNet Working Group Annual Reports, 2009 and 2010 and from Quarterly Reports 2011 to 09/2012). The current risk assessment includes discussion of outbreaks from 2013 onward.

Table 4 displays a summary of the total number of foodborne or potentially foodborne disease outbreaks investigated in NSW from 2013 to 2018, as well as the number of these outbreaks in which meat; alone or in a complex food(s), was identified as the suspected or responsible vehicle (Communicable Diseases Branch, 2014a, 2015, 2016, 2017, 2018, 2019). As can be seen in Table 4, the suspected/responsible food vehicle was identified in only a minority of outbreaks (37% ± 9%). A possible explanation for this is the delay between consumption of foods and reporting of illness, which impairs case recall of foods and ingredients consumed (Communicable Diseases Branch, 2015). This also reduces the ability of the NSW Food Authority to obtain specimens of implicated foods and timely environmental samples (Communicable Diseases Branch, 2015). In addition, not all reported outbreaks can be properly investigated due to factors such as lack of cooperation from cases (an outbreak is often reported by one case, representing many cases who may not want to collaborate) and prioritisation of resources (Communicable Diseases Branch, 2015). It is therefore acknowledged that the role of various food commodities as vehicles of foodborne disease may be underestimated.

Meat; alone or in a complex food(s), was identified as the suspected or responsible vehicle in a total of 9 outbreaks from 2013 to 2018 (Table 5). In 2018, no outbreaks were linked to meat or meat-related dishes. From 2013-2017, meat or meat-related dishes were identified as the suspected or responsible vehicle in 1-3 outbreaks annually. Liver dishes of chicken (*n* = 4), lamb (*n* = 1), pork (*n* = 1) and duck (*n* = 1) were the food vehicle responsible for the majority (7/9; 78%) of meat related outbreaks from 2013 to 2018. Insufficient cooking was identified as a contributing factor or a likely conceivable factor in all seven liver dish outbreaks. The remaining two meat related outbreaks were attributed to ham and roast beef. The gastroenteritis outbreak associated with beef at an aged care facility in 2014, was reported to likely be due to a toxin produced in food that was not subject to proper temperature control, however no microbiological evidence was available to confirm this (Communicable Diseases Branch, 2014b). Undercooking of meat and temperature abuse after cooking were therefore major factors in outbreaks in NSW from 2013 to 2018.

Campylobacteriosis became a notifiable condition in NSW on 7 April 2017 (Communicable Diseases Branch, 2019). *Campylobacter* was the causative agent for the majority (56%; 5/9) of meat related outbreaks from 2013 to 2018 (Table 5). The other four outbreaks across this time period were linked to *L. monocytogenes*, *S.* Typhimurium, HEV and an unknown agent. Of particular note, this was the first reported locally acquired HEV outbreak in Australia (Yapa et al., 2016).

Restaurants were the most common outbreak setting from 2013 to 2018 and were implicated in 67% (6/9) of all meat-related outbreaks (Table 5). The other three outbreaks occurred in an aged care facility, a bakery and a community setting.

Across all years from 2013 to 2018 several outbreaks occurred in which a complex food containing meat was identified as the suspected/responsible vehicle, however the specific ingredient responsible was not identified. Appendix 1 contains a table of outbreaks reported in the NSW OzFoodNet annual reports from 2013 to 2018, in which a specific meat species was identified as part of a complex food in the “suspected or responsible vehicle”. However, whether the meat within these meals was the source of the outbreak remains unknown.

It should be noted that within the OzFoodNet Working Group Annual Report, further information is provided on a select number of significant outbreaks. As a situation evolves, new findings may lead to differing conclusions over time. For example, in April 2017 an outbreak of *Campylobacter* occurred at a commune affecting 21 adults and the suspected/responsible vehicle was recorded as unknown on page 32 of the 2017 Annual Surveillance Report (Communicable Diseases Branch, 2018). However, further detail was provided on this outbreak in a section on a select number of significant enteric outbarks on page 36 (Communicable Diseases Branch, 2018). While no food was available for testing, epidemiological and laboratory investigations indicated that the cluster was likely caused by undercooked chicken (Communicable Diseases Branch, 2018). As the suspected/responsible vehicle was recorded as unknown, this outbreak is not included in Table 5 or Appendix 1 of this Risk Assessment.

Table 4: Summary of foodborne or potentially foodborne disease outbreaks reported in NSW from 2013 to 2018

	2013	2014	2015	2016	2017	2018
Total number of foodborne or potentially foodborne disease outbreaks	39	44	58	70	38	50
Number of people affected in all outbreaks	> 417	> 480	> 569	> 1,625	> 437	> 560
Percentage of all outbreaks in which the suspected/responsible vehicle was known	33% (13/39)	52% (23/44)	45% (26/58)	36% (25/70)	26% (10/38)	32% (16/50)
Total number of outbreaks in which meat; alone or in a complex food(s), was specifically identified as the suspected/responsible vehicle [a]	1	2	3	2	1	0

[a] In Table 11 (page 20) of the 2013 OzFoodNet Working Group Annual Report (Communicable Diseases Branch, 2014a), a column titled "responsible vehicle" lists the food item(s) for each outbreak where available, otherwise "unknown" is recorded. The evidence used to categorize the food item(s) as a responsible vehicle, are either solely or a combination of descriptive, analytical or microbiological evidence. From 2014 onwards, the OzFoodNet Working Group Annual Reports list the food item(s) for each outbreak where available as "Suspected / Responsible vehicle", otherwise "unknown" is recorded. The evidence used to categorize the food item(s) as a "Suspected / Responsible vehicle", is as listed above for the 2013 OzFoodNet Working Group Annual Report.

Table 5: Foodborne disease outbreaks reported in NSW between 2013 and 2018[a], in which meat; alone or in a complex food(s), was specifically identified as the responsible vehicle

Year	Month of onset	Setting	Pathogen	No. affected	No. hospitalised	Suspected or responsible vehicle
2018	-	-	-	-	-	-
2017	Dec	Restaurant	*Campylobacter*	2	0	Undercooked lamb liver
2016	Nov	Restaurant	*Campylobacter*	3	0	Undercooked chicken liver pâté
	Feb	Community	*L. monocytogenes*	3	3	Ham contaminated from environment
2015	Dec	Restaurant	*Campylobacter*	2	1	Undercooked chicken liver pâté

Year	Month of onset	Setting	Pathogen	No. affected	No. hospitalised	Suspected or responsible vehicle
	May	Restaurant	*C. jejuni*	2	1	Likely undercooked chicken liver pâté
	Sep	Bakery	*Salmonella* Typhimurium	12	9	Vietnamese pork rolls in which undercooked egg and chicken liver products were used & cross contamination occurred
2014	Apr	Restaurant	HEV	14	4	Pork liver pâté
	Sep	Aged care facility	Unknown	8	0	Roast beef
2013	Sep	Restaurant	*Campylobacter*	17	1	Duck liver parfait

[a] Data was obtained from the NSW OzFoodNet annual reports from 2013 to 2018 (Communicable Diseases Branch, 2014a, 2015, 2016, 2017, 2018, 2019)

2.3.2 Notable foodborne illness reports

2.3.2.1 *Campylobacter* and *Salmonella* outbreaks linked to undercooked liver dishes

As discussed above, liver dishes were the food vehicle responsible for the majority (7/9; 78%) of meat related outbreaks from 2013 to 2018 (Table 5). Liver dishes of chicken (*n* = 4), lamb (*n* = 1), pork (*n* = 1) and duck (*n* = 1) were responsible for these outbreaks and undercooking was identified as a contributing factor leading to all seven outbreaks.

In December 2017, descriptive evidence linked undercooked lamb liver to an outbreak at a restaurant (Communicable Diseases Branch, 2018). The outbreak caused illness in 2 people due to *Campylobacter*. No significant hygiene or food handling issues (including cooking of the lamb's fry) were reported at inspection by the local council. Based on epidemiological and laboratory investigations, it was thought that the cluster was caused by the consumption of undercooked lamb's fry, which may have been undercooked on this one occasion.

In November 2016, microbiological evidence was used to link chicken liver pâté from a restaurant to an outbreak of *Campylobacter* that led to 3 illnesses (Communicable Diseases Branch, 2017). Undercooking was identified as a contributing factor leading to the outbreak.

In 2015, three outbreaks were linked to undercooked chicken liver pâté (Communicable Diseases Branch, 2016). In May, descriptive evidence was used to determine the cause of an outbreak at a restaurant involving *Campylobacter jejuni* in which 2 people were ill, with one person hospitalised. During inspection of the restaurant, the NSW Food Authority found that a digital thermometer was not in use to confirm that livers reached the correct safe cooking temperature. It was therefore deemed possible that contaminated livers could have resulted in a batch of pâté that caused infection in this case. In September, microbiological evidence was used to link an outbreak caused by

Salmonella Typhimurium to Vietnamese pork rolls from a bakery. This outbreak resulted in 12 illnesses and 9 hospitalisations. The NSW Food Authority inspected the bakery and samples of food and the environment were taken, of which samples of cooked pork, chicken liver pâté, a swab of the pâté blender and a boot swab were all positive for *Salmonella* Typhimurium. Contributing factors leading to the outbreak were found to be the use of undercooked egg and chicken liver products and cross contamination. In December, using descriptive evidence, an outbreak in a restaurant involving *Campylobacter* was associated with undercooked chicken liver pâté. The outbreak led to two illnesses and one hospitalisation.

In September 2013, an outbreak of gastroenteritis due to *Campylobacter* affected people who attended a wedding reception (Communicable Diseases Branch, 2014a). Seventeen people were ill and one person was hospitalised. In a univariate analysis, the strength of association between becoming ill and 17 food and drink exposures at the wedding reception or attending a pre-wedding function on the night before were calculated. The only significant association with illness was for consumption of the duck entree that contained duck liver parfait. Fifteen of the 17 cases (88.2%) ate the duck entrée. The NSW Food Authority visited the venue to review the preparation and handling of foods. No food samples were available for collection, but the chefs were advised of the proper cooking method required to render poultry livers free from bacterial pathogens.

From 2013-2018, OzFoodNet recorded six outbreaks linked to the consumption of Vietnamese rolls. Vietnamese rolls typically contain raw egg mayonnaise and often chicken liver pâté, both of which require expertise in their safe preparation and storage. As discussed above, undercooked egg and chicken liver products and cross contamination were linked to an outbreak involving *S.* Typhimurium which occurred in 2015 (Table 5). In the remaining five cases, which occurred in 2015 (n = 1), 2014 (n = 3) and 2013 (n = 1), a specific ingredient within the Vietnamese rolls was not identified as the source of the contamination. Raw egg was however noted as an ingredient in the Vietnamese rolls associated with two outbreaks in 2014 and one outbreak in 2013 and is the most common risk factor in these types of products. *S.* Typhimurium was causative agent in all outbreaks, apart from the outbreak which occurred in 2015, in which the causative agent remains unknown.

Foodborne illness outbreaks in Australia and overseas have long been linked to poultry liver dishes such as pâté or parfait where the liver was undercooked. Lanier et al. (2018) undertook a review of chicken liver–associated outbreaks of campylobacteriosis and salmonellosis that occurred in the U.S.A between 2000 and 2016 (Lanier, Hale, Geissler, & Dewey-Mattia, 2018). Lanier et al. (2018) identified a total of 28 reported outbreaks associated with chicken liver, of which 23 (82.1%) were caused by *Campylobacter* only and 3 (10.7%) by *Salmonella* only and, in 2 (7.1%) of the outbreaks both pathogens caused illnesses. Chicken liver pâté or other blended dishes (e.g., spread, mousse, or butter) were implicated in 24 (85.7%) of the outbreaks. Common outbreak features included the responsible vehicle being pâté or other blended dishes (e.g., spread, mousse, or butter) (24/28, 85.7%), inadequate cooking (26/28, 92.8%) and preparation in foodservice settings (e.g. restaurants) (25/28, 89.3%). Lanier et al (2018) concluded that chicken liver–associated outbreaks may, in large part, be explained by the interplay of two factors: inadequate cooking and pathogen contamination. Lanier et al. (2018) also proposed that a possible explanation for the greater number of campylobacteriosis outbreaks associated with poultry liver dishes, may be inferred from the fact that several published studies have demonstrated the presence of *Campylobacter* in the internal tissues of chicken liver, while no such studies for *Salmonella* have been reported. Lanier et al. (2018) proposed that although internal *Salmonella* presence may simply not have been assessed, it is also possible that *Campylobacter* could more likely be present than *Salmonella* in internal chicken liver tissues. Liver as an organ can concentrate microorgansims and post-slaughter provides an ideal medium for microbial growth with high water activity and neutral pH. *Campylobacter* does not grow below 28°C and although its viability decreases during chilled storage, cells can still persist after several weeks of storage at chilled or frozen temperatures (Harrison, Corry, Tchórzewska, Morris, & Hutchison, 2013). As the prevalence of *Campylobacter* in chicken livers is high (see Section 2.3.7.1.2), undercooking is a hazardous practice (NSW Food Authority, 2018a). Survey work has also been conducted by NSW Food Authority to gather information on

the prevalence (presence/absence) of *Campylobacter* and *Salmonella* on beef, lamb and pork liver at retail level in NSW (NSW Food Authority, 2018b). *Salmonella* was detected in 19% of the pork liver samples (6/31) and in none of the lamb (*n* = 15) or beef (*n* = 3) liver samples. The percentage of *Campylobacter* positive liver samples was 80% (12/15) for lamb, 22% (7/31) for pork and, 0% for beef (*n* = 3). While the number of samples surveyed was small, the results indicate that lamb livers are more likely to be contaminated with *Campylobacter* than beef or pork. These results align with the high prevalence of *Campylobacter* on lamb livers reported in studies conducted in Scotland (78%) (Strachan et al., 2012), New Zealand (66%) (Cornelius, Nicol, & Hudson, 2005) and Northern Ireland (80%) (Scates, Moran, & Madden, 2003). The NSW Food Authority survey report concluded that there was room for improvement in the microbiological quality of lamb and pork offal and that thorough cooking and safe handling of these foods are essential.

2.3.2.2 Australia's first hepatitis E outbreak linked to consumption of pork liver pâté

Hepatitis E is a liver disease caused by HEV. HEV infection is usually self-limiting and resolves within 2–6 weeks. The majority of HEV infections are asymptomatic. When symptoms of HEV infection occur, they may include fever, fatigue, loss of appetite, nausea, vomiting, abdominal pain, jaundice, dark urine, clay-coloured stool or joint pain. Occasionally a serious disease, known as fulminant hepatitis (acute liver failure) develops, and a proportion of people with this disease can die. Fulminant hepatitis occurs more frequently when HEV infection occurs during pregnancy. Pregnant women with HEV infection, particularly those in the second or third trimester, are at increased risk of acute liver failure, foetal loss and mortality. Up to 20–25% of pregnant women can die if they contract a HEV infection in the third trimester. Cases of chronic HEV infection have been reported in immunosuppressed people, particularly organ transplant recipients on immunosuppressive drugs.

