

Supporting Document 3

Assessment of the microbiological hazards associated with the minor and wild game meat species – Proposal P1014

Primary Production & Processing Standard for Meat & Meat Products

Executive Summary

The objective of this assessment is to evaluate any key gaps or inconsistencies in production and processing risk factors between major meat species (cattle, sheep, pig and goat) and minor and wild game meat species, which may necessitate different risk management measures to control relevant microbiological hazards. Minor species assessed were: deer, camel, buffalo, emu, ostrich, crocodile and rabbit, with wild game species: wild boar, mutton birds, wallaby and kangaroo.

In addressing this objective, and within the context of the assessment, the following question was considered:

• Are there differences in risk factors associated with different production and processing requirements for minor and wild game species (ie rabbit, ratite etc.) compared to major meat species?

This assessment outlined key risk factors, including inputs and stages of production and processing of minor and wild game species, compared to the major meat species. The report also evaluated published and unpublished microbiological and epidemiological data from Australian and international sources (where available).

The evaluation of production factors for the minor meat species against those employed for cattle showed very little differences. Some differences were evident for wild game species as they are not subject to husbandry practices, and source food and water from their surroundings. However, there was no evidence to suggest these differences had a major influence on the microbiological quality of the raw meat.

Abattoir and slaughtering operations are currently mandated under Australian Standards to ensure that meat produced for human consumption is wholesome and safe. Regardless of the type of animal, or husbandry practices employed to rear or harvest the animal, once the animal is received at the abattoir gate and enters lairage, slaughtering operations are undertaken using very similar processing steps. Minor differences exist depending on the plant's capabilities and design but the main steps remain the same.

Limited data are available on the type, prevalence and levels of microorganisms present on animals prior to slaughter, or on carcasses post-processing from the minor and wild game meat species. This is particularly evident within the Australian context. Where evidence is available, the domestic and international data indicate the same pathogenic microorganisms are associated with minor and wild game animals as other meat producing animals. Further, little evidence exists, either domestically or internationally, that foodborne illness is associated with consumption of meat from minor and wild game species.

Conclusions

No substantial differences exist in the production and processing risk factors for minor and wild game meats compared to those of the major meat species. Microbiological hazards associated with minor and wild game species are consistent with those identified for other meat animals commonly consumed in Australia and are controlled by current meat processing requirements.

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Introduction

Currently, the safety of meat and meat products in Australia is implemented largely through reference to Australian Standards which place obligations relating to on-farm activities on processors but impose no corresponding obligations on producers. In accordance with the <u>Overarching Policy Guideline on Primary Production and Processing Standards</u> for through-chain food safety measures, FSANZ is considering risk management measures for the meat industry. The first stage (Proposal P1005)¹ considered meat and meat products from the major meat species (farmed cattle, pigs, sheep and goats including rangeland goats) and rendered products for human consumption, while the second stage considers minor and wild game meat species.

Animal species included in the second stage are those animals defined under existing Australian Standards:

- AS 4696:2007 Hygienic Production and Transportation of Meat and Meat Products for Human Consumption (excluding cattle, sheep, goats and pigs)
- AS 4466:1998 Hygienic Production of Rabbit Meat for Human Consumption
- AS 4467:1998 Hygienic Production of Crocodile Meat for Human Consumption
- AS 5010:2001 Hygienic Production of Ratite Meat for Human Consumption
- AS 4464:2007 Hygienic Production of Wild Game Meat for Human Consumption

To avoid confusion, when used to describe an animal species or meat in this report, the terms 'major', 'minor' and 'wild game' mean:

- 'major' refers to farmed cattle, sheep, goat (including rangeland goats) and pig
- 'minor' refers to farmed or collected species covered in AS 4696 (excluding cattle, sheep, goats and pigs), AS 4466, AS 4467 and AS 5010
- 'wild game' refers to species slaughtered in the wild, covered under AS4464.

1 Objective of the Assessment

The objective of this assessment is to evaluate whether any key gaps or inconsistencies exist in production and processing risk factors between the major, minor and wild game meat species which may necessitate different risk management measures.

2 Scope

Acknowledging information and data for all minor and wild game species would be scarce, advice was sought from the Minor Meat and Wild Game Working Group² regarding species to include and sources of available. A decision to include a particular species in the assessment was based on a number of considerations:

- whether an Australian Standard applied to a single species (ie: AS 4466)
- industry size or production volumes
- availability of data
- unusual or unique aspects to production factors

Included within the scope of this assessment are the minor species: deer, camel, buffalo, emu, ostrich, crocodile and rabbit, and wild game species: wild boar, mutton birds, wallaby and kangaroo.

¹ Proposal P1005 Primary Production and Processing Standard for Meat and Meat Products and is available at http://www.foodstandards.gov.au/code/proposals/pages/proposalp1005primary4220.aspx

² The Minor Meat and Wild Game Working Group is a working group of the P1005 Standard Development Committee (SDC).

3 Approach

Recognising many similarities exist in the husbandry practices, transportation and processing for the major and minor and wild game meat species, assessment work undertaken for the major species is used as a foundation for this work.

Consequently, this assessment encompasses an overview of the production and processing practices, including associated inputs and key stages of the meat supply chain for the minor and wild game meat species. Where available, data on the microbiological status of assessed species and level of foodborne illness associated with consumption of these meats is also considered.

Analysis of the production and processing practices for the minor and wild game species reflects the relevant processing standards. This should assist with identification of hazards common to production and processing practices for all meat species and whether any gaps exist which may require further analysis.

4 Question

Within the context of the assessment, the following question is addressed.

• Are there differences in risk factors associated with different production and processing requirements for minor and wild game meat species compared to major meat species?

5 Summary of major species assessment³

In 2009, FSANZ began consideration of a primary production and processing standard for the meat industry, initially considering the major meat species. Development and application of primary production and processing standards depends on an analysis of the public health and safety risks, economic and social factors and current regulatory and industry practices. Analysis of the public health and safety risk is based on scientific assessment the type of which is determined by the objective and the availability, quality and quantity of data.

The assessment sought to identify risk factors along the meat supply chain, the associated microbiological food safety hazards and the influence each risk factor has on the hazards.

Recognising considerable data and information already existed about meat production in Australia, the assessment aimed to identify any gaps and areas where further risk assessment may be required. Information on the key stages involved in the primary production and processing of meat, associated inputs and activities and potential microbiological hazards was collated and reviewed. Information on the prevalence and levels of microorganisms which may be found on animals, carcasses and at retail was also reviewed, as was epidemiological evidence of meat associated foodborne illness. Additionally, the assessment considered existing scientific assessments and risk profiles on Australian meat.

For the assessed species, a number of common inputs and activities during animal (on-farm) production were identified which influenced the manner in which hazards may be introduced or amplified. Steps where controls may be applied were also noted (Table 1).

³

 $http://www.foodstandards.gov.au/code/proposals/documents/P1005\%20PPPS\%20 for \%20 Meat\%20_\%20 Meat\%20Products\%201AR\%20SD1.pdf$

Input and/ or activity	Comment	Step in chain where control may be applied
Animal health	Pathogens may exist in the animal with or without exhibiting clinical signs	 Animals with clinical signs of disease or illness are identified and managed at: Dispatch from farm/saleyard Arrival at abattoir Ante-mortem inspection Without clinical signs, potential hazards may be identified and managed at: Slaughter to minimise contamination from external surfaces or internal spillage Post-mortem inspection
Stress	Animals may be more susceptible to infection and/or have increased faecal shedding. Pathogens colonise the gut	 Minimise exposure of animals to stress during: Transport Lairage Abattoir/Slaughtering operations to prevent carcass contamination
Feed	Feed has the potential to introduce pathogens into the gut or environment	 Management of input of manure and fertiliser onto pasture Control supplements Oversight of ensilage operations
Water	Contributes to internal and external contamination	Access of animals to suitable drinking water.
Environment and management of biosecurity	Pathogens may contaminate external surfaces of animal, or can lead to ingestion or infection of the animal	 Pasture management Vermin and pest control Good agricultural practices Sound animal husbandry

Table 1 Identified on-farm risk factors for the major meat species

Once an animal is received at the abattoir, slaughter operations are also very similar for the major species, with only minor differences in processing steps arising from the type of animal processed and the design, capability and systems particular to the abattoir. Essentially, contamination of carcasses arises from:

- external sources: from the animal (hide, skin, fleece, hooves, faeces, etc) and the environment (including personnel)
- internal sources: during evisceration and dressing operations and where spillage of gastrointestinal contents occurs.

The report identified a range of microbiological hazards that may be associated with meat and pathogenic microorganisms that, if unmanaged present a risk to public health. *Salmonella* spp was the principal microbiological hazard identified for all meat species during the on-farm phase of meat production and after slaughtering. Additionally, for beef, sheep and goat meat production, pathogenic *Escherichia coli* was also noted as a principle microbiological hazard. *Campylobacter* spp. was identified with both pig and cattle primary production stages, while *Yersinia enterocolitica* and *Toxoplasma gondii* were associated with pig primary production.

From the reviewed epidemiological and microbiological data, the report concluded a low likelihood that foodborne illness occurs from consumption of meat in Australia. The evidence suggests Australian meat has a low microbial load and generally low prevalence of pathogens, with many of the pathogens listed in the assessment occurring infrequently or not at all. Where incidences of meat associated foodborne illness had occurred, these were

mainly due to *Clostridium perfringens* and *Staphylococcus aureus* with post cooking temperature abuse a major contributing factor.

While the level of risk was not specifically evaluated, the report did conclude a significant body of evidence indicated that Australian meat (from cattle, sheep, goat and pig) presented a low risk to public health. The evidence also indicated that industry personnel were mature in their knowledge and management of food safety risks.

Evidence base for minor and wild game species

6 **Presence of pathogens**

6.1 Literature review

A structured search was undertaken of the EBSCO database to capture relevant scientific literature regarding pathogens associated with minor and wild game meat species.

The structured review was restricted to studies examining the prevalence and level of contamination associated with wild or farmed animals, before, during or after processing. Studies involving zoo or experimental animals, or those that specifically related to genetic characterisation of pathogens were omitted as they do not provide information on potential human exposure through the consumption and handling of meat. Additionally, studies of pathogens typically associated with occupational exposure or waterborne transmission were also excluded.

Details of the search terms and inclusion criteria applied, as well as an analysis of included articles, are contained at Appendix 1.

6.1.1 Summary

A comprehensive search of the literature found no published articles describing the prevalence or level of contamination of microbiological hazards in buffalo, deer, camel or ratites, either farmed or wild, on carcasses or on final processed meat products in Australia. Only internationally published data were available for these species.

Limited Australian data were available for microbiological hazards associated with kangaroos, and both international and Australian data were available for crocodiles, wild boar/feral pigs and rabbits. No data were identified that describes the pathogens associated with Tasmanian muttonbirds.

The principal microbiological hazards identified in all minor and wild game meat species, except crocodiles and muttonbirds, were pathogenic *E. coli* and *Salmonella* spp. with some variation between the different species, between countries and in some cases, whether species were farmed or wild. Other microbiological hazards identified included *Campylobacter jejuni, C. coli, Listeria monocytogenes, Yersinia enterocolitica* and *Y. pseudotuberculosis*. Enterotoxin producing *Staphylococcus aureus* and pathogenic *Aeromonas* spp. were identified on the processed carcasses of farmed rabbits in Europe.

Salmonella spp. was the principal microbiological hazard identified for crocodiles and no data were available to identify microbiological hazards for Tasmanian mutton birds.

Toxoplasma gondii was reported to be prevalent in deer, camel, rabbit, kangaroo and wild boar populations with wide variation between countries. Evidence indicates that *T. gondii* cysts remain infective in these species. Serological evidence indicates that buffalo and ratites

in a number of countries are exposed to *T. gondii*, but they are not likely to be a source of human toxoplasmosis since viable *T. gondii* are infrequently isolated from these animals.

Trichinella spiralis, the most common cause of human trichinellosis worldwide, has never been detected in any State or Territory in Australia. No *Trichinella* spp. has ever been detected in any animal species on the Australian mainland and extensive routine testing by industry of exported wild pig and horse meat supports the absence of this foodborne parasite in Australian meat animals. *Trichinella* spp. were identified in wild boar populations in Asia, Europe, South America, North America and in the Torres Strait. *Trichinella* spp. were also identified in crocodile populations of Africa and Papua New Guinea.

Hepatitis E virus (HEV) was identified in wild deer and pig populations in Europe and Asia. Data on HEV in meat animals in Australia is scarce and is limited to a serological survey of Australian farmed and wild pigs, which is indicative of a previous infection but does not inform potential exposure to humans through meat consumption and handling.

6.2 *E. coli* and *Salmonella* Monitoring program (ESAM)

Minor and wild game meats in the export sector are subject to *E. coli*, Total Viable Count (TVC) and *Salmonella* spp. testing under the ESAM program. Data was available for two wild game species (kangaroo and wild boar) and four minor species (camel, deer, emu and ostrich) for the period 2008 to 2010 (refer Appendix 2).

Over the three year period, the vast majority (96%: 4924/5130) of *E. coli* counts for all carcasses were classed as acceptable or better⁴ with only 0.6% (30/5130) deemed unacceptable. Similar results are shown for TVC with 96.9% (4884/5043) within the acceptable range or better.

Overall prevalence of *Salmonella* spp. was 0.9% (31/3370), with all species except emu having one or more positive detections during the three year period. Camel had the highest number of detections: 7/64 (10.9%) in 2009 and 6/97 (6.2%) in 2010, although overall sample numbers were small. A number of different *Salmonella* serovars were isolated, the most frequent being *S*. Anatum and *S*. Give.

6.3 Conclusion

International evidence suggests the minor and wild game species are susceptible to the same pathogenic microorganisms as other meat animals commonly consumed in Australia.

Little or no Australian evidence was found describing the prevalence and levels of microbiological hazards associated with minor and wild game species. However, data available from the Australian export sector suggest these meats have a low microbial load and prevalence of contamination.

7 Foodborne illness

Sources of foodborne illness are generally determined through epidemiological and/or microbiological associations in outbreak investigations. Critically important in this process is the ability to identify an outbreak through the existing surveillance system to enable an investigation to then proceed. Difficulties in identifying and attributing illness to a particular food include:

⁴ ESAM *E. coli* limits:Acceptable: 10 – 100 cfu/cm²; Marginal: 100 – 1000 cfu/cm²; Unacceptable >1000 cfu/cm²

- Time delays in recognition or notification of an outbreak, including:
 - the time taken for infected persons to seek medical treatment
 - obtaining stool samples
 - laboratory confirmation of the presence of pathogenic organisms
 - notification to public health authorities, and
 - identification and subsequent investigation of the outbreak
- Food recall biases when gathering food consumption histories (compounded by pathogens with long incubation periods, e.g. hepatitis A virus)
- Long exposure windows for specific pathogens (e.g. L. monocytogenes)
- Inability to trace food products to their source
- Inability to obtain representative food samples for analysis
- A lack of precision in, or suitable methods for, sample analysis and pathogen identification
- Food attribution in dishes with multiple food items
- The potential for variation in categorising features of outbreaks depending on investigator interpretation and circumstances

It is important to recognise that outbreak data are likely to only represent a small proportion of cases of foodborne illness. Many illnesses may go unrecognised and/or unreported to health authorities and not all notified cases may be investigated. People do not always seek medical attention for mild forms of gastroenteritis, medical practitioners do not always request collection of specimens for analysis and not all foodborne illnesses require notification to health authorities. In Australia, factors for underreporting of foodborne illness have been estimated at 6.9 (95% CrI: 4.0, 16.4) for salmonellosis, 9.6 (95% CrI: 6.2, 22.4) for campylobacteriosis and 8.2 (95% CrI: 3.3, 75.1) for STEC infection (Hall et al. 2006).