In April 2014, the first reported HEV outbreak was reported in Australia. Analytical evidence linked the outbreak to consumption of pork liver pâté (Communicable Diseases Branch, 2015). The outbreak occurred at a restaurant and led to 14 illnesses and 4 hospitalisations. The NSW Food Authority inspected the restaurant on two occasions and witnessed the preparation and cooking of the pork pâté. The restaurant was found to be well-run with no issues identified in food handling, cooking or cleaning. The pork pâté was made with pork livers and included only one short cooking step. Pork samples from the restaurant were tested for HEV. All samples were negative. It was considered conceivable that on more than one occasion the pork livers had been inadvertently undercooked, allowing the HEV to survive when the pâté was made. Trace back of the pork livers revealed that a single pig farm supplied the livers that were served as pork pâté on the days the cases reported eating at the restaurant. In addition to the HEV cases above, three notifications of locally acquired HEV from 2013 with no known source of infection were re-investigated. Interviews revealed that two cases had also eaten pork pâté at the same restaurant during their incubation period (the third case was thought to be person to person transmission). An additional case from October 2013, identified on retrospective testing of stored sera was also linked to the cluster. The viruses from 11 out of the 18 cases linked to the restaurant (three from 2013 and eight from 2014) were genetically sequenced and were found to be closely related, suggesting a common source.

Domestic pigs are the main animal reservoirs of HEV worldwide and the consumption of raw or undercooked pork products (e.g. pâté, sausages, salami) have been identified as risk factors for HEV infection in developed countries (EFSA Panel on Biological Hazards et al., 2017). The European Food Safety Authority (EFSA) Panel on Biological Hazards recently undertook a review of information on the occurrence and control of HEV as a food-borne pathogen (EFSA Panel on Biological Hazards et al., 2017). HEV is an important infection in humans in EU/EEA countries and over the last 10 years more than 21,000 acute clinical cases with 28 fatalities have been notified; the majority (80%) of cases were reported from France, Germany and the U.K. However, it has been predicted that as infection in humans is not notifiable in all Member States, and surveillance differs between countries, the number of reported cases is not comparable and the true number of cases is probably higher. Food-borne transmission of HEV appears to be a major route in Europe; pigs and wild boars are the main source of HEV. In the description of foodborne HEV outbreaks over

the last 10 years, frequent association was found with the consumption of products containing raw or undercooked pig liver and also other pork products, such as pork pies, homemade sausages, undercooked or raw pork meat, processed pork products and offal. Outbreaks and sporadic cases were identified in immune-competent persons as well as in recognised risk groups such as those with pre-existing liver damage, immunosuppressive illness or receiving immunosuppressive treatments.

2.3.3 Beef

2.3.3.1 National Surveys

2.3.3.1.1 Survey of beef and veal carcases for *E. coli* and *Salmonella*

MLA commissioned a survey of beef and veal carcases from Australian export meat processing establishments to demonstrate the level of process control and the resulting hygienic quality of beef/veal carcases (MLA, 2017a). The survey was initiated in response to the announcement that the Food Safety and Inspection Service (FSIS) was conducting a nationwide beef and veal microbiological baseline data collection program in the U.S.A which commenced in August 2014 (FSIS, 2016a). The objectives of the MLA survey were to estimate the prevalence of *Salmonella* and prevalence and concentration of indicator organisms on beef and veal carcases immediately after hide removal and at the end of all slaughter floor operations after any processing interventions, and to establish Australian beef and veal baseline data. Carcase sponge samples (n = 5452) were collected from different beef and veal processing establishments throughout Australia. The results are summarised in Table 6. The MLA report concluded that Australian beef and veal carcases have a low prevalence of *Salmonella* and that Australian dressing procedures in export processing establishments were effective in terms of reducing *Salmonella* detection and the microbiological load on the carcases.

The larger area sampled for the beef (4,000 cm^2) and veal (2,000 cm^2) carcases in the MLA survey, complicates direct comparison with the results obtained in Australia's national *Escherichia coli* and *Salmonella* Monitoring Program (ESAM) during that time period (300 cm^2). Comparison of the results of the MLA survey (summarised in Table 6) and the FSIS collection program was hindered by differences in the method of sampling and the reporting of results. However, in general, Australian produced beef and veal carcases had a lower prevalence level of *Salmonella* and generic *E. coli*. FSIS reported that the percentage of *Salmonella*-positive beef carcases was 27.12% at post-hide-removal and 3.36% at pre-chill (FSIS, 2016a). The percentage of beef carcases positive for generic *E. coli* was 75.75% at post-hide-removal and 13.82% at pre-chill (FSIS, 2016a). While for veal, FSIS reported that the percentage of *Salmonella*-positive carcases was 12.04% at post-hide-removal and 1.82% at pre-chill (FSIS, 2016a). The percentage of veal carcases positive for generic *E. coli* was 70.44% at post-hide-removal and 32.48% at pre-chill (FSIS, 2016a).

Table 6*:* Results from beef and veal sponge samples collected from Australian export establishments (MLA, 2017a)[a]

	Post-hide Removal				Pre-chilling			
	Beef		Veal		Beef		Veal	
	FQ	HQ	FQ	HQ	FQ	HQ	FQ	HQ
TVC Median (cfu/cm^2)	2.29 (0.36)[b]	4.17 (0.60)	12.88 (1.11)	17.38 (1.24)	0.81 (-0.09)	1.00 (0.00)	8.91 (0.95)	9.12 (0.96)
E. coli prevalence	32.9%	43.7%	47.0%	75.0%	15.6%	14.0%	39.5%	53.9%

	Post-hide Removal				Pre-chilling			
	Beef		Veal		Beef		Veal	
	FQ	HQ	FQ	HQ	FQ	HQ	FQ	HQ
E. coli Median (cfu/cm^2)	0.01 (-2.00)[b]	0.01 (-2.00)	0.09 (-1.06)	0.13 (-0.90)	0.01 (-2.00)	0.01 (-2.00)	0.01 (-1.90)	0.04 (-1.43)
Salmonella prevalence[c]	17/1318 (1.29%)	18/1317 (1.37%)	0/40 (0%)	3/40 (7.5%)	6/1329 (0.45%)	3/1331 (0.23%)	1/37 (2.7%)	0/39 (0%)

[a] Samples were collected from the hindquarter (HQ) and forequarter (FQ) of beef and veal carcases by sponging designated areas. Beef HQ and FQ has an assumed surface area of 4000 cm^2, whereas veal HQ and FQ have an assumed are of 2000 cm^2 per carcase quarter. For beef carcases, the limit of detection was -1.2 $\log_{10}$ (0.063 cfu/cm^2) for the total viable count (TVC), -2.2 $\log_{10}$ (0.0063 cfu/cm^2) for *E. coli* and -2.2 $\log_{10}$ (0.0063 cfu/cm^2) for *Salmonella*. For veal, the limits of detection were; TVC (-0.9 $\log_{10}$ = 0.12 cfu/cm^2), *E. coli* (-1.9 $\log_{10}$ = 0.012 cfu/cm^2) and *Salmonella* (-1.9 $\log_{10}$ = 0.012 cfu/cm^2).

[b] $\log_{10}$ cfu/cm^2

[c] *Salmonella* serovars isolated from beef carcases in the survey post-hide removal were: *S.* Hvittingfoss, *S.* Bredeney, *S.* Muenster, *S.* Adelaide, *S.* Infantis, *S.* subspecies II serotype: 42:g,t-, *S.* Poona, *S.* Bovismorbificans, *S.* Typhimurium, *S.* Senftenberg, *S.* Havana, *S.* Anatum, *S.* Oranienburg, *S.* Chester, *S.* Cerro. While *Salmonella* serovars isolated from beef carcases in the survey pre-chilling were: *S.* subspecies 1 serotype: 16:l,v:-, *S.* Tennessee, *S.* Zanzibar, *S.* Mbandaka, *S.* Havana, *S.* Dublin. *Salmonella* serovars isolated from veal carcases in the survey post-hide removal were: *S.* Chailey, *S.* Havana and *S.* St Paul. *Salmonella* serovars isolated from veal carcases in this survey pre-chilling were: *S.* Chailey.

2.3.3.1.2 Survey of STEC in beef and veal cattle faeces

Mellor et al. (2016) undertook a national survey of STEC serotypes O26, O45, O103, O111, O121, O145, and O157 in Australian beef cattle faeces (Mellor et al., 2016). The survey involved collection of 1,500 faecal samples at slaughter from adult (*n* = 628) and young (*n* = 286) beef cattle, adult (*n* = 128) and young (*n* = 143) dairy cattle, and veal calves (*n* = 315) across 31 Australian export-registered processing establishments, representing more than 85% of the annual beef production for export in Australia. Samples were collected from 5 February to 20 March and from 6 August to 25 September in 2013. Most establishments (87%) provided samples on both sampling occasions. Pathogenic STEC (pSTEC; isolates that possess *stx*, *eae*, and an O antigen marker for O157, O26, O45, O103, O111, O121 or O145) were isolated from 115 samples (7.7%), of which 100 (6.7%) contained *E. coli* O157, and 19 (1.3%) contained serotype O26, O45, O103, O111, O121 or O145. Four of the 115 samples contained multiple pSTEC serotypes. Among samples confirmed for non-O157 pSTEC serotypes (O26, O45, O103, O111, O121 and O145), 15 (1%) contained *E. coli* O26 and 4 (0.3%) contained *E. coli* O111. pSTEC of serotypes O45, O103, O121, and O145 were not isolated from any sample. Analysis of animal classes revealed a higher pSTEC prevalence in younger animals, including veal (12.7%), young beef (9.8%), and young dairy (7.0%), than in adult animals, including adult beef (5.1%) and adult dairy (3.9%). The authors concluded that the findings of their study suggest that Australian cattle are a potential reservoir for pSTEC serotypes O26 and O111. The lack of isolation of serotypes O45, O103, O121, and O145 suggests that these serotypes are not present, are uncommon, or are present in levels too low to detect in Australian cattle faeces. Mellor et al. (2016) state that their pSTEC prevalence results are comparable to those previously reported for cattle faecal (Barlow & Mellor, 2010; Delphine Bibbal et al., 2015; D. Bibbal et al., 2014; Hofer, Stephan, Reist, & Zweifel, 2012; Joris, Pierard, & De Zutter, 2011; Monaghan et al., 2011) and ground beef (Bosilevac & Koohmaraie, 2011) samples but lower than their past estimates of *E. coli* O157 in Australian cattle (Barlow & Mellor, 2010; Fegan, Vanderlinde, Higgs, & Desmarchelier, 2004). Although the prevalence of *E. coli* O157 in their study is comparable to those observed in other countries (Elder et al., 2000; García, Fox, & Besser, 2010; Masana et al., 2010; Omisakin, MacRae, Ogden, & Strachan, 2003), the rate reported represents an increase from their 2008 survey (1.7%) (Barlow & Mellor, 2010) but a reduction from values reported in 2004 (13%) (Fegan et al., 2004). Mellor et al. (2016) state that while the exact cause of this variation is unclear from their results, previous studies have correlated

the prevalence of STEC with multiple factors, including animal age, seasons, herds, rainfall, production types, and feed types.

2.3.3.1.3 Survey of the microbiological status of lymph nodes of cattle at slaughter

Salmonella contamination of ground beef has been viewed as originating from the surface of carcases. Recent studies have identified lymph nodes as a potential source of *Salmonella* contamination because these tissues play an active role in containment of pathogens in the live animal and because some lymph nodes are unavoidably present in manufacturing beef trimmings or primal cuts that may be incorporated into ground beef. Bailey et al. (2017) conducted a survey of the microbiological status of lymph nodes from Australian cattle at the time of slaughter to determine the prevalence of microbiological contamination (Bailey, Huynh, Govenlock, Jordan, & Jenson, 2017). Samples were collected from five processing facilities, one in each of the states of Queensland, New South Wales, Victoria, Tasmania, and South Australia. Sets of lymph nodes (n = 197) were collected from five abattoirs over a period of 14 months from October 2015 to December 2016. The 197 sets of lymph nodes collected contained only 1,464 individual nodes, owing to the difficulty of locating nodes and excising them from carcases while they were being processed. Samples were tested for the presence of *Salmonella* spp. and STEC by BAX PCR assay. Aerobic plate count, *E. coli*, and coliforms were enumerated with a lower limit of detection of 80 cfu per node. The observed prevalence of *Salmonella* within peripheral lymph nodes was 0.48% (7/1,464), which was notably lower than the prevalence of *Salmonella* spp. observed in similar studies (Arthur et al., 2008; Brichta-Harhay et al., 2012) reporting prevalences of 1.6 and 0.80%. The seven *Salmonella* isolates came from six different animals and from five different lots of animals. In six of seven nodes, the maximum possible *Salmonella* level was below the limit of detection of 80 cfu per node. Grass-fed, grain-fed, and cull dairy cattle were all found to have detectable *Salmonella* in lymph nodes. All *Salmonella* detections occurred during cooler months of the year. Aerobic microorganisms were detected above the limit of quantification in 3.2% of nodes (median count 2.24 log per node), and *E. coli* was detected in 0.8% of nodes (median count 3.05 log per node). No STEC were detected on enrichment. The authors concluded that overall bovine lymph nodes in Australian slaughter-age cattle are not likely to contain *Salmonella* and are unlikely to add significantly to the *Salmonella* burden of ground beef produced from Australian manufacturing beef.

2.3.3.2 International risk assessments

Tesson et al. (2020) conducted a systematic review of beef meat Quantitative Microbiological Risk Assessments (QMRAs) (Tesson et al., 2020). A total of 2343 articles were collected and 67 were selected for inclusion in their study. The authors collated the beef QMRA models to identify steps of the farm-to-fork chain considered, analyse inputs and outputs included, modelling methods adopted and to identify future challenges. The collated studies focused mainly on western countries and considered Enterohemorrhagic *Escherichia coli* (EHEC) and *Salmonella*. Tesson et al. (2020) reported that collected studies tended to emphasize the main contribution of contamination at the farm level, with contaminated faeces or hide, to the chilling of the carcase, and the contaminations associated with carcase dehiding, evisceration, or splitting. These findings led the authors to encourage risk managers to focus on these steps on the farm and at the slaughterhouse.