7.1 OzFoodNet

The OzFoodNet⁵ Outbreak Register contains data on reported outbreaks of gastrointestinal disease in Australia since 2001. The register was examined to determine any minor and wild game meat associated outbreaks (details provided at Appendix 3).

Between January 2001 and June 2011 there were no foodborne or suspected foodborne outbreaks in which the food vehicle was identified, or suspected, as being a minor meat.

There were three foodborne or suspected foodborne outbreaks where a minor meat (kangaroo, roast rabbit and deer, respectively) was mentioned as being consumed, however, these were not suspected as the source of infection for these outbreaks.

This summary is subject to some limitations given that it is often very difficult to identify the key vehicle causing outbreaks, or critical factors contributing to their occurrence.

7.2 Literature review

The structured search described in section 6.1 also captured relevant articles reporting outbreaks of foodborne illness associated with consumption of minor and wild game meats.

In summary, no evidence was found in the published literature, either internationally or domestically, of any outbreaks of foodborne illness associated with consumption of buffalo, camel, rabbit, crocodile, ratite, kangaroo or muttonbird meat.

⁵ Established in 2000, OzFoodNet is collaboration of Australia's state and territory health authorities to provide better understanding of the causes and incidence of foodborne disease in the community and provide an evidence base for policy formulation (http://www.ozfoodnet.gov.au/)

Several STEC O157 outbreaks and sporadic human cases have been traced to contaminated venison in the USA with epidemiological and microbiological evidence linking the case isolates to isolates from raw venison product (Keene et al. 1997; Rabatsky-Ehr et al. 2002; Ahn et al. 2009; Rounds et al. 2012). In Japan, human hepatitis E virus (HEV) infections have been traced to venison (Tei et al. 2003).

No articles were found describing outbreaks of foodborne illness associated with consumption of meat from deer or wild boar in Australia, although some evidence was identified internationally. Cases of trichinellosis and HEV associated with consumption of wild boar or venison has limited applicability to the Australian context. No human trichinellosis cases have been acquired in Australia, further supporting the evidence that *Trichinella* spp. are absent from Australian meat animals. Outbreaks of human trichinellosis associated with the consumption of wild boar meat have been reported from a number of European and Asian countries including Italy, France, Lithuania, Sweden, Spain, Turkey, Korea and Thailand (Frongillo et al. 1992; Jongwutiwes et al. 1998; Ranque et al. 2000; Heper et al. 2005; Gari-Toussaint et al. 2005; Gallardo et al. 2007; Khumjui et al. 2008; Bartuliene et al. 2009; Kusolsuk et al. 2010; Romano et al. 2011; Intapan et al. 2011; Kim et al. 2011a).

To date, only overseas acquired human HEV cases have been reported from Australia and have been linked to travel to HEV endemic countries. Human cases definitively linked to foodborne exposure have been associated with consumption of uncooked liver or bile from infected wild boar or deer and have been limited, thus far, to North Asia. Several cases have been reported from Japan and Korea without detection of virus in the boar meat (Matsuda et al. 2003; Kim et al. 2011b) and from venison in Japan (Takahaski et al. 2004; Li et al. 2005). In this same survey, HEV RNA was isolated from three of seven wild boars (Takahashi et al. 2004).

7.3 Summary

Very little evidence is available establishing consumption of meat from minor and wild game species as a cause of foodborne illness. In Australia, no cases of illness have been recorded in the Outbreak Register or the published literature, while international literature provides some information on foodborne illness associated with consumption of wild boar meat and venison.

8 **Production practices**

The microbiological status of meat is influenced by many factors along the supply chain.

Assessment for the major meat species determined each step of the production and processing chain and where hazards may be introduced, modified or controlled. It detailed inputs and key stages including husbandry (intensive, extensive and collected), transport, lairage and processing practices.

To allow comparison, a similar detailed analysis was undertaken for each of the included minor and wild game meat species, which is provided at Appendix 4.

8.1 Comparison of primary production and processing steps

Using the production and processing stages identified for meat produced from cattle as a basis, the following compares the stages involved for minor and wild game species.

8.1.1 Primary Production

The major stages of cattle primary production where hazards may be introduced and controls applied were identified as animal production, feed, drinking water, animal husbandry and the environment (Table 2).

Analysis of the primary production factors for the minor and wild game species showed these stages were also applicable for farmed species, namely: deer, rabbit, crocodile, emu and ostrich. For animals initially collected from the wild and kept in holding yards (camel and buffalo) these stages only apply once the animals are collected. The influence that feed, water, health status and the environment have on the introduction of microbiological hazards prior to collection is uncertain. The same situation was also identified for rangeland goats in the major species assessment.

Differences were observed in primary production stages for animals slaughtered in the wild (e.g. kangaroo, wild boar, muttonbird) in that controls cannot be applied to animal production, feed, water or the environment and that animals are not subject to any form of husbandry. Requirements do exist in relevant documentation for where animals can be harvested from and for determining their health status prior to slaughter.

Species	Animal production (birthing, health status, zoonoses)	Feed (pasture, feeds (including roughages, grains, silage), concentrates and supplements)	Drinking water (town, reticulated, ground, surface and run-off water)	Animal husbandry (handling practices, veterinary chemicals)	Environment (premises, building and equipment, personnel)
Deer	\checkmark	\checkmark	\checkmark	\checkmark	\checkmark
Buffalo	*	*	*	*	*
Camel	*	*	*	*	*
Rabbit	\checkmark	\checkmark	\checkmark	\checkmark	\checkmark
Crocodile	\checkmark	\checkmark	\checkmark	\checkmark	\checkmark
Emu/ostrich	\checkmark	\checkmark	\checkmark	\checkmark	\checkmark
Kangaroo	#	#	#	×	#
Wild boar	#	#	#	×	#
Muttonbird	#	#	#	×	#

Table 2	Primary production stages for minor and wild game species compared to those
	for cattle

same/similar to cattle,* Unable to be determined prior to collection, but same/similar to cattle following collection, # Some controls/restrictions applicable, * not applicable

8.1.2 Transport to lairage

Little difference was evident in the steps for preparation and transport to abattoir and lairage between cattle and the farmed minor species (Table 3). Farmed minor species are transported directly from the farm to the abattoir thereby bypassing the saleyard. Camel and buffalo can be held in holding yards during collection prior to transport to the abattoir.

Determination of an animal's "fitness for slaughter" is assessed at various stages including when animals are selected for transport to the abattoir and again at lairage for ante-mortem inspection. This determination is also applicable to farmed/collected animals and wild game, although can occur at a different points. For game animals, harvesters are required to make an assessment of an animal's fitness for slaughter prior to kill. Kangaroo and wild boar carcasses are then eviscerated in the field and transported, with pluck⁶ intact, to the abattoir for additional inspection. Similar pre-slaughter determinations are made for muttonbirds, but whole carcasses (not eviscerated) are then transported directly to on-site processing sheds where ante-mortem inspection occurs.

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	Preparation and transport to market/abattoir selection of animals and handling operations, transport, feed curfew	Saleyards holding and processing	Lairage environment, water, ante-mortem
Deer	\checkmark	×	\checkmark
Buffalo	\checkmark	subject to holding yards during collection prior to transport to abattoir	\checkmark
Camel	\checkmark	subject to holding yards during collection prior to transport to abattoir	\checkmark
Rabbit	\checkmark	×	\checkmark
Crocodile	\checkmark	×	✓ integrated with farm
Emu/ostrich	\checkmark	×	\checkmark
Kangaroo	Transport of eviscerated (pluck intact) carcass to abattoir	×	ante-mortem inspection by shooter /harvester
Wild boar	Transport of eviscerated (pluck intact) carcass to abattoir	×	ante-mortem inspection by shooter /harvester
Muttonbird	Transport of carcass to on-site processing shed	×	ante-mortem inspection by shooter /harvester

✓ same/similar to cattle, ★ not applicable

⁶ Pluck' includes heart, lung and liver

8.1.3 Processing

Comparing processing operations for the minor and wild game species and cattle showed only minor differences (Table 4). For emu and ostrich, there is an additional step to remove feathers following bleeding prior to legging and skin removal. Muttonbirds also require steps to remove feathers or skin depending on whether they are processed as plucked (skin-on) or skin-off product. Processing of crocodile has similar unit operations to other slaughter practices but may not follow the same order. For example, after the carcass wash post killing, the carcass is chilled overnight prior to being processed; legging may follow skinning; and carcasses may or may not be eviscerated prior to boning. Crocodile meat portions are also dipped in an anti-microbial solution prior to packing and freezing.

	Washing	Stunning & bleeding	Carcass washing	Legging	Hide / Skin clearing and removal	Bunging	Evisceration	Post mortem	Trimming	Carcass washing (optional)	Chilling	Boning / portioning	Storage
Deer	✓	\checkmark	\checkmark	✓	\checkmark	✓	\checkmark	~	~	\checkmark	✓	\checkmark	✓
Buffalo	✓	\checkmark	\checkmark	~	\checkmark	~	\checkmark	✓	✓	\checkmark	✓	\checkmark	✓
Camel	✓	\checkmark	\checkmark	✓	\checkmark	✓	\checkmark	✓	✓	\checkmark	✓	\checkmark	✓
Rabbit	×	✓	×	✓	\checkmark	×	\checkmark	✓	✓	~	✓	\checkmark	✓
Crocodile	✓	✓	\checkmark	✓	\checkmark	✓	\checkmark	✓	✓	✓	✓	\checkmark	✓
Emu / ostrich	×	~	×	✓	\checkmark^{\wedge}	✓	✓	✓	✓	✓	~	\checkmark	~
Kangaroo	×	In field	×	~	✓	×	In field. Pluck intact	~	~	✓	~	\checkmark	✓
Wild boar	×	In field	×	~	✓	×	In field. Pluck intact	~	✓	~	~	✓	✓
Muttonbird	×	In field	\checkmark	✓	$\checkmark^{\wedge\wedge}$	×	\checkmark	\checkmark	✓	\checkmark	✓	\checkmark	✓

Table 4Processing unit operations for minor and wild game species compared to those
identified for cattle

✓ same/similar to cattle, ★ not applicable, ^ Additional step (removal of feathers), ^ Plucked (skin-on) or skin-off.

8.2 Summary

Only minor differences exist in the factors identified during the rearing and transport of minor species to those outlined for cattle. For non-husbanded minor species (ie: some camel and buffalo), specific information regarding risk factors (ie: inputs, environment and health status) is uncertain until the animals are collected and enter the supply chain. Once collected, the same primary production and transport steps as cattle generally apply. In most cases, minor species are transported directly from farm to abattoir and are not subject to saleyards

therefore avoiding the effect that co-mingling can potentially have on increasing the microbiological load of the animal.

Some differences are evident for wild game species compared to farmed species, such as the sourcing of food and water from the surroundings, and not being subject to animal husbandry practices. Similar controls cannot therefore be placed on inputs and waste management as those proposed for the major species. Requirements do exist, however, in the Australian Standard (AS 4464) and relevant state and territory legislation, for where game animals can be sourced from, as well as assessing the animals' fitness for slaughter. Carcasses of wild game species may be held in cold storage facilities (in mobile chillers or field depots) prior to being transported to the processor. The Australian Standard (AS 4464) contains requirements for storage temperature and maximum times.

Regardless of the type of animal or husbandry practices employed to rear, collect or harvest the animal – once received at the processor, slaughtering operations are undertaken using very similar unit operations to those identified for the major species. Minor differences exist depending on the species of the animal and the plant's capabilities and design, but the main processing steps remain the same.

9 Discussion

FSANZ's evaluation of the hazards and current management practices in Australia (P1005) indicates that there are no unmanaged food safety risks for the major meat sectors (cattle, sheep, goats, pigs) i.e. controls are provided to protect public health and safety. It could therefore be assumed that meat from other species produced and processed under the same or similar requirements, would have the same outcome. If any differences were apparent, they would conceivably arise from the microbial flora and load particular to the species itself.

Microbiological status of raw meat reflects the conditions of the incoming livestock, slaughter practices, hygiene of equipment and workers during dressing and processing, chilling and potential for cross contamination during packaging, storage and transport.

The microbiological status of incoming livestock is influenced by a number of different factors. The primary production risk factors identified for the major meat species included health status of the animal, types of feed, water, husbandry practices, veterinary inputs and the animal's environment. Transportation, saleyards and lairage conditions were also noted as important risk factors. Nottingham (1982), notes that factors such as co-mingling of animals, intensive rearing methods and stress (such as starvation and transport) increase the shedding and transmission of pathogens in animals.

An evaluation of production factors for the minor species against those employed for cattle showed very little differences. Transport and lairage risk factors (where applicable) were also similar, except for the lack of movement of stock through saleyards. In most cases, minor species are transported directly from farm to abattoir and are not subject to saleyards. Some differences were evident for wild game species as they source food and water from their surroundings and are not subject to husbandry practices. However, there was no evidence that these differences had a significant influence on the microbiological quality of the raw meat.

Abattoir and slaughtering operations are currently mandated under Australian Standards to ensure that meat produced for human consumption is wholesome and safe. Regardless of the type of animal, or husbandry practices employed to rear, collect or harvest the animal, once the animal is received at the abattoir gate and enters lairage, slaughtering operations are undertaken using very similar processing steps. Minor differences exist depending on the plant's capabilities and design but essentially the steps are the same. 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 (FSANZ 2009; ICMSF 2011).

Little or no Australian data were available to ascertain the type, prevalence and levels of microorganisms associated with minor and wild game species. Evidence that is available mostly reflects international conditions and has limitations to the domestic situation. For all minor and wild game except crocodiles and muttonbirds, pathogenic *E. coli* and *Salmonella* spp were identified as the principal microbiological hazards. Some variation was evident between species, between countries and whether or not the animals were farmed or wild. Other microbiological hazards identified included *Campylobacter jejuni, C. coli, Listeria monocytogenes, Yersinia enterocolitica* and Y. pseudotuberculosis.

Toxoplasma gondii was reported in deer, camel, rabbit, kangaroo and wild boar populations with wide variation between countries. *Trichinella* spp. have been identified in wild boar populations in Europe and Asia, however evidence available from Australia indicates absence of this foodborne parasite from Australian meat animals. Similarly, although HEV has been identified in minor and wild game species internationally, there is no data from Australia that indicates that people are exposed through the consumption and handling of meat from major, minor or wild game species.

The available evidence indicates the same pathogenic microorganisms are associated with minor and wild game animals as other meat producing animals. This is not unexpected considering minor species are often reared in similar environments and under similar production practices as major meat producing animals. Collected animals (camel and buffalo) and wild game have the same potential for exposure to pathogenic microorganisms from the environment as other meat producing animals grazing similar terrain. Indeed, pathogenic *E. coli* and *Salmonella* spp. were identified as the principal microbiological hazards for both kangaroo and cattle.

Limited Australian data exists describing the frequency and level of contamination on carcasses post processing from the minor and wild game meat species. Some carcass hygiene related data exists for minor and wild game species in the export market which indicates low contamination on carcasses processed at export certified establishments. These data suggest current processing controls are effective in minimising contamination of carcasses during processing. Additionally, there is little epidemiological evidence available internationally and domestically, describing foodborne illness associated with consumption of minor and wild game species.