2.3.4 Sheep

2.3.4.1 National surveys

2.3.4.1.1 Survey of lamb and sheep faeces for STEC, *Salmonella* and *Enterococcus*

MLA (2019) funded a large national survey on the prevalence and concentration of key foodborne pathogens from sheep faeces at slaughter (MLA, 2019). A total of 14 Australian sheepmeat processors participated in the survey, collectively representing 65% of total Australian lamb production and 83% of total Australian mutton production. The survey comprised 800 faecal samples, collected weekly throughout two sampling windows (400 samples per window), with the first sampling window occurring over an 11-week period between September and November 2017 and the

second over a 19-week period between February and July 2018. The 800 sampled animals were sourced from five states; NSW (34%), VIC (26%), WA (15%), SA (20%), QLD (0.75%) and unknown origin (4.5%), representing more than 200 different postcodes. Samples were tested for the presence of Shiga toxin-producing *E. coli* serogroups O26, O45, O103, O111, O121, O145 and O157 (Top 7 STEC), *Salmonella*, *Enterococcus* and generic *E. coli*. A summary of the results of the survey are in Table 7. Of the Top 7 STEC recovered from 28 of the 800 samples processed (3.5%); 27 samples contained STEC O157 (3.4%), two samples contained STEC O26 (0.3%), with one sample containing both O157 and O26. Top 7 STEC serogroups O45, O103, O111, O121, and O145 were not isolated from any sample. Counts of STEC O157 were generally low with 17 of the 27 samples (63%) containing O157 at concentrations less than 1 $\log_{10}$ MPN/g faeces. The remaining samples contained O157 at 1 (n = 1), 1.7 (n = 1), 1.8 (n = 2), 2.3 (n = 1), 3.3 (n = 2), 3.7 (n = 2) and 6.3 (n = 1) $\log_{10}$ MPN/g of faeces. The two STEC O26 isolates were present at 0.15 and 3.0 $\log_{10}$ MPN/g faeces. Characterisation data showed that STEC O157 isolates most often possess *stx1a* and *stx2c* toxin subtypes (72%), which places them into level 3 of the risk classification scheme proposed by the Joint Food and Agriculture Organization (FAO)/World Health Organization (WHO) Meetings on Microbiological Risk Assessment (JEMRA) and is consistent with the predominant *stx* subtypes observed in Australian cattle populations. The risk classification scheme proposed by JEMRA consists of a set of criteria which includes 5 risk levels (where 1 is the highest and 5 is the lowest) based on virulence gene combinations and the estimated potential to cause diarrhoea, bloody diarrhoea and haemolytic uraemic syndrome (HUS) (JEMRA, 2018). The remaining O157 isolates were shown to possess *stx1a* alone (16%; JEMRA level 4) and *stx2c* alone (12%; JEMRA level 3). The two O26 isolates possessed a single toxin type, *stx1a* (JEMRA level 4), which is also consistent with the predominant profile observed in Australian cattle isolates. The results indicate that Australian sheep are a potential reservoir for STEC O157 and O26; however, the very low prevalence of STEC O26 and lack of isolation of other Top 7 STEC suggests that these serogroups are uncommon, or not present in Australian sheep populations. The authors concluded that the prevalence of Top 7 STEC and *Salmonella* from sheep are consistent with previous Australian surveys of beef cattle.

Table 7: Prevalence and concentration of key foodborne pathogens from sheep faeces at slaughter. Data summarised from MLA (2019).

Microbiological analyses	**Pasture-fed lamb (*n* = 414)**	**Feedlot lamb (*n* = 163)**	**Sheep (*n* = 223)**	**Total (*n* = 800)**
Top 7 STEC prevalence (% detection)	2.4%	4.3%	4.9%	3.5% (28/800)
Salmonella prevalence (% detection)	7.5%	4.3%	19.3%	10.1% (81/800)
Salmonella mean count ($\log_{10}$ MPN/g faeces)	0.4	0.9	0.6	Not recorded
E. coli (% detection)	Not recorded	Not recorded	Not recorded	96%

Microbiological analyses	Pasture-fed lamb (*n* = 414)	Feedlot lamb (*n* = 163)	Sheep (*n* = 223)	Total (*n* = 800)
Enterococcus (% detection)	Not recorded	Not recorded	Not recorded	98%
Enterococcus faecium (% detection)	Not recorded	Not recorded	Not recorded	5.3% (42/800)
Enterococcus faecalis (% detection)	Not recorded	Not recorded	Not recorded	4.3% (34/800)

2.3.4.1.2 Survey of lamb mincemeat for *T. gondii*

Dawson et al. (2020) undertook a survey of *T. gondii* contamination in a total of 79 lamb mincemeat parcels from a supermarket in South Australia over a defined six-month period in 2017. Samples were subjected to PCR testing and the probability of *T. gondii* contamination of the meat product was conservatively estimated at 43% (Dawson et al., 2020). It is important to note that each mincemeat parcel product is sourced from multiple (15-20) animals and therefore does not reflect the prevalence of *T. gondii* in these animals (Dawson et al., 2020). This study did not include an assessment of viability.

2.3.5 Pig meat

2.3.5.1 National Surveys

2.3.5.1.1 Survey of pig faeces for *Salmonella*

Weaver et al. (2017) investigated *Salmonella* shedding in five pig herds located in two southern states of Australia (Weaver et al., 2017). Pooled faecal samples were collected quarterly in 2014 and 2015. *Salmonella* was detected in 43% of samples, which is comparable to data from the U.S.A in which *Salmonella* was reported to be present in pig faecal samples at a prevalence level of 50% in sows and 35% in market swine (FDA, 2017). Weaver et al. (2017) reported that when *Salmonella* was cultured, multiple colonies were characterized by serotyping and where *S.* Typhimurium-like serovars were confirmed, isolates were further characterized by phage typing and multiple locus variable number tandem repeat analysis (MLVA). Multiple *Salmonella* serovars were detected in each of the study herds, as has commonly been reported elsewhere. *Salmonella* 1,4,[5],12:i- was one of several serovars that persisted within the herds. Monophasic variants of *S.* Typhimurium with the serotype 1,4,[5],12:i:- have risen to international prominence due to increasing isolation and implication in human disease (CDC, 2016; Gossner et al., 2012; Mossong et al., 2007; Nguyen, 2014). Pigs have been identified as a major reservoir of *S.* Typhimurium 1,4,[5],12:i:- in Europe (Hauser et al., 2010; Hopkins et al., 2010). Weaver et al. (2017) reported that virtually all *S.* Typhimurium 1,4,[5],12:i:- isolates were phage type 193, but exhibited 12 different, closely-related MLVA profiles. *Salmonella* Typhimurium 1,4,[5],12:i:- diversity within herds was low and MLVA profiles were stable indicating colonization throughout the herds and suggesting each farm had an endemic strain. This study reported persistent, high levels of *S.* Typhimurium 1,4,[5],12:i:- PT193 shedding among pig herds destined for slaughter in five independent production systems, thereby identifying a potential hazard source in the Australian food chain.

2.3.5.1.2 Survey of pig caeca for *E. coli* and *Salmonella*

Kidsley et al. (2018) undertook a national survey to investigate the occurrence of AMR among commensal *E. coli* and *Salmonella* spp. isolated from caecal specimens obtained using a systematic-random sampling method from healthy Australian finisher pigs at slaughter (Kidsley et al., 2018). Samples were collected from 19 farms distributed throughout Australia during July-December 2015. Not surprisingly, *E. coli* was isolated from all caecal samples collected (*n* = 201). *Salmonella* spp. were recovered from caecal samples from 14 of the 19 (73.7%) farms sampled. The overall prevalence of *Salmonella* in caeca was 34% (69/201), which is comparable to a similar Italian survey reporting a prevalence level of 34.64% (*n* = 306) (Pesciaroli et al., 2017) and a survey conducted in Northern Ireland reporting a prevalence level of 31.4% (*n* = 513) (McDowell, Porter, Madden, Cooper, & Neill, 2007). Kidsley et al. (2018) did not further characterise any isolates or enumerate pathogen levels. There have been no surveys to characterise STEC contamination of Australian pork meat since the work of Hamilton et al. (2011), which was cited in the previous meat risk assessment (NSW Food Authority, 2014). Hamilton et al. (2011) reported that STEC were not detected in sow meat (*n* = 101), sausages (*n* = 116) or mince (*n* = 148) (Hamilton et al., 2011).

2.3.5.1.3 Survey of sow hearts for *T. gondii*

Hodgson et al. (2017) undertook a study to estimate the prevalence of *T. gondii* in sow meat from Western Australia (WA) (Hodgson, Tan, Torok, Holds, & Hamilton, 2017). The sampling strategy was based on the numbers of sows required for a national baseline survey (a minimum of 300 samples would be required to give 95% confidence in a national prevalence estimate) using a randomised sampling framework and pig numbers proportional to annual production. Western Australia has 12% of the Australian sow population resulting in a total sample of 40 sow hearts from six free range and 14 intensive farms in WA. *T. gondii* DNA was detected in two samples from different intensive indoor production herds, resulting in an estimated prevalence of *T. gondii* in sow hearts from WA of 5%. An earlier pilot study using the same methodology estimated the prevalence in sow hearts (*n* = 92 from 62 herds) from south-eastern Australia at 9.8%. Combined, the prevalence of *T. gondii* in sow hearts was estimated to be 8.3%, with no statistically significant difference between the prevalence estimates for WA and south-eastern Australia. These studies did not include an assessment of viability.

2.3.5.1.4 Survey of HEV in wild-caught and commercial pigs

The presence of HEV in Australian pigs was first noted in 1999 by a study that used an in-house assay and reported seropositivity rates of 17% (15/59) in wild-caught pigs and 92-95% in commercial pigs by 16 weeks of age in two piggeries (*n* = 45) (Chandler, Riddell, Li, Love, & Anderson, 1999). Chandler et al. (1999) concluded that their study indicated that swine HEV infection may be widespread in Australian commercial piggeries and in wild pigs. To date, no further studies investigating the epidemiology of HEV in Australian pigs appear to have been conducted.

2.3.5.2 International surveys of STEC, *Salmonella* and HEV

Jung et al. (2019) undertook a survey of intact and non-intact raw pork collected at retail stores in the mid-Atlantic region of the U.S.A for the seven regulated serogroups of STEC (O26, O45, O103, O111, O121, O145, or O157:H7) (Jung et al., 2019). A total of 514 pork samples (395 ground or non-intact and 119 intact samples), representing 60 brands, were purchased at 107 retail stores between July and December 2017. The results of the survey revealed that none of the 514 retail raw pork samples were positive for any of the seven regulated serogroups of STEC. Four of 514 raw pork samples harboured *E. coli* of unknown serogroup (i.e. none of these isolates displayed the serogroup-specific O-antigens for the seven regulated serogroups of STEC) and contained *stx* and *eae*. Therefore, these isolates would or could probably cause human illness if the raw pork was not properly cooked, handled, or stored. For these reasons, the authors suggested that efforts should be made to determine the specific serotype of these isolates to ascertain whether these serotypes have caused human illnesses from pork or other foods. The authors concluded that the seven regulated serogroups of STEC are uncommon in retail raw pork samples in the U.*S.* mid-Atlantic region.

Essendoubi et al. (2020) undertook a study to determine the prevalence of STEC O157:H7 in colon content and on carcases from pigs slaughtered at provincially licensed abattoirs in Alberta, Canada (Essendoubi et al., 2020). In 2017, carcase sponge samples and colon content samples were collected from 504 healthy market hogs at thirty-nine abattoirs. The respective prevalence of *E. coli* O157:H7 on carcase swabs and colon content was 1.8% (9/504) and 1.4% (7/504). These positives were found in 12.8% (5/39) of the abattoirs, from hogs originating from eight farms. The *E. coli* O157:H7 isolates recovered from the positive samples (1 isolate per sample) were clonal, as determined by pulsed-field gel electrophoresis (PFGE). All these strains were reported to harbour *eae* and *ehxA*, and were of *stx*2a subtype, suggesting that swine can carry *E. coli* O157:H7 of importance to human health. Essendoubi et al. (2020) concluded that the results of their study supported the idea that while the incidence of *E. coli* O157:H7 on pork carcases is low, it is still present and, if not well controlled, during processing and handling could result in foodborne illness. In contrast with the very few outbreaks of *E. coli* O157:H7 involving pork products globally, there have been three major outbreaks associated with pork products in Alberta in the last 5 years (2014, 2016 and 2018) (Alberta Health Service, 2018; Honish et al., 2017). The outbreak in 2014 had 115 laboratory-confirmed cases, representing the second largest foodborne *E. coli* O157 outbreak in Canadian history (Honish et al., 2017). The outbreak in 2018 had 42 laboratory-confirmed cases and one fatality likely related to the *E. coli* O157:H7 infection (Alberta Health Service, 2018).

In a study undertaken by Scott et al. (2020) in the U.S.A, the FSIS conducted a baseline study from June 2017 through to May 2018 to characterize and determine the prevalence of *Salmonella* and assess the occurrence of STEC in a variety of raw pork products (Scott et al., 2020). In total, 4,014 samples from slaughter and processing establishments were analysed for *Salmonella*; a subset of these samples (1,395) from slaughter establishments were also analysed for STEC. Analyses determined that the national prevalence of *Salmonella* in raw pork products was highest in comminuted products (28.9%), followed by intact cuts (5.3%) and non-intact cuts (3.9%). Of the 545 isolates recovered from the 4,014 samples analysed, 52 distinct *Salmonella* serotypes were represented. The top five serotypes were Anatum at 13.8% (75/545), Infantis at 13.0% (71/545), Johannesburg at 9.0% (49/545), Derby at 8.6% (47/545), and 1,4,[5],12:i:- at 6.0% (33/545). Less than 1% of samples analysed were positive for the top seven STEC. Of the 1,395 samples analysed for STEC, 3 (0.2%) were positive, 2 were positive for *E. coli* O103, and 1 was positive for *E. coli* O157. All were recovered from comminuted pork products. The authors concluded that their findings indicate there is a need for additional pathogen reduction strategies for raw pork products.

Domestic pigs are the main animal reservoirs of HEV worldwide (EFSA Panel on Biological Hazards et al., 2017). Published surveys have reported on the detection and prevalence of HEV antibodies in pig populations and HEV RNA in swine faeces, bile, liver, serum and muscles from swine sampled across various stages of the production chain in multiple countries. Where studied, very high seroprevalence of HEV antibodies in pig populations has been reported around the world (EFSA Panel on Biological Hazards et al., 2017). In New Zealand, HEV seroprevalence was 91% in commercial herds (20/22) (Garkavenko et al., 2001). In a recent survey of HEV in pigs from slaughterhouses in the U.S.A from 2017–2019, approximately 40% of pigs were seropositive for HEV, indicating prior HEV infection of the pigs on the farms (Sooryanarain et al., 2020). Despite the relatively high seropositivity, a small proportion (6%) of the pigs had detectable HEV viremia (Sooryanarain et al., 2020). Sooryanarain et al. (2020) proposed that this is likely because HEV viremia is transient and the window for detecting HEV RNA in serum is narrow. Active HEV infection occurs naturally in most farm pigs around 2 months of age (Huang et al., 2002; Meng et al., 1997). Therefore, most market-weight pigs >6 months of age at the time of slaughter are no longer actively infected by HEV. Nevertheless, studies have shown that 5.7% of UK (Grierson et al., 2015), and 44.4% of Scotland (Crossan et al., 2015) slaughterhouse market-weight pigs were viremic. In Europe, EFSA (2017) reviewed information on the occurrence and control of HEV and stated that a proportion of pigs, likely to be less than 10%, remain viraemic at slaughter and are a probable cause of prime meat cuts containing HEV (EFSA Panel on Biological Hazards et al., 2017).

A limited number of studies have reported on the detection of HEV in retail pork cuts and pork products. Mykytczuk et al. (2017) surveyed various brands of pork pâté, raw pork sausages, and raw pig livers collected from local grocery stores in Canada (Mykytczuk, Harlow, Bidawid, Corneau, & Nasheri, 2017). Overall, HEV was detected in 47% of the pâtés (36/76) and 10.5% of the pork livers (2/19) sampled. No HEV was detected in the raw pork sausages screened (*n* = 35). Mykytczuk et al. (2017) concluded that the prevalence of HEV in pâtés in their study (47%) was in agreement with reports of pork products in other developed countries (Berto et al., 2013; Di Bartolo, Angeloni, Ponterio, Ostanello, & Ruggeri, 2015; Di Bartolo et al., 2012; Szabo et al., 2015; Barbara Wilhelm et al., 2014), and is representative of the overall HEV infection in the swine herds used for manufacturing pâtés. Failure to detect HEV RNA in the screened sausages was hypothesised to be due to a number of factors including a low amount of liver in the making of the sausages, low virus recovery rates, varying amounts of fat and salt concentrations, and/or to the food processing procedures (Mykytczuk et al., 2017). In an earlier Canadian survey of HEV on retail pork chops and pork livers, 5.7% of liver (16/283) and no pork chop (0/599) samples contained detectable HEV by quantitative real-time polymerase chain reaction (qRT-PCR) assay (B. J. Wilhelm et al., 2016). Wilhelm et al. (2016) reported that their finding that pork chops had reduced odds of HEV detection, is consistent with studies in swine which identify the liver as a site having the longest duration of viral detection and greatest load during infection (de Deus et al., 2008; Leblanc, Poitras, Gagné, Ward, & Houde, 2010). In the Netherlands, Boxman et al. (2019) assessed the presence of HEV RNA in liver and pork products (Boxman et al., 2019). HEV RNA was detected in 27.3% of 521 products sampled from Dutch retail stores. A total of 12.7% of livers were positive for HEV RNA (*n* = 79), 70.7% of liverwurst (*n* = 99), 68.9% of liver pâté (*n* = 90), but in none of the pork chops (*n* = 98) and fresh sausages (*n* = 103). It should be noted that these retail surveys include products such as liverwurst and liver pâté, which may undergo heat treatment sufficient to inactivate HEV. Therefore, the detection of HEV in these products is not necessarily indicative of viable virus that could be transmissible.

2.3.6 Goat meat

2.3.6.1 National surveys

2.3.6.1.1 Survey of goat faeces for *Salmonella*

The Australian goat-meat industry is dominated by rangeland goats, which are typically unmanaged (undomesticated) and opportunistically captured and utilised for meat production (Al-Habsi, Jordan, et al., 2018). *Salmonella* and *Campylobacter* occur naturally in the gut as commensals, and infections are often asymptomatic (Al-Habsi, Yang, et al., 2018). A study undertaken in Western Australian (WA) investigated the rate of faecal carriage of *Salmonella enterica* recovered from rangeland goats (Al-Habsi, Jordan, et al., 2018). A total of 400 faecal samples were collected at slaughter from four consignments of goats (100 samples per consignment), each from one of four localities in WA. The overall rate of detection of *Salmonella* faecal carriage was 26.5% (106/400), with faecal carriage in the four consignments ranging between 23–30%. The serotypes detected were Typhimurium (84.9%), Chester (10.4%) and Saintpaul (4.7%). The rate of faecal carriage of *Salmonella* was high (26.5%), but comparable to a previous study that observed 26% *S.* enterica faecal carriage in rangeland goats on arrival at a feedlot (Al-Habsi, Yang, et al., 2018). Survey results cited in the previous Risk Assessment (2014), reported that *Salmonella* was detected in the faeces (46.3%), rumen samples (45.5%) and on carcases (28.9%) of 121 free-ranging feral goats destined for slaughter at 2 Australian abattoirs (L. Duffy, Barlow, Fegan, & Vanderlinde, 2009). Duffy et al. (2009) also reported that the three *S.* enterica serovars identified in the study by Al-Habsi, Jordan, et al. (2018) (Typhimurium, Chester and Saintpaul), were the dominant serotypes detected in their study [Saintpaul (31%), Typhimurium (13%) and Chester (11%)].

2.3.6.1.2 Survey of goat faeces for *Campylobacter*

Al-Habsi, Yang, et al. (2018) reported on the faecal carriage of *Campylobacter* spp. of rangeland goats (*n* = 125) captured from a rangeland grazing property in WA (Al-Habsi, Yang, et al., 2018). Faecal samples were collected from

each goat immediately after arrival at a commercial goat depot (feedlot). *Campylobacter* spp. were identified in 8% of samples and all *Campylobacter*-positive samples were identified as *C. jejuni*.

2.3.6.2 International surveys of *E. coli* O157, *Salmonella* and *Campylobacter*

Hanlon et al. (2018) undertook a study to evaluate the presence of *Salmonella*, *Campylobacter* and *E. coli* O157 in goat faeces and, the presence of *Salmonella* and *E. coli* O157 found on hides (Hanlon et al., 2018). Faecal samples were obtained from abattoirs (California, Texas and New Mexico) and farms (Bahamas, Mexico, California and Texas). Sampling of goat faeces revealed the presence and rate of faecal carriage of *Salmonella* (10.3%), *E. coli* O157 (19.7%) and *Campylobacter* (71.0%). Hide samples were collected from goats at small (1–30 animals per day) and large (800–1200 animals per day) sized abattoirs located in California, New Mexico, and Texas. On goat hides, *Salmonella* was detected on 3.3% of samples and *E. coli* O157 was present on 1.7% of samples. The study did not quantify organism presence at any point in time. The rate of faecal carriage of *Salmonella* reported by Hanlon et al. (2018) is much lower than those rates reported in Australian studies (Al-Habsi, Jordan, et al., 2018; Al-Habsi, Yang, et al., 2018; L. Duffy et al., 2009). While the rate of faecal carriage of *Campylobacter* reported by Hanlon et al. (2018) is much higher than the rate reported in the Australian study by Al-Habsi, Yang, et al. (2018). The differences observed may be due to a number of factors, including the effect of region, environmental factors and production practices. While no recent Australian studies could be found on the presence of *E. coli* O157 in goat faeces and on hides, the results reported by Hanlon et al. (2018) are comparable to survey work cited in the previous Risk Assessment (2014) by Jacob et al. (2013). In an American study, Jacobs et al. (2013) reported prevalences of 11.1%, 2.7%, and 2.7%, in the faeces, on hides and carcases of meat goats, respectively (Jacob, Foster, Rogers, Balcomb, & Sanderson, 2013). While a study in the United Arab Emirates by Al-Ajmi et al. (2020) reported a much lower carriage rate of *E. coli* O157 at 2% of 150 faecal samples of goats collected from the slaughterhouse (Al-Ajmi, Rahman, & Banu, 2020).

2.3.7 Chicken meat

2.3.7.1 National surveys

2.3.7.1.1 NSW Food Authorities poultry verification program

Campylobacter and *Salmonella* are the principal pathogens of concern found on poultry meat. In January 2015, the NSW Food Authority commenced a new annual microbiological testing program for raw poultry. This program was introduced due to the commencement of Standard 4.2.2 Primary production and processing standard for poultry meat, the increased growth of the poultry industry in NSW and the inherent food safety risks associated with the poultry industry. The program involves the collection of raw poultry samples from processing facilities and retailers in NSW for subsequent testing for *Campylobacter* and *Salmonella*. One of the aims of this program is to gather ongoing data on the prevalence and levels of these organisms so that any changes can then be analysed and the effect of the introduction of the Standard can be monitored. Prior to the commencement of Standard 4.2.2 Primary production and processing standard for poultry meat, NSW participated in two baseline surveys that were led by FSANZ. A baseline survey of the microbiological quality of chicken portions and carcases at retail in two Australian states was conducted from 2005 to 2006 (Pointon et al., 2008). A baseline survey on the prevalence and concentration of *Salmonella* and *Campylobacter* in chicken meat on-farm and at primary processing was conducted in 2008 and published in 2010 (FSANZ/SARDI, 2010). Results of the two baseline surveys and the last 5 years of data collected in the NSW Food Authority poultry verification surveys are summarised in Table 8. The key findings were:

- Compared to the baseline data, prevalence of *Salmonella* has been reduced at both processing plants and retail. The prevalence was the lowest in 2017-18 and increased in 2018-19 but remained below the baseline levels.
- The prevalence of *Campylobacter* remains high for samples collected from both processing plants and retail.

- The concentration of *Salmonella* and *Campylobacter* in retail portions (for positive samples) remained low but at levels higher than found in the baseline study. However, the proportion of portions samples with concentrations of *Salmonella* and *Campylobacter* above the limit of detection was low.
- The concentrations of *Salmonella* and *Campylobacter* in carcase samples collected from processing plants remained at much higher levels than found in retail portions. However, the proportion of carcase samples with concentrations of *Salmonella* and *Campylobacter* above the limit of detection was low.
- The prevalence of *E. coli* in samples collected from processing plants has been reduced and has remained low. However, the concentration for positive samples collected as part of the verification program remains higher than the baseline data for samples collected from both processing plants and at retail.

In the poultry verification survey, serotyping was undertaken on one isolate per *Salmonella*-positive sample. *S.* Abortusovis, of which human infections with this serovar appear to be very rare, was most frequently isolated from the processing plant (2015-2016, 2016-2017, 2017-2018, 2018-2019) and retail (2014-2015, 2016-2017, 2017-2018). Non-pathogenic *S*. Sofia was the most frequently detected serovar in samples from the processing plant in 2014-2015 and at retailers in 2015-2016. *S.* Typhimurium has been detected in samples taken from processing plants (2014-2015) and retailers (2014-2015, 2015-2016, 2016-2017, 2017-2018) and was the most isolated serovar at retailers in 2018-2019.

2.3.7.1.2 National surveys of chicken meat and offal

Abraham et al. (2019) undertook a survey of all major chicken-meat producers in Australia. A total of 200 pooled caecal samples, each consisting of five composite caeca, were collected between June and November 2016 (Abraham et al., 2019). Samples were collected from twenty poultry abattoir plants owned by seven commercial companies that process approximately 11 million chickens per week, representing 95% of Australian chicken meat production. *Salmonella* spp. was recovered from 53 pooled samples (26.5%) with twelve different serotypes. The most frequent serovar was *S.* Sofia (34.0%), followed by *S.* Abortusovis (15.1%), *S.* Adelaide (15.1%), and *S.* Typhimurium (7.6%).

Walker et al. (2019) studied the prevalence and distribution of *C. coli* and *C. jejuni* in a variety of fresh and frozen meat and offal (giblet and liver) products collected from retail outlets in NSW, QLD and VIC (Walker et al., 2019). Chicken product was identified as either conventionally farmed or free range. Chicken meat samples were collected from Australian supermarkets and butcher shops over a 2-year sampling period (October 2016 to October 2018) and included breast, drumstick, Maryland (thigh and drumstick), thigh, wing and whole bird products. In total, 785 samples of chicken (meat and offal) were tested for *Campylobacter* spp. Walker et al. (2019) reported that the prevalence of *Campylobacter* on chicken meat was 84% in NSW, 90% in QLD and 96% in VIC. The prevalence of *Campylobacter* on chicken offal was slightly lower, 83% in NSW, 65% in QLD and 88% in VIC. However, it is important to note that Walker et al. (2019) state that a limitation of their study was that samples collected in NSW, QLD and VIC were processed independently by their respective NATA accredited laboratories. As described by Walker et al. (2019), this may lead to some differences in procedure by state and therefore direct comparisons between the survey results for each state should be made with caution. Individual chicken meat portions ranged in prevalence from 73 to 100%. Whole chicken carcases had a lower prevalence of *Campylobacter* than most meat cuts across the three jurisdictions, whereas thighs and wings had the highest prevalence. Although retail chicken meat was frequently contaminated with *Campylobacter*, the level of contamination was generally low. Where quantitative analysis was conducted, 98% of chicken meat samples, on average, had <10,000 cfu *Campylobacter* per carcase, with 10% <21 cfu per carcase. Higher levels of contamination were observed on whole bird samples, where 11% of samples positive for *Campylobacter* spp. had >10,000 cfu per carcase detected. All (100%) of the drumstick, Maryland, and wing samples positive for *Campylobacter* spp. had <10,000 cfu per carcase detected. However, a small proportion of chicken product, particularly whole bird (10%), thigh (5%), and breast (3%), had levels of *Campylobacter* that exceeded the

current FSANZ microbiological target (<10,000 cfu per carcase) for raw chicken meat before distribution. Reducing bacterial load below this target would limit the risk of campylobacteriosis to consumers. Chicken products from poultry raised using conventional farming methods were found to have a lower prevalence of *Campylobacter* spp. compared with poultry that were reared free range. Conventionally farmed fresh prepacked chicken product (300/361, 83.1%) had a lower prevalence of *Campylobacter* compared with fresh prepacked chicken product farmed by free range (144/159, 90.6%). *Campylobacter coli* was the most frequently recovered species in chicken meat collected in NSW (53%) and VIC (56%) and in chicken offal collected in NSW (77%), QLD (59%) and VIC (58%).

The prevalence of *Campylobacter* spp. on chicken meat reported by Walker et al. (2019) for three Australian states (84% in NSW, 90% in QLD and 96% in VIC), is comparable to the prevalence data reported by the NSW Food Authority in the poultry verification surveys (80-100% in processor samples and 70-89.9% in retailer samples) (Table 8). Walker et al. (2019) report that their results are comparable with other Australian reports (83 to 95.8%) (L. L. Duffy, Blackall, Cobbold, & Fegan, 2014; FSANZ/SARDI, 2010; King & Adams, 2008; Pointon et al., 2008), but are higher than that in surveys from Canada, the United Kingdom and the United States (75, 73.3, and 46.6%, respectively) (Bohaychuk et al., 2006; FSIS, 2008; Jorgensen, Madden, Arnold, Charlett, & Elviss, 2015). In discussing the results of their quantitative analysis, in which 2% of chicken meat samples had >10,000 cfu *Campylobacter* per carcase, Walker et al. (2019) state that their findings are relatively consistent with those of Habib et al. (2019). Habib et al. (2019) reported that 18.7% of retail chicken samples from Western Australia (WA) had >20,000 cfu per carcase (Ihab Habib, Coles, Fallows, & Goodchild, 2019).