10 Conclusion

This 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. This is primarily a consequence of minor and wild game meat species being exposed to essentially the same microbial ecosystem as the major meat species pre-slaughter. Events occurring prior to slaughter for the wild game species are uncertain, however, the geographical range and grazing patterns for the harvested species are well documented and unmanaged exposures to unique microbial pathogens is highly unlikely.

Only minor differences exist in the factors identified during the rearing and transport of minor species to those outlined for cattle. Some differences are evident for wild game species compared to farmed species, such as the sourcing of food and water from the surroundings, and not being subject to animal husbandry practices. However, ccontrols are employed at various stages of the supply chain regarding where animals may be sourced (which may influence types of food and water the animal is exposed to), traceability and ante and post mortem inspection.

Regardless of the type of animal or husbandry practices employed to rear, collect or harvest the animal – once received at the processor, slaughtering operations are undertaken using very similar unit operations to those identified for the major species.

Microbiological hazards associated with minor and wild game species are consistent with those identified for other meat animals commonly consumed in Australia and are controlled by current meat processing requirements.

11 Response to question

Are there differences in risk factors associated with different production and processing requirements for minor and wild game species (ie rabbit, ratite etc.) compared to major meat species?

Microbiological hazards associated with minor and wild game meat species are consistent with those identified for major meat species. The analysis of the production and processing steps identified no major differences in practices undertaken for meat production from the minor and major meat species. Some differences were noted for wild game species during harvest and transport stages, but not once carcasses enter the processing stage. Analysis of microbiological and epidemiological evidence suggests these differences have minimal, if any, impact on public health.

No substantial differences exist in risk factors associated with different production and processing requirements for minor and wild game meat species compared to those for the major species.

Appendix 1

Review of pathogens associated with minor and wild game meat species

1 Background

A structured search was undertaken of the EBSCO database (Food Science Source; FSTA – Food Science and Technology Abstracts; Medline; Medline with Full text) to capture relevant scientific literature regarding pathogens associated with minor and wild game meat species.

Titles and abstracts were used to select studies reporting prevalence in animals or levels of contamination on carcasses or product, or human outbreaks associated with consumption. Excluded studies included those regarding zoo or experimental animal, genetic characterisation of pathogens, occupational exposure or waterborne transmission.

2 Search strategy

Initial searches for both primary and secondary terms were conducted in the MEDLINE -MeSH 2013 (Medline medical health) function of EBSCO to identify universal identifiers and explode search terms. The primary and secondary search terms were then combined by "OR" in the general EBSCO window using Boolean/Phrase search mode, which searched in Food Science Source, FSTA and Medline. No time delimiters were placed on the search.

The search string used is listed in Table 1.

Minor or wild game species	Primary search term/s	Secondary search term/s (linked with primary by "AND")	Secondary search applied to
Kangaroo and wallaby	(MM "Macropodidae") OR ("Kangaroo") OR ("Wallaby") OR ("Wallabies") OR ("Kangaroos") OR ("Macropod") OR ("Macropus")	(MH "Salmonella+") OR (MH "Salmonella Food Poisoning") OR (MH "Salmonella Infections, Animal") OR (MH "Salmonella Infections+")	All species
Buffalo	(MH`"Buffaloes")́ OR (MH "Bison")	(MH "Escherichia coli+") OR (MH "Shiga-Toxigenic Escherichia coli+") OR (MH "Escherichia coli Infections+") OR (MH "Enterohemorrhagic Escherichia coli+") OR (MH "Enteropathogenic Escherichia coli") OR (MH "Enterotoxigenic Escherichia coli") OR (MH "Escherichia coli O157")	All species
Deer	(MH "Deer") OR ("Venison")	(MH "Enterobacteriaceae+")	All species
Crocodiles	(MH "Alligators and Crocodiles") OR ("crocodile meat")	(MH "Toxoplasma") OR (MH "Toxoplasmosis+")	All species
Wild boar	(MH "Sus scrofa+") OR ("wild boar") OR ("wild boar meat")	(MH "Listeria monocytogenes") OR (MH "Listeria+") OR (MH "Listeriosis+")	All species
Ratites	(MH "Dromaiidae") OR (MH "Rheiformes") OR ("ostrich") OR (MH "Struthioniformes") OR ("emu") OR ("ratite") OR (MH "Palaeognathae+")	(MH "Campylobacter+") OR (MH "Campylobacter Infections") OR (MH "Campylobacter jejuni")	All species

Table 1 Search string applied to structured review of literature

Minor or wild game species	Primary search term/s	Secondary search term/s (linked with primary by "AND")	Secondary search applied to
Rabbit	("rabbit meat") OR ("rabbit carcass") OR ("farmed rabbit") OR ("wild rabbit")	(MH "Clostridium+") OR (MH "Clostridium Infections+")	All species
Camels	(MH`"Camels")	(MH "Bacillus+")	All species
Mutton bird	("mutton bird") OR ("short tailed shearwater") OR ("Puffinus tenuirostris")	(MH "Staphylococcus+") OR (MH "Staphylococcus aureus+")	All species
	·····	(MH "Shigella+")	All species
		(MH "Yersinia+") OR (MH "Yersinia enterocolitica") OR (MH "Yersinia Infections+") OR (MH "Yersinia pseudotuberculosis")	All species
		(MH "Vibrio+") OR (MH "Vibrio Infections+")	All species
		(MH "Zoonoses+")	All species
		(MH "Foodborne Diseases+")	All species
		(MH "Disease Outbreaks+") (MH "Taepia sagipata") OR (MH	All species
		"Cysticercosis+") OR "cysticercus bovis"	and camel
		(MH "Trichinella+") OR (MH	Crocodile, wild
		"Trichinellosis")	boar and ratites
		(MH "Chlamydia+") OR (MH	Crocodile
		"Chlamydia Infections+") OR (MH	
		(MH "Spirometra+") OR (MH	Crocodile and
		"Sparganum")	wild boar

MH, medline medical health term; +, explode function applied



Titles and abstracts were screened for applicability and used to select studies reporting prevalence in animals or levels of contamination on carcasses or product, or human outbreaks associated with consumption. Studies of zoo animals, pathogen characterisation, experimental studies and review articles were excluded. Diseases associated with occupational exposure or consumption of milk, including *Bacillus anthracis* (anthrax), *Mycobacterium bovis* (bovine tuberculosis), *Brucella* spp. (brucellosis), *Coxiella burnetti* (Q fever), *Burkholderia pseudomallei* (melioidosis) and buffalopox virus were excluded from this search. *Cryptosporidium* spp and *Giardia duodenalis* were also excluded as meat-borne

transmission has not been demonstrated. *Taenia solium* and *T. asiatica* were excluded from the wild boar/feral pig search since these tapeworms are exotic to Australia.

From an initial 2256 articles, 149 articles were selected for inclusion and are discussed, by species, below.

3 Key findings

3.1 Buffalo

A comprehensive search of the literature found no published articles describing the prevalence or level of contamination of microbiological hazards in buffalo livestock, either farmed or wild, on buffalo carcasses or on final processed meat products in Australia. International literature provides data on a number of foodborne pathogens.

No articles were found describing foodborne illness associated with consumption of buffalo meat.

3.1.1 Summary

Microbiological evidence

The prevalence of *Salmonella* infection in farmed water buffalo has been examined in the Lao Peoples' Democratic Republic (Boonmar et al. 2008) and in farmed bison in Canada (Woodbury and Chirino-Trejo 2011). Boonmar et al (2008) found that 8% of buffalo (4/50) slaughtered at the abattoir in Vientiane were caecum positive for *Salmonella enterica* subspecies *enterica* serovar 9, 12: –:1,5, *S.* Derby and *S.* Javiana. In Canada, a small survey found no *Salmonella* spp. in the faeces of 96 animals sampled from 10 captive herds, including 12 animals from two zoo populations (Woodbury and Chirino-Trejo 2011).

The prevalence of pathogenic bacteria on bison carcasses during processing, including *Salmonella*, has been reported in the USA (Li et al. 2004). The prevalence of *Salmonella* isolation of 0.0 (0/116), 2.6 (3/116), 2.6 (3/116), 3.5 (4/116) and 2.9% (7/239) were observed at pre-dehiding, post-evisceration, post inspection, post-washing at 80°C and on 24h chilled carcasses, respectively. No bacterial load data were reported (Li et al. 2004). In Nepal, a small survey of a Kathmandu wet market found 13.5% (5/37) of buffalo meat samples were contaminated with *Salmonella* (Maharjan et al. 2006), although the wet market environment of Kathmandu has little relevance to the Australian meat industry.

Li et al (2004) reported high prevalence of carcasses contaminated with generic *E. coli*. Prevalence of *E. coli* isolation of 88.8 (103/116), 73.3 (85/116), 52.6 (61/116), 56.9 (66/116) and 11.3% (27/239) were observed at pre-dehiding, post-evisceration, post inspection, post-washing at 80°C and on 24h chilled carcasses, respectively. Pathogenic *E. coli* O157:H7 was only detected at pre-dehiding (4/116) and post-evisceration (1/116) (Li et al. 2004). In contrast, 70% of buffalo meat samples collected from retail butchers in Bangladesh were PCR positive for either stx_1 , stx_2 or stx_1/stx_2 genes and *E. coli* O157 was isolated from 6.7% (2/30) of buffalo meat samples (Islam et al. 2010).

Studies assessing the prevalence of pathogenic *E. coli* in farmed buffalo (including bison), with a particular focus on *E. coli* O157, have been conducted in a number of countries. In the USA, a survey of 342 bison sampled at an abattoir found a prevalence of *E. coli* O157:H7 in either faeces or recto-anal swabs of 47.4% (162/342). Of the 212 isolates, all were positive for *stx*₂, *eae*, *hlyA* and *fliC* virulence genes (Reinstein et al. 2007). In Bangladesh, shiga toxin-producing *E. coli* (STEC) O157 was isolated from the faeces of 14.4% (25/174) of water buffalo that were sampled post-slaughter and in the same study, non-O157 STEC were recovered from 23.6% (41/174) of water buffalo (Islam et al. 2008). *E. coli* O157:H7 was detected in the faeces of 3.7% (11/300) Anatolian water buffalo sampled from government and private farms in Turkey (Seker and Yardimci 2008) and *E. coli* O157 was detected in the

faeces of 14.5% (42/289) Mediterranean water buffalo sampled from 65 herds in southern Italy (Galiero et al. 2005). A survey of Asiatic water buffalo in central Vietnam found 27% (64/237) of rectal swabs were positive for STEC, a small subset of 64 buffalo isolates were further categorised, no buffalo isolates tested were O157, O145 or O26 positive and none carried the *eae* gene, however 81% (52/64) and 78% (50/64) of the buffalo isolates were PCR positive for the *ehxA* and *saa* virulence genes, respectively (Vu-Khac and Cornick 2008). Similarly, 37% (37/100) of water buffalo sampled from nine dairy farms in Brazil had STEC isolated from rectal swabs. No isolates were O157, O145, O111, O103 or O26 positive and no isolates were *eae* gene positive (Oliveira et al. 2007). Like the Vietnamese study, *ehxA* and *saa* virulence genes were detected in approximately 80% of the Brazilian buffalo STEC isolates (Oliveira et al. 2007).

Comparisons are difficult to make between the different studies in the various countries due to different laboratory and sample collection protocols used and the different production systems from which the farmed buffalo or bison were raised.

Only one study was identified that reported the prevalence of pathogenic *E. coli* in the faeces of wild buffalo or bison. A small survey in the USA did not detect *E. coli* O157 in the faeces of 57 wild bison and the authors hypothesised that the extensive grazing reduced the potential for exposure and colonisation in comparison to intensively raised ruminants (Rice et al. 2003).

Two surveys of *Listeria spp.* infections of buffalo have been conducted at slaughterhouses in India. *Listeria monocytogenes* was isolated from 2.4 (3/125), 1.6 (2/125), 4.0 (5/125), 2.4 (3/125) and 2.4% (3/125) of meat, blood, faeces, nasal and vaginal samples tested (Chaudhari et al. 2004). In a second slaughterhouse survey, 2.4% (4/167) of buffalo meat samples were positive for *L. monocytogenes* (Barbuddhe et al. 2002). In both studies, all *L. monocytogenes* isolates were lethally pathogenic for mice. Woodbury and Chirino-Trejo (2011) found 7.3% (7/96) of buffalo faecal samples collected from 10 captive herds in Canada were positive for *Listeria*-like isolates.

Only one international study has reported the prevalence of *Campylobacter* spp. in the faeces of farmed buffalo. Samples were collected from the caecum (184) and bile of Asiatic water buffalo at the Vientiane slaughterhouse in Lao PDR and 1.1% (2/184) of caecum samples and 1% (1/100) of bile samples were positive for *C. jejuni* (Boonmar et al. 2007).

A survey of Canadian farmed bison (Woodbury and Chirino-Trejo 2011) found 2.1% (2/96) of animals had *Yersinia enterocolitica* detected in their faeces at mean count of 3.5×10^4 cfu/g.

Few international studies have reported the prevalence of *Toxoplasma gondii* in buffalo or bison. The prevalence of *T. gondii* antibody in buffalo ranges from zero in Egypt and China (Dubey et al. 1998; Yu et al. 2007), 3% in India and Vietnam (Huong et al. 1998; Sharma et al. 2008), 4% in Brazil (Pita Gondim et al. 1999) and 9% in Iran (Navidpour and Hoghooghirad 1998). However, the serological tests used in these studies had not been validated for buffalo or diagnostic performance criteria for buffalo had not been reported. In the Brazilian study, serum from goats was used as controls. Furthermore, the relationship between *T. gondii* antibody detection and the detection of viable cysts has not been established for buffalo. Cattle are a poor host for *T. gondii* infection and in the absence of good quality data, the international literature tends to suggest that *T. gondii* infection in buffalo is similar to that of cattle. This is further supported by the finding that buffalo meat rarely harbours viable *T. gondii* tissue cysts (Tenter 2009).

Asiatic water buffalo are susceptible to bovine cysticercosis caused by the larval stage of the tapeworm *Taenia saginata*. A serological survey of buffalo and cattle in northern Lao PDR found 38% (228/604) of buffalo infected with *T. saginata* cysticerci (Vongxay et al. 2012). No data is available for bovine cysticercosis of buffalo in Australia.

3.1.2 Conclusion

No published literature was available describing the prevalence or concentration of microbiological hazards associated with buffalo in Australia. Similarly, no evidence was found in the published literature, either internationally or domestically, of any foodborne illness associated with consumption of buffalo meat. International data indicate buffalo are susceptible to infections from the same pathogenic microorganisms as cattle and other ruminants.

3.2 Deer

A comprehensive search of the literature found no published articles describing the prevalence or level of contamination of microbiological hazards of deer or venison, either farmed or wild, on deer carcasses or on final processed venison products in Australia. International literature provides data on a number of foodborne pathogens and some information on foodborne illness associations.

3.2.1 Summary

Microbiological evidence

The prevalence of *Salmonella* isolation from the faeces of farmed and wild deer, including white-tailed deer, roe deer, red deer, fallow deer and reindeer, has been reported from the USA, Sweden, Finland and Norway. No *Salmonella* was detected in the faeces of 2,243 semi-domesticated deer from eight herds in northern Finland and Norway (Kemper et al. 2006), 484 harvested wild deer in Norway (Lillehaug et al. 2005), nor in the faeces of 200 wild roe deer in Sweden (Wahlstrom et al. 2003). In the USA, no *Salmonella* was detected in the faeces of white-tailed deer collected from 30 farms in Ohio (French et al. 2010) and *S. enterica* serovars Litchfield (1), Dessau (1), Infantis (2) and Enteritidis (1) were isolated from the faeces of 500 free-ranging white-tailed deer harvested by hunters in Nebraska for an overall prevalence of 1% (Renter et al. 2006). Two out of 26 (7.7%) wild white-tailed deer that were simultaneously grazing the same rangeland as cattle and sheep at a university farm in Texas had *Salmonella* cultured from rumen contents (Branham et al. 2005).