The NSW Food Authority undertook a survey of poultry livers from supermarkets and butchers between March 2015 and December 2016 (NSW Food Authority, 2018a). The prevalence of *Campylobacter* in chicken livers was very high, with a total of 96% of the individual livers testing positive for *Campylobacter* (*Campylobacter* was detected both externally and internally in 88% of samples). This result was similar to a New Zealand (NZ) study (Whyte, Hudson, & Graham, 2006) which found 90% of livers tested had internalised *Campylobacter*. A Scottish study which only examined external prevalence found 81% of poultry livers purchased at retail were positive for *Campylobacter* (Strachan et al., 2012). In the NSW Food Authority survey *Campylobacter* was detected at the level of greater than 10^3 cfu/ml in 12.3% of the surface of chicken livers tested (NSW Food Authority, 2018a). This result was lower than a NZ study (Whyte et al., 2006) which found 30% of chicken liver surfaces sampled had greater than 1.1 x10^3 cfu/sample, but higher than a UK study (Firlieyanti, Connerton, & Connerton, 2016) which found 2.8% of retail chicken liver surfaces had *Campylobacter* greater than 10^3 cfu/g. As for the *Campylobacter* level inside the chicken liver, the NSW Food Authority survey revealed that 1.6% of samples had *Campylobacter* at the level of greater than 10^3 cfu/g (NSW Food Authority, 2018a). This result is similar to the findings from the NZ and the UK studies which found 6% and 4.6% of samples had *Campylobacter* levels of greater than 10^3 cfu/g inside the chicken livers, respectively (Firlieyanti et al., 2016; Whyte et al., 2006).

2.3.7.2 International risk assessments and studies on risk reduction

Dogan et al. (2019) undertook a farm-to-fork quantitative microbial risk assessment (QMRA) of *Campylobacter* in broiler chickens, to evaluate processing interventions in the U.S.A (Dogan, Clarke, Mattos, & Wang, 2019). Dogan et al. (2019) concluded that the results of their study indicate that consumer education is a critical factor in reducing the risk of foodborne illnesses, as undercooking was the most important input parameter affecting the risk estimates of their model. Processing operations were also found to be crucial for the safety of the final product and to reduce the overall disease burden, with the prevention of faecal-leakage (cloacal plugging) and the use of chemical processing aids offering the most promising results in terms of efficacy.

González et al. (2019) developed a risk-based prioritization framework to rank chicken meat processing interventions that achieve the greatest *Salmonella* relative risk reduction in the U.S.A (González, Sampedro, Feirtag, Sánchez-Plata, & Hedberg, 2019). Results showed the combination of chlorine at the bird wash station and peroxyacetic acid at

the on-line reprocessing and chill stages as the most common processing scenario in the U.S.A. Irradiation at packaging and acidified sodium chlorite at evisceration were the most effective single processing interventions (98.8 and 91.6% risk reduction, respectively); however, no single intervention was able to comply with the current FSIS *Salmonella* postchill performance standards. The combination of peroxyacetic acid in at least one of the chicken processing stages with the current set of baseline interventions achieved >99% *Salmonella* relative risk reduction and ensured FSIS compliance. Adding more than one intervention to the current practice did not enhance (<2%) the overall *Salmonella* risk reduction.

EFSA recently published an update and review of control options for *Campylobacter* in broilers at primary production (EFSA Panel on Biological Hazards et al., 2020). The specific aims of the review were to identify and rank the possible control options at the primary production level and where possible, to quantify the expected efficiency in reducing human campylobacteriosis cases. The median values of the relative risk reduction of the eight prioritised control options were judged to be as follows; vaccination 27%; feed and water additives 24%; discontinued thinning 18%; employing few and well-trained staff 16%; avoiding drinkers that allow standing water 15%; addition of disinfectants to drinking water 14%; hygienic anterooms at the broiler house entrance 12%; designated tools per broiler house 7%. Not surprisingly, it was noted that multiple control activities would be expected to have a higher effect preventing *Campylobacter* spp. from entering the broiler house and infecting the birds.

Table 8: Data obtained in baseline surveys and the NSW Food Authorities poultry verification program

Point of sampling	Microorganisms	Type of product[1]	Parameter[2]	Baseline data	2014-15 data	2015-16 data	2016-17 data	2017-18 data	2018-19 data
Processing plant	SPC	carcase	Mean	2.52	3.58	3.09	3.02	2.65	2.16
	E. coli	carcase	Prevalence	96.3%	32.6%	36.2%	17.1%	6.7%	8.0%
		carcase	Mean	0.55	2.00	1.86	1.43	1.14	1.79
	Salmonella	carcase	Prevalence	48.4%	33%	19%	17.1%	10%	16.1%
		carcase	No. with levels ≥ LOD (%)	-	6 (22.2%)	5 (10.6%)	2 (5.7%)	0	2 (2.3%)
		carcase	Mean	-	3.17	3.63	2.15	-	2.45
	Campylobacter	carcase	Prevalence	95.1%	88.9%	100%	85.7%	96.7%	89.7%
		carcase	No. with levels ≥ LOD (%)	-	7 (25.9%)	14 (29.8%)	8 (22.9%)	7 (23.3%)	11 (12.6%)
		carcase	Mean	4.07	3.94	4.37	4.39	4.60	4.68

Point of sampling	Microorganisms	Type of product[1]	Parameter[2]	Baseline data	2014-15 data	2015-16 data	2016-17 data	2017-18 data	2018-19 data
Retail	SPC	skin-on	Mean (SD)	5.66 (1.14)	5.86 (0.91)	5.62 (1.09)	4.76 (1.35)	5.10 (1.20)	5.34 (1.13)
		skin-off	Mean (SD)	5.64 (1.17)	5.55 (1.03)	5.31 (1.08)	4.67 (1.29)	5.22 (1.32)	5.06 (1.33)
	E. coli	skin-on & skin-off	Mean (SD)	0.60 (0.85)	1.68 (0.56)	1.72 (0.58)	1.53 (0.58)	1.35 (0.40)	1.53 (0.47)
	Salmonella	skin-on & skin-off	Prevalence	47.7%	20%	23%	25.3%	10.8%	25.8%
		skin-on & skin-off	No. with levels ≥ LOD (%)	-	10 (4.8%)	18 (6.0%)	4 (1.4%)	0	4 (1.3%)
		skin-on & skin-off	Mean	0.66	1.63	1.68	1.38	-	1.60
	Campylobacter	skin-on & skin-off	Prevalence	87.8%	70%	84%	87%	89.5%	89.9%
		skin-on & skin-off	No. with levels ≥ LOD (%)	-	10 (4.8%)	20 (6.7%)	24 (8.3%)	32 (10.8)	19 (6.4%)
		skin-on & skin-off	Mean	0.96	1.20	1.32	1.51	1.53	1.52

[1] Carcase means whole chicken. Skin-on means chicken portions with the skin still attached e.g. drumsticks, wings and marylands. Skin-off means chicken portions with skin removed from the products e.g. breast fillets, thigh fillets, lovely legs and tenderloins.

[2] All mean values were calculated from samples with enumeration results only. The limit of detection (LOD) for *E. coli* is 10 cfu/cm^2. The LOD for *Salmonella* for carcases is 65 cfu/carcase and for portions is 13 cfu/100cm^2. The LOD for *Campylobacter* for carcases is 5000 cfu/carcase and for portions is 10 cfu/cm^2.

2.3.8 Game meat

As game meat animals are not husbanded like farmed animals and are legally slaughtered in a wild state, controls cannot be applied in the primary production stages which include feed, water and the environment (FSANZ, 2013b). The microbiological condition of meat obtained from large game animals and birds will depend upon the types of microorganisms carried by each species, on the hide, in the gastro-intestinal tract, or in the muscle tissue itself; the circumstances in which the creature is killed; and the conditions under which the carcase is dressed and butchered (Gill, 2007). The 2014 meat Risk Assessment (NSW Food Authority, 2014) included results of a microbiological survey of game meats (Boar, Buffalo, Emu, Kangaroo, Rabbit, Venison) in NSW retail outlets conducted by the NSW Food Authority between 11/2011 and 06/2012. Based on the Australian Meat Standards Committee guidelines, 68% of all samples were classified under the marginal category for TVC and 18% marginal for *E. coli* counts. A review of the published literature revealed that since this time, no other microbiological surveys have been conducted on Australian game meat animals or retail game meat products. The National Carcase Microbiological Monitoring program (NCMMP) (formerly the ESAM program), is performed by all export registered meat establishments (including wild game meat and meat processing establishments) and requires Aerobic Plate Count (APC) and *E. coli* (process control verification), and *Salmonella* testing (pathogen reduction), to verify slaughtering and chilling operations. While the NCMMP would capture data for exported wild game meat species, such as kangaroo and wild boar, the data is not publicly available.

Aside from bacterial hazards, a recent review of diseases and pathogens of invasive animals in Australia (DEDJTR, 2016) identified a wide range of pathogenic viruses, parasitic helminths and protozoa that may present additional food safety and human health risks. However, relevant studies are scarce on the prevalence and concentration of pathogens in live game meat animals and to what extent their presence may result in contamination of meat cuts. While there are significant knowledge gaps, a number of the viruses and parasites identified in the report (DEDJTR, 2016) may be of particular concern in food products where wild game meat is consumed raw (e.g. uncooked comminuted fermented meat). Further discussion on these hazards in relation to UCFMs, can be found below in Section 2.3.9.1.

2.3.9 Processed meat products

Processed meat is defined in Clause 76 of the Food Regulation 2015 as:

a meat product intended for human consumption that contains not less than 300 grams per kilogram of meat, where the meat has undergone a method of processing other than boning, slicing, dicing, mincing or freezing, and includes cured or dried meat flesh in whole cuts or pieces.

UCFMs are discussed in Section 2.3.9.1, in light of recent queries from NSW manufacturers who are seeking approval to produce products in a manner which may introduce microbial hazards capable of causing foodborne illness.

2.3.9.1 UCFMs

UCFM products are traditionally made with farmed beef or pork, for which the UCFM production process can reduce the level of key foodborne bacterial pathogens to an acceptable level to ensure food safety. Recently, the NSW Food Authority has experienced an increase in the number of applications from UCFM manufacturers seeking approval to produce products containing wild game meats. In comparison to the farmed meat species typically used to make UCFMs (e.g. beef and pigs), wild game species are not subject to the same husbandry practices and may harbour complex parasite communities and zoonotic viruses (Bordes & Morand, 2011; DEDJTR, 2016). As UCFM products are not cooked, any harmful microorganisms present in the raw materials and/or the processing environment could survive and/or grow to cause illness. Unlike bacteria and viruses, the infective unit for parasites varies (e.g. tissue cyst, oocyst, egg). Important determinants of parasite viability include the parasite species and its developmental stage, as well as

characteristics of the specific food matrix (e.g. meat species/fat content) (Franssen et al., 2019). Therefore, control measures need evaluation for specific parasites and food commodity contexts (FAO/WHO, 2014; Franssen et al., 2019). Any NSW business producing UCFM products must complete a production process pro forma, which is a written description of the steps used to make a particular product. The NSW Food Authority will review the pro forma and must provide approval before manufacture can begin. If a UCFM manufacturer would like to use a different type of meat (i.e. other than beef or pork), the approval process will take longer, as a literature review and risk assessment will need to be conducted for the specific type of meat species to be used and to assess the microorganisms that may be present (NSW Food Authority, 2020g). There will also be additional conditions (e.g. raw meat testing, additional RTE meat testing) imposed upon the approval of the UCFM process (NSW Food Authority, 2020g).

The NSW Food Authority has also received an increase in the number of enquiries from UCFM manufacturers wanting to remove nitrate/nitrite from their UCFM products. Sodium nitrate and sodium nitrite have been used in meat products as curing agents and preservatives for centuries. However, nitrate is seldom used today because it must be converted to nitrite to be effective, which is a slow process achieved by microbial reductase. Nitrite, in combination with salt and pH, is used in cured meats to ensure their safety with respect to a number of pathogens including *Clostridium botulinum*. Spores formed by *Cl. botulinum* are ubiquitous in the environment and ensuring complete absence from meat during the slaughter process is impossible to achieve with current technologies. To cause illness, spores of *Cl. botulinum* must germinate, grow and produce neurotoxin. The botulinum neurotoxins are the most potent poisons known, and foodborne botulism may be caused by consuming as little as 50 ng of neurotoxin (Michael W. Peck & van Vliet, 2016). Botulinum toxins block nerve functions and can lead to respiratory and muscular paralysis. While botulism poisoning is rare, because of its severe, debilitating symptoms and relatively high mortality rate of approximately 5–10% of cases (M.W. Peck, 2006), it remains a major hazard. To prevent foodborne botulism, it is necessary to destroy spores, or prevent spore germination, cell multiplication and neurotoxin formation. The removal of nitrite can be likened to the removal of a hurdle to the growth of *Cl. botulinum*. To maintain the safety of the food, another similar hurdle must be used to replace nitrite or otherwise the 'height' of the remaining hurdles has to be increased to prevent *Cl. botulinum* from growing. Unless manufacturers take preventive measures to inactivate *Cl. botulinum*, or to inhibit its growth and toxin production, botulism outbreaks could occur. To date, no effective single replacement material has been identified as an alternative to nitrite. If a UCFM manufacturer would like to remove nitrate/nitrite from their product, they must conduct a full validation of the new preservation system in their product/s (NSW Food Authority, 2020g). The alternative process must be approved by the NSW Food Authority before products can be manufactured for sale (NSW Food Authority, 2020g).

2.3.10 Chemicals in meat

Sulphur dioxide (SO_2) is a chemical used as a preservative and colour fixative in some foods. It is permitted in controlled doses in certain products such as sausages but is not permitted at all in raw meat cuts or minced meat. Some people, particularly asthmatics, are sensitive to SO_2. When ingested it may trigger typical asthma symptoms. Due to this, its use in foods is strictly controlled by the Food Standards Code. Standard 1.3.1 of the Code permits the use of SO_2 in sausage and sausage meat to a maximum of 500 mg/kg. Raw meat however is not permitted to contain any SO_2. To assess compliance during audits of licensed retail meat businesses, meat samples may be subjected to a field test for SO_2. Samples taken during audits are usually raw meat samples that have failed a field test for sulphur dioxide (SO_2) which is not permitted in raw meat (SO_2 is permitted in sausages). If a field test is positive, a three-part sample is then taken and submitted to a NATA accredited laboratory for SO_2 analysis.

Sulphur dioxide test results of raw meat samples collected from retail premises by the NSW Food Authority and submitted to a NATA accredited laboratory for SO_2 analysis, are shown in Table 9. Across the 5 years for which SO_2 test results are shown, a total of 160 samples were collected, of which 83% (132/160) tested positive. The samples which tested positive for the presence of SO_2 displayed a large range in concentration (13 - 5,000 mg/kg).