Surveys of pathogenic E. coli in the faeces of farmed and wild deer, including white-tailed deer, roe deer, red deer, fallow deer and reindeer, has been reported from Germany, USA, Sweden, Finland, Norway, Spain and Belgium. In Belgium, STEC or EPEC was present in 15% (20/133) of roe and red deer and 12% (16/133) were positive for one or both the stx_1 or stx₂ gene, no pathogenic isolates belonging to serogroups O157, O26, O111, O103 or O145 were detected. In Spain, STEC O157:H7 was isolated from 1.5% (3/206) of wild red deer and no STEC O157 isolates were recovered from wild roe deer (0/20) or fallow deer (0/6) (Garcia-Sanchez et al. 2007). In contrast non-STEC O157 were detected in 25% (51/206) of red deer, 5% (1/20) of roe deer and 33% (2/6) of fallow deer (Sanchez et al. 2009). Lillehaug et al (2005) were unable to detect STEC in the faeces of 206 Norwegian roe deer and 1.5% (2/135) of red deer were stx gene-positive. In northern Finland and Norway, E. coli was isolated from the faeces of 95% (2,123/2,243) of semi-domesticated reindeer, no pathogenic strains were detected after screening by PCR for stx_1 , stx_2 , eae and hly_{FHFC} virulence genes (Kemper et al. 2006). Wahlstrom et al (2003) were unable to detect STEC O157 from the faeces of 285 wild and farmed roe, red and fallow deer in Sweden and STEC O157:H7 was cultured form the faeces of 0.25% (4/1,608) wild deer in Nebraska, USA (Renter et al. 2001). In the USA state of Louisiana, 0.3% (1/338) and 1.8% (1/55) of wild and farmed white-tailed deer, respectively, had STEC O157 cultured from faecal samples (Dunn et al. 2004) and in Ohio, 3.3% (1/30) of deer farms had STEC O157 detected in deer faeces (French et al. 2010). In a recent German study of wild red and roe deer, 72% (43/60) of deer excreted stx gene-positive faeces and STEC was isolated from 42% (25/60) of deer irrespective of the serogroup (Eggert et al. 2012).

The review identified two studies that assessed STEC contamination of raw or processed venison. In Belgium, 46% (52/113) of wild venison samples were *stx* gene-positive by PCR and 16% (19/119) were culture positive; no isolates were STEC O157 (Pierard et al. 1997). In Spain, 46% (22/48) of frozen venison and 5% (2/37) of venison ready-to-eat meat products were *stx*-gene positive by PCR, for the same products 8% (4/48) and 3% (1/37), respectively, were culture positive and all were non-STEC O157 (Diaz-Sanchez et al. 2012).

Campylobacter jejuni was isolated from the faeces of 3% (5/172) of wild roe deer, no red or fallow deer (0/90) in Sweden (Wahlstrom et al. 2003) and 3% (1/38) of wild roe deer, no red deer or reindeer (0/203) in Norway (Lillehaug et al. 2005). *C. hyointestinalis* was isolated from the faeces of 0.04% (1/2243) reindeer in northern Finland and Norway, no *C. jejuni* was detected in this study (Kemper et al. 2006).

Kemper et al (2006) isolated *Yersinia* spp. from the faeces of 5% (108/2243) of reindeer in northern Finland and Norway and of these isolates, 28 were identified as *Y. enterocolitica*. In the USA, 30.3% of deer farms in Ohio (9/30) had deer infected with *Y. enterocolitica* (French et al. 2010).

Listeria monocytogenes has been isolated from farmed deer in the USA. One out of thirty (3.3%) deer farms in Ohio isolated *L. monocytogenes* from faecal samples (French et al. 2010).

In Norway, faecal samples from 166 semi-domesticated reindeer were tested for *Clostridium perfringens* and 59% (98/166) were culture positive and all carried the gene for α -toxin (Aschfalk et al. 2002). In the USA state of Ohio, 37% (11/30) of deer farms were positive for *C. difficile*, 7 of these farms yielded isolates with a toxigenic gene profile and 4 farms yielded isolates with the human epidemic ribotype 078 strain (French et al. 2010).

Surveys for the detection of antibodies to *Toxoplasma gondii* have been conducted in a variety of wild and farmed deer species, including sika, white-tailed, black-tailed, mule, red, roe and reindeer, in Japan, Brazil, USA, France, Spain, Belgium, Czech Republic, Finland and Sweden (Lindsay et al. 1991; Chomel et al. 1994; Vanek et al. 1996; Ferreira et al. 1997; Dubey et al. 2004; Vikoren et al. 2004; Lindsay et al. 2005; Omata et al. 2005; Gauss et al. 2006; Bartova et al. 2007; Gamarra et al. 2008; Dubey et al. 2008; Dubey et al. 2009; Jokelainen et al. 2010; Panadero et al. 2010; Aubert et al. 2010; Malmsten et al. 2011; De Craeye et al. 2011; Matsumoto et al. 2011). The surveys indicate that toxoplasmosis is highly prevalent and widely distributed in the USA, Europe and Brazil with very low prevalence observed in the two surveys of sika deer in Japan.

Unlike cattle and buffalo, deer are not resistant to *T. gondii* infection and several studies have successfully demonstrated viability of *T. gondii* tissue cysts by feeding heart muscle from seropositive animals to mice. In one study in the USA, *T. gondii* was isolated from the hearts of 61% (21/34) of seropositive white-tailed deer (Dubey et al. 2004) and in another study; isolates were obtained from 21% (4/19) of seropositive white-tailed deer (Lindsay et al. 1991). In France, *T. gondii* cysts were isolated from 36% (12/33) of seropositive roe deer and 25% (1/4) of red deer (Aubert et al. 2010). Genotype II *T. gondii* has been isolated from deer in the USA and France (Dubey et al. 2004; Aubert et al. 2010).

Epidemiological evidence

The structured review of the international literature did not identify studies reporting microbiological or epidemiological evidence linking venison consumption with salmonellosis in humans. Similarly, no outbreaks or sporadic human cases of campylobacteriosis have been associated with venison.

Several STEC O157 outbreaks and sporadic human cases have been traced to contaminated venison in the USA with epidemiological and microbiological evidence linking the case isolates to isolates from raw venison product (Keene et al. 1997; Rabatsky-Ehr et al. 2002; Ahn et al. 2009; Rounds et al. 2012).

In Japan, human hepatitis E virus (HEV) infections have been traced to venison. Human case isolates had identical nucleotide sequence homology with HEV isolated from frozen venison kept by one of the case patients, family members who did not eat the venison remained uninfected (Tei et al. 2003).

3.2.2 Conclusion

No published literature was available describing the prevalence or concentration of microbiological hazards associated with deer in Australia. However, international data indicate deer are susceptible to infections from the same pathogenic microorganisms as other ruminants and meat animals, and susceptibility of deer to *T. gondii* infection is similar to sheep and goats rather than cattle and buffalo.

Internationally, consumption of venison has been associated with cases of foodborne illness.

3.3 Camel

A comprehensive search of the literature found no data describing the prevalence or level of contamination of microbiological hazards of camels, either farmed or wild, on carcasses or on final processed meat products in Australia. International literature shows limited data on a number of foodborne pathogens associated with camels.

No articles were found describing foodborne illness associated with consumption of camel meat.