Occasionally, sausage samples are also submitted for analysis to ensure that any SO_2 present is below the maximum permitted level. From July 2015 to June 2016, 172 sausages were tested for SO_2 as part of a targeted project and during audits. A total of 37 samples (22%) had SO_2 levels above the maximum level permitted, with the concentration of SO_2 ranging from 510 to 2700 mg/kg. A survey was also carried out across 2013 to 2014 and continued throughout 2014 to 2015, in which 29 samples of sausages and mince were tested. Six sausage samples were found to be non-compliant. From July 2018 to June 2019, nine samples of sausages and/or sausage meat were taken during audit and submitted for SO_2 analysis. Of these samples, 33% (3/9) had values in excess of the maximum permitted level, with concentrations ranging from 870 to 3,200 mg/kg.

Table 9: Sulphur dioxide (SO_2) test results of raw meat samples collected from retail premises by the NSW Food Authority

	Year of sampling[a]				
	2014 - 2015	**2015 - 2016**	**2016 - 2017**	**2017 - 2018**	**2018 - 2019**
Audits of licensed retail meat businesses	1,032	2,755	1,206	1,177	1,598
Samples tested	61 samples	30 samples from 8 butchers	17 samples from 8 butchers	21 samples from 10 butchers	31 samples from 14 butchers
Positive samples	43	29	15	17	28 samples from 13 butchers
SO_2 range (mg/kg)	15 – 1,900	36 – 1,400	40 - 700	65 - 5,000	13 - 3,600

[a] In all years sampling was conducted within the financial year (July – June), apart from 2014-2015 in which sampling was conducted from October 2014 to June 2015.

2.3.11 Recalls and import border failures for meat and meat products

Analysis of consumer level recalls and imported foods which failed inspection and testing requirements at Australia's borders, provides some information on the foods and safety hazards that do or could enter the food supply from either domestic or imported food sources and pose a health risk. Information on consumer level recalls of meat and meat products in Australian States and Territories can be accessed on the FSANZ website (FSANZ, 2020). Table 10 lists consumer level recalls between the 17/10/2015 and 15/10/2020 due to the presence of microbial contamination, foreign material and issues around food safety checks and labelling. Where further information has since come to light on the source of microbial contamination of any recalled food item and meat is not the suspected source, the recalled food item has been excluded from Table 10. Food recalls due to the presence of undeclared allergens were also excluded from Table 10. The presence of pesticide, veterinary and other residues in red meat and poultry meat, could cause allergic reactions in sensitized individuals. However, chemical hazards are well controlled at primary production under existing regulatory and non-regulatory measures (see Section 2.1.1.2). Between the 17/10/2015 and 15/10/2020, fourteen recalls were due to microbial contamination and six recalls were due to the presence of foreign material, such as plastic (n = 2), metal (n = 2), rubber (n = 1) and bone fragments (n = 1). A further two recalls were due to incorrect best before dates on the product label and routine food safety checks being unable to verify the safety of the manufacturing process for the products in question. Recalls involving potential microbial contamination of meat were due to *L. monocytogenes* (n = 9), *Salmonella* (n = 1), *E. coli* (n = 1), unidentified microbial contaminants (n = 2) and a potential/unconfirmed microbial contaminant (n = 1). Recalls due to *L. monocytogenes* contamination occurred

in German sausages (*n* = 3), ham (*n* = 2), frozen meals (*n* = 2), silverside (*n* = 1) and chicken liver pâté (*n* = 1). The recall involving *Salmonella* was due to pork pies. The recall involving *E. coli* was due to chorizo. Recalls due to an unidentified microbial contaminant were due to hotdogs (*n* = 1) and paunch (lamb stomach) (*n* = 1). The recall due to a potential/unconfirmed microbial contaminant involved German sausages (*n* = 1).

Table 10: Consumer level recalls of meat and meat products in Australia from 17/10/2015 to 15/10/2020[a]

Date	Location	Product	Outlet type	Reason
28/8/2020	VIC and NSW	Chicken Wurst	Supermarkets, retailers	*L. monocytogenes* contamination
27/8/2020	SA	Leberwurst	Retailers	*L. monocytogenes* contamination
3/8/2020	QLD	Beef sausages	Retailer	Foreign material (plastic)
24/1/2020	SA	Mettwurst	Supermarkets, retailers	Potential microbial contamination
27/11/2019	SA	Mettwurst	Supermarkets	*L. monocytogenes* contamination
20/9/2019	NSW, ACT, QLD and SA	Frozen meals	Meals on Wheels and community organisations	*L. monocytogenes* contamination
22/5/2019	NSW, QLD, VIC and WA	Sweet Chilli Chicken Kiev	Supermarkets	Foreign material (blue rubber)
22/3/2019	SA	Frozen meals	Meals on Wheels SA	*L. monocytogenes* contamination
21/12/2018	NSW, QLD, VIC and WA	Bone-in Ham Half Leg	Butcher, retailer	*L. monocytogenes* contamination
11/10/2018	SA	Silverside	Supermarkets	*L. monocytogenes* contamination
6/04/2018	National	Frozen Sweet Chilli Chicken Breast Tenders	Supermarkets	Foreign material (plastic)
5/12/2017	National	Skinless Hot Dogs	Supermarkets	Microbial contamination and foreign material (bone fragments)
15/09/2017	NSW and QLD	Chorizo	Supermarkets	*E. coli* contamination
21/03/2017	SA	Pork Pie	Butchers, retailers	*Salmonella* contamination

Date	Location	Product	Outlet type	Reason
18/11/2016	QLD	Paunch (lamb stomach)	Butchers	Microbial contamination
8/11/2016	National	Frozen meals	Direct to consumers	Foreign material (metal)
14/10/2016	NSW	Fresh pork, lamb and beef mince	Supermarket	Foreign material (metal)
23/09/2016	VIC and SA	Mettwurst and Pepperoni	Supermarkets, retailers	Routine food safety checks being unable to verify the safety of the manufacturing process for these products
11/03/2016	NSW, ACT, QLD, VIC, TAS, SA and NT	Chicken Liver Pâté	Supermarkets	*L. monocytogenes* contamination
25/01/2016	NSW, ACT, QLD, VIC and SA	Ham	Supermarkets	*L. monocytogenes* contamination
13/01/2016	NSW	Chicken Meatballs (Chilled)	Supermarkets	Incorrect best before dates on the label

[a] Data accessed from the FSANZ website (FSANZ, 2020)

Meat and meat products are imported under strict import rules and are inspected under the Imported Food Inspection Scheme (IFIS) (IFIS, 2020). To ensure imported food meets food safety requirements, products must be covered by a recognised foreign government certificate and are subject to microbiological verification testing. Meat and meat products are tested against a published list of potential hazards, including microorganisms and contaminants, which can be found on the DAWE website (DAWE, 2020c). Reports of imported foods that fail inspection and testing requirements under the IFIS are published on the DAWE website (DAWE, 2020a). Reports between January 2014 to August 2020 revealed ten imported meats and meat products that failed inspection and testing requirements (Table 11). The majority of failures (7/10, 70%) were due to *L. monocytogenes* contamination of ham originating from Spain (n = 6) or Italy (n = 1). This correlates with the findings of the previous meat risk assessment (NSW Food Authority, 2014), where the most common reason for failure of imported meat and meat products from 2010 to March 2014 was the presence of *L. monocytogenes* in ham products (11/27, 41%). Between January 2014 to August 2020, two failures were due to *L. monocytogenes* contamination of prosciutto originating from Italy (Table 11). One failure was due to the presence of an antibiotic (enrofloxacin) in a boneless pork product from the U.S.A (Table 11).

Table 11: Imported meats and meat products that failed inspection and testing requirements from January 2014 to August 2020[a]

Date of fail	Product description	Country of Origin	Test failed
22/11/2018	Boneless pork	U.S.A	Enrofloxacin 0.003mg/kg
2/02/2017	Jamon serrano ham	Spain	*L. monocytogenes*
18/10/2016	Whole deboned ham	Italy	*L. monocytogenes*
12/10/2015	Spanish serrano dry cured ham	Spain	*L. monocytogenes*
4/12/2014	Prosciutto	Italy	*L. monocytogenes*
11/12/2014	Serrano ham	Spain	*L. monocytogenes*
9/09/2014	Serrano ham	Spain	*L. monocytogenes*
1/07/2014	Prosciutto	Italy	*L. monocytogenes*
30/05/2014	Jamon serrano ham	Spain	*L. monocytogenes*
27/02/2014	Sliced iberico ham	Spain	*L. monocytogenes*

[a] Data for Failing Food Reports accessed from the DAWE website (DAWE, 2020a)

2.4 Risk characterisation

2.4.1 Beef, sheep, pig and goat meat

There have been a number of recent microbiological surveys of domestically reared cattle (Bailey et al., 2017; Mellor et al., 2016; MLA, 2017a), sheep (MLA, 2019), pig (Kidsley et al., 2018; Weaver et al., 2017) and goats (Al-Habsi, Jordan, et al., 2018). These surveys generally reveal a low prevalence and/or concentration of key foodborne pathogens, or results that are lower than or equivalent to comparable domestic and international reports. The survey results indicate that when processed under existing standards, these meat species present a low risk to public health. This is also supported by foodborne illness reports in NSW from 2013 to 2018 (Communicable Diseases Branch, 2014a, 2015, 2016, 2017, 2018, 2019).

However, it is important to recognise that outbreak data represents a small proportion of actual cases of foodborne illness, many outbreaks go unrecognised and/or unreported to health authorities. Of those cases which are reported, a variety of methods exist for pathogen characterisation to assist outbreak investigations. In NSW, whole genome sequencing (WGS) has been used to routinely sequence clinical and environmental isolates of *S.* Typhimurium, *S.* Enteritidis and *L. monocytogenes*. The discriminatory power of WGS for pathogen characterisation is unrivalled, making it possible to detect more outbreaks with fewer cases and to link human illness to specific foods or production environments with greater confidence than ever before. Australian epidemiological approaches for STEC surveillance are currently confined to conventional serotyping and therefore the ability to differentiate sporadic infections from potential point-source outbreaks is limited (Dallman et al., 2015; Ingle et al., 2019). Currently, human-associated

STEC isolates in Australia are sent for serotyping and detection of Shiga toxin(s) to a national reference laboratory for epidemiological typing (Microbiological Diagnostic Unit Public Health Laboratory, MDU PHL). In total, 435 human clinical STEC isolates were received at the MDU PHL for serotyping and detection of Shiga toxin(s) between 1 January 2007 and 31 December 2016 (Ingle et al., 2019). Ingle et al. (2019) reported that the most common serotypes reported amongst the 435 Australian human clinical STEC isolates were O157 (234/435, 54%), O26 (48/435, 11%) and O111 (31/435, 7%). None of the human clinical isolates belonged to serotype O45 and there was a low representation of serotypes O103 (2/435, 0.5%), O121 (1/435, 0.2%) and O145 (1/435, 0.2%). Detailed epidemiological data for each of the 435 cases was not available (Ingle et al., 2019). However, like other countries, the main reservoirs of STEC in Australia are healthy ruminants, particularly cattle. The dominance of the O157, O26 and O111 serotypes amongst Australian clinical isolates reported by Ingle et al. (2019), correlates with survey results describing the presence of STEC O157, O26 and O111 in Australian beef faeces (Mellor et al., 2016) and O157 and O26 in Australian sheep faeces (MLA, 2019). As proposed by Ingle et al. (2019), a national WGS approach to the characterisation of STEC during public health surveillance and outbreak investigations, would enhance our understanding of STEC epidemiology. While previous studies indicate that the incidence and burden of disease due to STEC and HUS in Australia appears comparable to or lower than similar developed countries (Rivas et al., 2015; Vally et al., 2012), an enhanced understanding of the risk of STEC illness from consumption of Australian meat could provide information enabling the optimisation and/or adoption of new prevention and control efforts to drive further improvements in food safety.

Overall the evidence suggests that Australian meat from domestically reared cattle, sheep, pig and goats, has a low microbial load and generally low prevalence of pathogens. However, continued baseline monitoring of the prevalence of foodborne pathogens in the meat production environment is necessary to ensure that existing prevention and control efforts remain adequate to mitigate food safety risks and to monitor for emerging hazards. A recent study of particular relevance to the pork industry, was the first report of persistent, high levels of *S.* Typhimurium 1,4,[5],12:i:- PT193 shedding in five independent production systems (Weaver et al., 2017). The global prevalence of *S.* Typhimurium 1,4,[5],12:i:- has increased considerably in recent years, indicating the emergence of this strain, particularly on pig farms (Tassinari et al., 2019). A study by Rajtak et al. (2012) demonstrated the superior ability of this serotype to survive in this environment, by revealing that isolates of *S.* Typhimurium 1,4,[5],12:i:- were associated with long-term survival in pig faeces compared to other serotypes (Rajtak, Boland, Leonard, Bolton, & Fanning, 2012). It has also been proposed that persistently high rates of shedding of *S.* Typhimurium 1,4,[5],12:i:- PT193 might increase the bacterial load introduced into the slaughter facility and its concomitant potential to establish as resident flora (Kawakami et al., 2019). Pork has been identified as a principal *S.* Typhimurium 1,4,[5],12:i:- reservoir and source of foodborne outbreaks in Europe and, more recently, in the United States (Elnekave et al., 2018; Nguyen, 2014; Self, Luna-Gierke, Fothergill, Holt, & Vieira, 2017). Outbreaks of *S.* Typhimurium 1,4,[5],12:i:- have also been linked to consumption of beef, lamb and poultry products (CDC, 2018; Imanishi et al., 2014), indicating that this serotype has a wide host range. Weaver et al. (2017) concluded that *Salmonella* I 4,[5],12:i: has emerged recently in Australia and has likely spread widely. However, the nature of emergence, via parallel evolution or introduction, and time frame requires further investigation (Weaver et al., 2017). In the previous meat risk assessment (NSW Food Authority, 2014), *S.* Typhimurium 1,4,[5],12:i:- PT 193 was discussed as the cause of an outbreak in Victoria in 2011 and a homemade pork salami was attributed as the food responsible. Of note, in Australia in 2017 *S.* Typhimurium 1,4,[5],12:i:- was responsible for the fifth highest number of *Salmonella* notifications in NSW (133 cases, 4% of all serotypes of *Salmonella* in 2017), up 36% from the previous year (Communicable Diseases Branch, 2018). Subsequently in 2018, *S.* Typhimurium 1,4,[5],12:i:- was responsible for the fourth highest number of *Salmonella* notifications in NSW (137 cases, 4% of all serotypes of *Salmonella* in 2018), up 2% from the previous year (Communicable Diseases Branch, 2019). Further insight into other possible meat and poultry sources of *S.* Typhimurium 1,4,[5],12:i:- in Australia, may help focus preventative strategies along the primary production pathway to

prevent *S.* Typhimurium 1,4,[5],12:i:- entering into the human food chain. The Australian National University (ANU), in collaboration with others, is currently conducting a source attribution analysis for *Salmonella* infections acquired in NSW between January 2008 and August 2019. This work may shed more light on whether other meat and poultry sources play a role in foodborne transmission of *S*. Typhimurium 1,4,[5],12:i:-.

Also of relevance to the pork industry, Australia recently experienced its first recorded local HEV outbreak, which was linked to consumption of pork liver pâté. The presence of HEV in Australian pigs was first noted over 20 years ago and it was proposed at this time that swine HEV infection may be widespread in Australian commercial piggeries and in wild pigs (Chandler et al., 1999). Currently there is no commercially available vaccine for HEV and infected animals often do not show symptoms of infection; therefore, they can be sent for slaughter and contaminated organs and meat will enter the food supply chain (EFSA Panel on Biological Hazards et al., 2017). Recently published risk profile and risk assessment studies on HEV in pigs and pork meat conducted in Switzerland (Müller, Collineau, Stephan, Müller, & Stärk, 2017) and Canada (B. Wilhelm, Fazil, Rajić, Houde, & McEwen, 2017), identified specific data gaps requiring additional information for any future full and complete risk assessment. Firstly, there is a lack of information with regard to the infectious dose of HEV or the dose–response relationship. The HEV dose-response is likely to vary individually, especially if co-morbidities such as pre-existing liver disease are present. There is also a lack of data available on the prevalence and load of HEV in pork products, which may vary geographically according to pig husbandry. There are also gaps in knowledge concerning the survival of HEV in food matrices such as RTE raw meat products containing pork or pork liver. To improve the accuracy of data for risk assessments, internationally standardized HEV PCR assays are also needed, that specifically target infectious virus (EFSA Panel on Biological Hazards et al., 2017; Müller et al., 2017). Methodologies that allow for the detection, characterisation and quantification of HEV and the prevalence of HEV in relevant farm stock and their importance as a source of foodborne infection, will assist in informing the most appropriate risk mitigation measures needed to control HEV transmission from food animals and food to humans. Presently, the only efficient control option for HEV infection from consumption of meat, liver and products derived from animal reservoirs is sufficient heat treatment (EFSA Panel on Biological Hazards et al., 2017). EFSA (2017) reported that in Europe the level of awareness of HEV risk associated with pig meat products and other reservoirs and sources is low, so dissemination of information and advice to consumers and those working with potential sources of infection should be optimised. This is especially likely to be the case in Australia, as this country has not experienced the number of locally acquired cases of HEV infection observed in Europe. At the time of the HEV outbreak in Australia, a media release was issued urging the public to cook pork products thoroughly and, in particular, to cook pork livers to 75°C at the thickest part for 2 minutes (Yapa et al., 2016). A useful initiative for future prevention of HEV infections would be the implementation of education campaigns, especially for the meat industry and butcheries and for consumers within risk groups. Provision of information on the risk of consumption of raw or undercooked pork products to vulnerable groups may help prevent the most serious HEV infections. Vulnerable groups and host risk factors include those with a weakened immune system, pre-existing liver disease, diabetes and those using immunosuppressive medication and gastric acid inhibitors (EFSA Panel on Biological Hazards et al., 2017; Tulen, Vennema, van Pelt, Franz, & Hofhuis, 2019).

Foodborne transmission is considered to be the main mode for transmission of *T. gondii* to humans (EFSA Panel on Biological Hazards et al., 2018). Ingesting raw or undercooked meat contaminated with *T. gondii* oocysts and tissue cysts is a major source of infection for humans (Guo et al., 2015). Recent surveys of *T. gondii* in Australian sow meat (Hodgson et al., 2017) and lamb mincemeat (Dawson et al., 2020) indicate that consuming raw or undercooked products of these meat species may be a risk factor for toxoplasmosis. The incidence and prevalence of toxoplasmosis in Australia is difficult to estimate, as toxoplasmosis is not a notifiable disease and mostly asymptomatic (FSANZ, 2014). In a 1979 review of previous epidemiological surveys conducted across five Australian states, it was estimated that there was a 30% mean population prevalence of *T. gondii* serum antibody amongst the human population (Johnson, 1979). While there is considerable variation in the reported seroprevalence of toxoplasmosis in

different countries, this figure is in keeping with estimates that up to one-third of the human population is infected with *T. gondii* (Montoya & Liesenfeld, 2004). The estimated annual median number of hospitalisations and deaths caused by domestically acquired foodborne *T. gondii* in Australia, circa 2010, was estimated to be 30 and 1 respectively (Kirk et al., 2014). Disease-burden estimates due to *T. gondii* infections in various countries have demonstrated the overall high public health impact of toxoplasmosis (EFSA Panel on Biological Hazards et al., 2018). In the U.S.A, after *Salmonella*, *T. gondii* is the pathogen responsible for contributing to the second highest percentage (24%) of domestically acquired foodborne illnesses resulting in death (CDC, 2018a). Currently there are no control methods for Toxoplasma available during meat inspection (EFSA Panel on Biological Hazards et al., 2018). Visual meat inspection cannot identify tissue cysts in the tissues of infected animals as they are normally only identifiable by microscopy (EFSA Panel on Biological Hazards et al., 2018). Recently, the Codex Alimentarius amended the general guidelines for the control of food-borne parasites in food, describing some basic concepts of food hygiene throughout the food chain, but guidelines for testing food-producing animals or specific food products for *T. gondii* are not yet in place. Despite the high number of studies estimating *T. gondii* prevalence through serology and/or direct detection of the parasite in animal samples, there is disagreement about the relative importance of different food animal species (Belluco et al., 2016). However, general messaging may be helpful to educate consumers on the risks related to consumption of rare or undercooked meat, which applies particularly to pregnant women, the elderly and immunocompromised persons (Dawson et al., 2020). In these groups, the infection is accompanied by more severe complications, such as encephalitis, retinochoroiditis, foetus abortion, splenomegaly and pneumonitis. While in immunocompetent people, *T. gondii* infection is mostly asymptomatic or results in non-specific flu-like symptoms, connection has been documented between certain mental health disorders, especially schizophrenia. Infection with atypical *T. gondii* strains can also be fatal in immunocompetent adults (Carme, Demar, Ajzenberg, & Dardé, 2009).

2.4.2 Chicken meat

2.4.2.1 Chicken meat

Results of the poultry verification surveys conducted over the last four years by the NSW Food Authority, indicate that the prevalence of *Salmonella* has been reduced at both the processing plant and retail level. However, the prevalence of *Campylobacter* remains high for samples collected from processing plants and retail. Results of the poultry verification surveys also indicated that while the concentration of *Salmonella* and *Campylobacter* in portions (for positive samples) remained low, that levels were higher than in the baseline study conducted from 2005 to 2006 (Pointon et al., 2008). The results of these surveys indicate that further improvements could be achieved through a focus on pathogen control during primary processing (live chickens entering the slaughterhouse through to chilling of the carcase) and secondary processing stages (cutting, portioning and deboning of carcases for sale as pieces). While the results of the foodborne illness reports in NSW from 2013 to 2018 (Communicable Diseases Branch, 2014a, 2015, 2016, 2017, 2018, 2019) do not indicate that poultry was responsible for a high level of foodborne outbreaks, as discussed previously, it is well established that outbreak data only represents a small proportion of actual cases of foodborne illness. *Campylobacter* is the most frequently notified enteric pathogen under surveillance by OzFoodNet with 141.5 cases per 100,000 population reported in 2019 (DoH, 2020b), making Australian rates of campylobacteriosis amongst the highest in developed countries (Wallace et al., 2020). Despite the variety of exposures to *Campylobacter*, there is a broad scientific agreement that poultry meat is a major transmission vehicle, and most probably the leading vehicle, in most countries for campylobacteriosis (NSW Food Authority, 2018a). A number of research projects have recently been undertaken in Australia, which aim to apply genomics, epidemiology, and source attribution modelling to identify locally relevant risk factors and sources to reduce human illness from *Campylobacter* (Moffatt et al., 2020; Varrone, Glass, Stafford, Kirk, & Selvey, 2020; Varrone et al., 2018; Walker et al., 2019). Walker et al. (2019) undertook a study to investigate the prevalence and distribution of *Campylobacter* species in a variety of fresh and frozen meat and offal products collected from retail outlets in NSW, QLD and VIC. The results

of the survey by Walker et al. (2019) in relation to poultry samples, were previously discussed in section 2.3.7.1.2. While the results of the survey revealed a high prevalence level of *Campylobacter* spp. in chicken meat (90%) and chicken offal products (giblet and liver) (73%), there was a significantly lower prevalence in lamb (38%), pork (31%) and beef (14%) offal (kidney and liver) (Walker et al., 2019). While Moffatt et al. (2020) reviewed the national register of enteric and foodborne disease outbreaks to summarize data on all *Campylobacter* outbreaks reported in Australia between 2001 and 2016. Moffatt et al. (2020) identified 84 *Campylobacter* outbreaks and after review of evidence data, 23 outbreaks (27%) were determined to have an unknown route of transmission. Foodborne or suspected foodborne transmission accounted for 61% (51/84) of outbreaks, of which a food vehicle was identified for 65% (33/51) of these outbreaks (Moffatt et al., 2020). Poultry meat or offal was implicated in 85% (28/33) of these outbreaks (Moffatt et al., 2020). Collectively the findings of these research projects show that poultry is a primary source of human *Campylobacter* infection in Australia. Similarly, in a recent year-long (12 March 2018 - 11 March 2019) study of notified campylobacteriosis cases in New Zealand, 84% of cases were infected with strains attributed to a poultry source (Lake et al., 2020). Also of note, Australians consume a much higher amount of chicken meat than other nations (Section 2.2.1). Industry and food regulatory agencies recognise that reducing the occurrence of *Campylobacter* on raw chicken meat is an important strategy to reduce campylobacteriosis. Foodborne illness caused by *Salmonella* has been significantly increasing over the past 20 years in Australia and, compared to many similar countries, has one of the highest rates (Franklin, Hope, Glasgow, & Glass, 2020; FRSC, 2018). As part of efforts to reduce total foodborne salmonellosis by 30% under the NSW Food Safety Strategy 2015-2021 (FRSC, 2018), *Salmonella* Typhimurium (the most common serovar linked to foodborne illness in Australia) declined by 65% in NSW between 2014 and 2018 (NSW Food Authority, 2019). Eggs accounted for the majority (40.1%, 1980/4905) of *Salmonella* foodborne illnesses in NSW from 2000 to 2017, while chicken accounted for the second highest number (11.8%, 579/4905) of *Salmonella* foodborne illnesses during this period (Franklin et al., 2020). The controls through the poultry meat production process which reduce counts of *Campylobacter* are the same as those which can control *Salmonella*.

In 2015-2016, FSANZ set process hygiene criteria for raw chicken meat, to assist industry in verifying that the whole process is under control. A microbiological target for *Campylobacter* was set at <10,000 cfu per whole chicken carcase at the end of processing (after final chill and just prior to dispatch). However, as 5,000 *Campylobacter* organisms per carcase is considered to be sufficient to cause a risk of cross contamination to RTE foods in the kitchen environment, FSANZ has recommended that a test to count down to a lower detection level is used as this can be readily achieved in the processing plant and can demonstrate good process control. While a microbiological target for *Salmonella* was not been proposed, it was recommended that serotypes be identified and that those of public health or industry significance (i.e. *S.* Typhimurium or *S.* Enteriditis) be notified to the relevant authority to ensure appropriate controls are applied. The high prevalence of *Campylobacter* in processing plant and retail poultry samples reported in the poultry verification surveys and the results of raw chicken meat surveys (Ihab Habib et al., 2019; Walker et al., 2019) which report samples that exceed the level of *Campylobacter* set by FSANZ (FSANZ, 2018), indicate that further improvements could be made to reduce the prevalence and bacterial load and limit the risk of campylobacteriosis to consumers. The process hygiene criteria set by FSANZ (2015-2016) are an initiative that forms part of the measures listed for the poultry sector within Australia's foodborne illness reduction strategy 2018-2021+ (FRSC, 2018), however this initiative is not linked to a target in terms of achieving a specific percentage reduction in human illness. The Australia and New Zealand Ministerial Forum on Food Regulation are supporting efforts to shift to national adoption of the poultry process hygiene criteria set by FSANZ, national performance reporting and consistent triggers for action (FRSC, 2018). All jurisdictions have now agreed to the criteria and they have been implemented. Overseas, a number of countries have already set process hygiene criteria to control contamination of carcases during the slaughtering process, through monitoring and setting requirements for corrective actions to be undertaken when the mandated targets are breached. In the U.S.A in 2016, the FSIS began assessing whether poultry meat processing

establishments met new performance standards (FSIS, 2016b). Samples were collected weekly and a record was kept of the percentage of samples positive in a moving 52-week window, enabling assessment of a processing plant's performance on a continuous basis. For broiler carcases, comminuted chicken, and chicken parts, the maximum acceptable % positive for *Campylobacter* in a 52-week period is 15.7%, 1.9%, and 7.7%, respectively (FSIS, 2019). For broiler carcases, comminuted chicken, and chicken parts, the maximum acceptable percentages of those positive for *Salmonella* in a 52-week period are 9.8%, 25%, and 15.4%, respectively (FSIS, 2019). The new and revised performance standards were designed to achieve The Healthy People 2020 (HP2020) goal to reduce human illnesses from *Salmonella* by 25% and *Campylobacter* by 33% by the year 2020 (FSIS, 2015). In Europe, slaughterhouses must sample whole poultry carcases with neck skin for *Salmonella* and *Campylobacter* analyses at least once a week (European Commission, 2017). Process hygiene criteria for *Campylobacter* came into effect in 2018. As of the 1st of January 2020, if 15 out of 50 samples of carcases after chilling have counts > 1,000 cfu/g, corrective actions must be taken. The EFSA estimates that a public health risk reduction from the consumption of broiler meat of more than 50% could be achieved if carcases complied with a limit of 1 000 cfu/g (European Commission, 2017). Process hygiene criteria are also in place for *Salmonella* and as of 2013, processors have to meet a target of fewer than five positive samples of *Salmonella* out of 50 (European Commission, 2011). In addition, corrective action must be undertaken if any regulated serovars (*S.* Typhimurium and *S.* Enteritidis) are identified during microbiological criteria sampling. In the UK, The Food Standards Agency (FSA) agreed with industry to reduce *Campylobacter* contamination in raw chicken (FSA, 2019). The target was to reduce the percentage of chickens produced in UK poultry slaughterhouses that were contaminated with >1,000 colony forming units (cfu) per gram (g), to 7% or less at retail level (FSA, 2019). The FSA has also incorporated a derogation for smaller slaughterhouses into their staged sampling framework [for a Review see (Hill et al., 2020)]. While it is important to ensure that meat from smaller poultry processors is safe and under appropriate control for *Salmonella* and *Campylobacter*, they will likely find it harder to resource and implement any mandated sampling schemes. Smaller processors also represent a small fraction of the poultry industry and it is speculated that their contribution to infection in humans is minimal (Hill et al., 2020). In Australia, the chicken meat industry is predominantly vertically integrated[2], with the two largest integrated chicken companies supplying approximately 70% of Australia's meat chickens (ACMF, 2020b).

Globally, there is regional variation in the process hygiene criteria set and the targets formulated. A recent Australian study by Habib et al. (2020), concluded that investing in refining a quantitative *Campylobacter* monitoring and process hygiene target would be most helpful for the Australian chicken meat industry in prioritizing risk-based corrective actions and tracing sources of unacceptable contamination. Cross-contamination during handling of fresh poultry meat is a significant source of *Campylobacter* infection. Habib et al. (2020) applied a QMRA model to assess human campylobacteriosis related to cross-contamination during handling of raw chicken meat. Habib et al. (2020) reported that their study aligned with conclusions from various researchers confirming the importance of the tail of the distribution of *Campylobacter* concentrations, which is driven by the proportion of highly contaminated chicken meats. The importance of the number of *Campylobacter* in retail chicken meat was also more evident compared to the predictive impact of *Campylobacter* prevalence (Ihab Habib, Coles, Fallows, & Goodchild, 2020). Habib et al. (2020) concluded that their finding indicates the importance of evaluating the applicability and implications of mitigation strategies aiming toward reducing the numbers (mean and/or standard deviation) of *Campylobacter* in retail chicken meat.

As most retail food businesses handle raw poultry and as the retail sector is a major source of foodborne illness, a focus on handling practices in the retail sector is warranted. *Campylobacter* can be easily spread from raw chicken to

[2] Vertically integrated companies own/operate and control all aspects of production from breeder operations, chick hatching, feed milling, nutrition and health advisory services, quarantine facilities, laboratories and meatprocessing.

other foods and surfaces during preparation. As the infectious dose of *Campylobacter* is small, haphazard cleaning of surfaces with soap and water might not eliminate the risk of cross contamination (Friedman et al., 2004). To this end, the NSW Food Authority, in conjunction with local councils undertook a survey of retail food outlets in NSW (NSW Food Authority, *In print*) as part of efforts to reduce total foodborne campylobacteriosis by 30% under the NSW Food Safety Strategy 2015-2021 (FRSC, 2018). The on-site survey of retail food businesses involved local council authorised officers completing a questionnaire on the food businesses' food handling practices, undertaking protein swabbing of "clean" surfaces that yielded instant indicative results of the surfaces' cleanliness, and taking samples of RTE chicken or liver products which were sent for microbiological analysis (NSW Food Authority, *In print*). The survey revealed some room for improvement for food businesses to ensure that they are limiting the risk of foodborne illness, and meeting food safety standards outlined in the Food Standards Code (NSW Food Authority, *In print*). The data revealed the most common areas with opportunities to improve include:

- damaged chopping boards used in food preparation
- sanitisers were not being used according to instructions
- sanitisers only being used at the end of food service
- poor temperature control of higher risk foods during processing and also when displayed
- 25% of food handlers do not have adequate skills and knowledge

A variety of recommendations were made to address these and other identified issues (NSW Food Authority, *In print*).

2.4.2.2 Chicken offal

Undercooked chicken liver dishes were identified as the responsible vehicle in four outbreaks which occurred from 2013 to 2018; for which a responsible vehicle was identified (4/9, 44%). *Campylobacter* was the responsible agent in the majority of chicken liver dish outbreaks (3/4, 75%) and in all cases the outbreaks occurred in a restaurant setting. Undercooked liver dishes were also a food vehicle of concern in the previous meat risk assessment and it was noted that guidance material was present on the websites of both FSANZ and the NSW Food Authority at that time (NSW Food Authority, 2014). This led to a recommendation to consider whether additional stakeholder engagement activities could be undertaken to reduce the risk of foodborne illness associated with these products (NSW Food Authority, 2014). As poultry liver dishes are an established and persistent vehicle of foodborne outbreaks domestically and internationally (Moffatt et al., 2020), continued strategic communication is required to ensure that educational material reaches those within the food service settings responsible for the safe preparation of these dishes. As outlined in the goals of the FDA's recently published blueprint for the future of food safety, new technologies, tools, and approaches may enhance the development of stronger food safety cultures by increasing message reach and influence to sustain widespread safe-food behaviour changes (FDA, 2020). Guidance material has already been prepared by the NSW Food Authority (NSW Food Authority, 2020a) and FSANZ (FSANZ, 2017) on the safe preparation of poultry liver dishes and warrants further promotion. Guidance material prepared by the NSW Food Authority (2020a) and FSANZ (2017) clearly states that as *Campylobacter* can penetrate animal livers, including chicken livers, they must be cooked so that the core temperature (measured using a digital probe thermometer) of the food reaches 70°C for 2 minutes. The recommendations may also be effective for other species. Undercooking was also identified as a contributing factor leading to outbreaks involving liver dishes of lamb, pork and duck. The predominance of foodservice preparation settings in reported liver–associated outbreaks indicates there may be value in targeting restaurants and other food service settings where liver dishes are prepared for prevention efforts, especially with regard to cooking adequacy. It has been reported that some food writers recommend using livers that have not been fully cooked when preparing chicken liver dishes and that recipes that call for the use of partially cooked chicken liver are readily available (Lanier

et al., 2018). A number of contributing factors have been identified in outbreaks linked to pâté that have led to the product being undercooked (NSW Food Authority, 2018a):

- Cooking to a core temperature of 65°C, but not holding it for the required length of time
- Shallow frying livers to retain a pink colour and not cooking to a high enough core temperature
- Only lightly cooking the liver to retain a pink colour
- Using a larger pot than normal, with no adjustment to the cooking time to compensate for the larger pan size

Further research would also be warranted to test practical and immediately applicable methods of chicken liver decontamination at the processor level. At the poultry abattoir, liver is removed by machine and then visually inspected. Damaged livers are removed manually, and the remaining livers are rinsed with chlorinated chilled water to remove any loose organic matter (NSW Food Authority, 2018a). An increase in the chlorine level in the rinse water or an extension of the time of the rinse may aid liver decontamination at the processor level (NSW Food Authority, 2018a). Other interventions have been reviewed and have been shown to reduce, but not eliminate, *Campylobacter* (FSIS, 2018; Lanier et al., 2018). Amongst those interventions commonly proposed are freezing, organic acid washes and high-pressure processing (FSIS, 2018; Gunther, Abdul-Wakeel, Ramos, & Sheen, 2019; Lanier et al., 2018). Important considerations have also been explored on the effect of processing parameters on the appearance and palatability of livers treated using these interventions (FSIS, 2018; Gunther et al., 2019; Lanier et al., 2018).

2.4.3 Game meat

Game meat is consumed world-wide and in most regions, including Australia, it contributes only a small part of the overall meat and food supply. Despite differences in game species, hunting or harvesting procedures and further handling of the carcase, there are common requirements regarding meat safety and quality. Requirements exist specifying where animals can be harvested from and for determining their health status prior to slaughter. The Australian Standard for the Hygienic Production of Wild Game Meat for Human Consumption (AS 4464:2007), sets the minimum standards required in hygiene for harvesting, transporting, processing, packaging and storage, to ensure a safe and wholesome product. These standards apply to wild game meat for domestic use and for export.

As previously discussed, the NCMMP captures data on the microbiological quality (APC, *E. coli* and *Salmonella*) of exported wild game meat species, such as kangaroo and wild boar. However, the data are not made publicly available. Relevant published studies are also scarce on the presence of pathogens, including parasites and viruses, in live game meat animals and to what extent this may result in contamination of meat cuts. Surveys and targeted research to generate the missing information would provide necessary data to inform future risk assessments concerning game meats.

Currently, time and temperature control treatments (freezing and heating) that will result in the reduction/elimination of viable parasites are the most commonly used preventative control measures (Codex, 2016; Franssen et al., 2019). Ideally, such treatments should be done in accordance with validated parameters which specify the specific time/temperature combination of treatment. The effectiveness of the treatment is dependent on the desired temperature being reached, maintained, and evenly distributed throughout the meat. Therefore, the inactivation of parasites during freezing and heating will also be determined by the food type and portion size. In addition, efficacy of freezing and heating depends on the parasite species and the developmental stage of the parasite.

There are currently gaps in knowledge concerning the survival of parasites in food matrices such as RTE raw meat products, including UCFMs. While many processing steps may, by themselves or in combination, provide further interventions for the reduction of parasites in the final product, further research is required before they can be confidently incorporated into a risk-based assessment. Indeed, in a review of public health risks associated with

food-borne parasites, the EFSA BIOHAZ Panel (2018) stated that while data is available on inactivation of parasites in meat products (the necessary concentrations of salt and other preservatives etc), it has not been collected systematically (EFSA Panel on Biological Hazards et al., 2018). Hence, further work is required to validate the control of parasites in meat products by specific processes.

3. Conclusion

Recent microbiological surveys of the main meat species (domestically reared cattle, sheep, pig and goats), combined with foodborne illness data, indicates that they present a low risk to public health when processed under existing standards. This aligns with the conclusions of the previous risk assessment (NSW Food Authority, 2014).

Results of the poultry verification surveys conducted over the last four years by the NSW Food Authority and other domestic surveys (Ihab Habib et al., 2019; Walker et al., 2019), combined with foodborne illness data, indicates that further improvements could be achieved in the microbiological quality of raw poultry meat. It is predicted that this will be assisted by the future introduction of poultry process hygiene criteria and national performance reporting. However, while poultry meat processors may drive further food safety improvements through optimisation of technical aspects of the slaughter process and routine processing parameters and attention to detail with hygienic practices (L. L. Duffy et al., 2014; FSA, 2017), novel interventions hold the most promise in realising additional significant gains. To date, no single intervention could be relied upon to eliminate the presence of all pathogens on the final poultry product, without affecting the sensory quality of the meat. Therefore, risk reduction through a series of interventions along the poultry processing line is likely the most effective method to achieve further reductions in the numbers of pathogens on finished poultry (safefood, 2017). While beyond the scope of this risk assessment, a number of novel poultry processing interventions are at various stages of research and development and are the subject of recent reviews (Lu, Marmion, Ferone, Wall, & Scannell, 2019; Thames & Theradiyil Sukumaran, 2020). Of course, food safety is best assured by an integrated, multidisciplinary approach that considers the entire food chain ("farm to fork"). The AgriFutures™ Chicken Meat Program invests in research to improve the food safety of Australian chicken meat, from genetic factors through to production and post-farm gate processing (The AgriFutures™ Chicken Meat Advisory Panel, Townsend, Beer, Hewson, & Murphy, 2019). Australian studies have also recently been undertaken to assess the effectiveness of various interventions at the primary production stage, including bacteriophage cocktails to control *Campylobacter* in broiler chickens (Chinivasagam et al., 2020). While at the consumer end, national Australian studies to assess domestic food safety and food handling practices concerning raw meat are scarce, with the last study undertaken almost twenty years ago (Ihab Habib et al., 2020; Jay, Comar, & Govenlock, 1999). A recent survey was undertaken in NSW to assess current food safety practices in the home in regard to defrosting, storage, preparation and cooking, managing leftovers, cleaning and hygiene (NSW Food Authority, 2020e). In regard to handling poultry meat, a number of practices were reported to be routinely undertaken that can increase the risk of foodborne illness (NSW Food Authority, 2020e). For example, of those NSW consumers surveyed, less than half (47%) were aware that they should store raw meat on the bottom shelf of the fridge, one third (33%) of those surveyed wash their chicken and 27% do not check that their meat is cooked right through to the centre (NSW Food Authority, 2020e). Information on the safe handling and correct cooking of raw poultry is available at the NSW Food Authority website (NSW Food Authority, 2020f).

Undercooking accounted for the majority of all meat related outbreaks in NSW from 2013 to 2018. Cooking meat to recommended internal temperatures is the safest method to destroy all pathogens, including parasites and viruses. Strategic communication is required to ensure that educational material reaches those within the food service settings responsible for the safe preparation of dishes which pose a particular risk (i.e. liver pâté). In addition, general messaging may be helpful to educate consumers on the risks related to consumption of 'rare' or undercooked meat, which applies particularly to pregnant women, the elderly and immunocompromised persons. Further information is also required to inform future risk assessments, around the presence of pathogens; especially parasites, in game meat and to what extent they may pose a threat to human health if meat is consumed 'rare' (i.e. 'rare' steaks) or raw (i.e. UCFMs).

Continued baseline monitoring of the prevalence of foodborne pathogens in the production, processing and retail environment of these meat species, will remain necessary for future risk assessments of existing prevention and

control efforts and whether they remain adequate to mitigate current and emerging food safety risks. In addition, new hazards or unfamiliar hazard/commodity combinations may be identified due to increased sensitivity in the surveillance methods available. WGS is increasingly being used by food regulatory and public health agencies to facilitate the detection, investigation, and control of foodborne bacterial outbreaks, and food regulatory and other activities in support of food safety. As WGS becomes more routinely used to sequence clinical and environmental microorganisms during public health surveillance and outbreak investigations, new transmission pathways may be identified for existing or new foodborne pathogens. This information would enable food safety breaches to be identified and addressed, leading to further reductions in the incidence of foodborne illness.

Appendix 1: Outbreaks reported in NSW OzFoodNet annual reports from 2013 to 2018[a], in which a complex food containing meat was identified as the suspected/responsible vehicle

Year	Month of onset	Setting	Pathogen	No. ill	No. hospitalised	Suspected or responsible vehicle	Contributing factors
2018	Oct	Take-away	*Salmonella* Virchow	3	3	Chicken and Mayonnaise sandwich/ wrap	Inadequate cleaning of equipment
2016	Dec	Commercial caterer	*Salmonella* Typhimurium	78	5	Duck pancakes	Cross contamination
2015	Dec	Take away	Unknown	2	0	Chicken curry	Unknown
	Feb	Take-away	Unknown	30	Unknown	Vietnamese style chicken & salad rolls	Unknown
	Oct	Restaurant	*Salmonella* Typhimurium	4	0	Beef burger	Cross contamination
	Apr	Restaurant	Unknown	4	0	Beef and Guinness pie	
	Apr	Restaurant	Unknown	3	0	Chicken burger	
	Feb	Restaurant	Unknown	4	0	Beef taco	
	Jan	Take-away	Unknown	3	0	Chicken burger	

[a] Data was obtained from the NSW OzFoodNet annual reports from 2013 to 2018 (Communicable Diseases Branch, 2014a, 2015, 2016, 2017, 2018, 2019)

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