3.3.1 Summary

Two studies report the prevalence of *Salmonella* in apparently healthy camels. An extensive survey of camels between 1987 and 1991 in the United Arab Emirates found 4% (165/3801) of camels were shedding *Salmonella* in faeces. In all, 28 serovars were detected, the most common being *S.* Saintpaul, *S.* Frintrop, *S.* Hindmarsh, *S.* Kottbus and *S.* Bovismorbificans (Wernery 1992). In a survey of camels between 2001 and 2002 in eastern Ethiopia, *Salmonella* was recovered from 15% (18/119) of faecal samples collected at slaughter from healthy animals. *Salmonella* was also recovered from 16, 12 and 14% of mesenteric lymph nodes, livers and spleen samples, respectively. Furthermore, Salmonellas were isolated from 20% of abdominal and diaphragmatic muscle samples collected from dressed carcasses. In all, 16 serovars were detected, the most common being *S.* Saintpaul, *S.* Braenderup, *S.* Muenchen, *S.* Kottbus and *S.* Havana (Molla et al. 2004).

A single study conducted in five African countries, Egypt, Somalia, Djibouti, Kenya and Sudan examined the prevalence of *E. coli* O157:H7 and non-O157 *E. coli* in the faeces of 400 camels. *E. coli* was isolated from all camels but no O157:H7 or *stx*-gene positive isolates were detected (EI-Sayed et al. 2008).

Camel meat purchased unpackaged from butchers in two Iranian cities in 2008 and 2009 was tested for the prevalence of pathogenic *Campylobacter*, with one of 107 samples contaminated with *Campylobacter coli* (Rahimi et al. 2010).

Camels are also a potential source of *Toxoplasma* spp. Published surveys from Saudi Arabia, Sudan, Egypt, Iran and Turkey have reported *T. gondii* seroprevalence of 16, 67, 17, 4 and 91%, respectively (Hussein et al. 1988; Elamin et al. 1992; Hilali et al. 1998; Sadrebazzaz et al. 2006; Utuk et al. 2012). Limited data on the viability of *T. gondii* in the

muscle tissue of camels suggests that it remains viable and infective for cats (Hilali et al. 1995), as is the case for deer, sheep and goats.

3.3.2 Conclusion

No published literature was available describing the prevalence or concentration of microbiological hazards associated with camel in Australia. However, international data indicate camels are susceptible to infections from the same pathogenic microorganisms as ruminants and other meat animals.

There have been no cases of foodborne illness associated with consumption of camel meat reported in the published literature.

3.4 Rabbits

A comprehensive search of the literature found limited data describing the prevalence or level of contamination of microbiological hazards of rabbits, either farmed or wild, on carcasses or on final processed meat products in Australia. International literature provides some data on a number of foodborne pathogens and microbiological quality of rabbit carcasses.

No articles were found describing foodborne illness associated with consumption of rabbit meat.

3.4.1 Summary

Two published studies provide data on the prevalence of pathogenic bacteria in wild rabbit populations of Europe. In the United Kingdom, 8% (8/97) of wild rabbits on six properties sharing grazing land with cattle in summer had *E. coli* O157 isolated from faecal samples. In the same region, no rabbits (0/32) were found to be shedding *E. coli* O157 in winter. Of the 97 samples collected in summer, 21% (20/97) of rabbits were shedding non-O157 VTEC (Scaife et al. 2006). Another study in northern Portugal found 48% (38/80) of wild rabbits shedding *Salmonella* in faeces, the serovars detected were Rissen (11), Enteritidis (10), Havana (9), Typhimurium (6) and Derby (2) (Vieira-Pinto et al. 2011).

Two European studies also report on carcass quality of rabbits at slaughter or rabbit meat at retail. A survey of 51 farmed rabbit carcasses and retail meat samples collected in Spain found no evidence of *Salmonella* or pathogenic *E. coli* contamination (Rodriguez-Calleja et al. 2006). Four samples were positive for *E. coli* but none were O157 and all were negative for *stx*₁/*stx*₂ genes. *Yersinia enterocolitica* was cultured from 4% (2/51) of samples but neither sample carried the *yst* gene which is a predictor of virulence. However, a further two samples were PCR positive for *yst* gene but *Y. enterocolitica* was not cultured.

Listeria monocytogenes was isolated from 6% (3/51) of samples and *Aeromonas spp.* were isolated from 35% (18/51) of samples. Furthermore, the *aerA/hlyA* genes were detected by PCR from 77% (39/51) of non-selective enriched samples which is predictive of virulent *Aeromonas* capable of causing gastroenteritis. *Staphylococcus aureus* was isolated from 53% (27/51) of samples, 23 samples were negative for the genes encoding enterotoxin A, B, C, D and E; two samples each were PCR positive for enterotoxin B and C genes, *seb* and *sec* (Rodriguez-Calleja et al. 2006). In Switzerland, a survey of 500 faecal samples and 500 carcasses of farmed rabbits at slaughter found no rabbit carcasses or faeces contaminated with *Salmonella* or *Listeria. Campylobacter* was not detected on carcasses but 0.04% (2/500) of faecal samples tested positive for *C. jejuni.* Of the faecal samples tested for pathogenic *E. coli*, 46% tested positive by PCR for *eae* gene, 1% for *stx* and 2% for both *stx* and *eae*.

Staphylococcus aureus was detected on 30% (151/500) of carcasses and staphylococcal enterotoxin genes were detected in 102 (20%) of the *S. aureus* isolates. No *S. aureus* isolates harboured the gene for methicillin resistance (*mecA*). *Enterobacteriaceae* were detected on 24% (118/500) of carcasses and total viable counts (TVC) from carcasses ranged from 2 - 5 log CFU/cm² and the daily mean TVC ranged from 3 - 4 log CFU/cm² (Kohler et al. 2008).

A survey of 1,697 wild rabbits from 24 sites in Victoria from 1971 to 1980 found high titre antibodies to *T. gondii* in rabbits sampled from 5 sites, Dartmouth (1%), Seaspray (3%), Dreeite (6%), Mud Island (13%) and the land filtration area of the Werribee sewage treatment plant (26%). Rabbits with low titre antibodies to *T. gondii* were detected in all locations (Cox et al. 1981). No data was identified on toxoplasmosis in Australian farmed rabbits.

3.4.2 Conclusion

No published literature was available describing the prevalence or concentration of microbiological hazards associated with rabbits in Australia. However, international data indicate rabbits are susceptible to infections from the same pathogenic microorganisms as ruminants and other meat animals.

There have been no cases of foodborne illness associated with consumption of rabbit meat reported in the published literature.

3.5 Crocodiles

A comprehensive search of the literature found limited Australian data describing the prevalence or level of contamination of microbiological hazards of crocodiles, either farmed or wild, on carcasses or on final processed meat products. International literature provides data on a number of foodborne pathogens, including *Salmonella* and *Trichinella* spp.

No articles were found describing foodborne illness associated with consumption of crocodile meat.

3.5.1 Summary

Salmonella have been isolated from the skin, cloaca and meat of farmed crocodiles in the Northern Territory (NT) and Queensland (Manolis et al. 1991; Rickard et al. 1995; Millan et al. 1997); from meat samples of captive Nile crocodiles in Zimbabwe (Madsen 1993; Madsen 1996); and from cloacal swabs of captive crocodiles in Argentina (Uhart et al. 2011) and wild Nile crocodiles in Zimbabwe (Madsen et al. 1998).

A 1989 study of two crocodile farms in the NT found 16% of crocodile meat swabs yielded 10 serotypes of *Salmonella* post-chlorine treatment, the most frequently isolated being *S*. Singapore (Manolis et al. 1991). Significant differences in prevalence of contamination on chlorine treated crocodile flesh were observed between the two farms, 22% of carcasses on farm 1 and 3% of carcasses on farm 2 yielded *Salmonella*. *Salmonella* was also detected in the faeces and cloaca of crocodiles on these farms two farms (Manolis et al. 1991). In Queensland, samples were collected from the skin and meat of crocodiles harvested and processed on two farms. A study was conducted in July 1991 on one farm (n=23) and a follow-up study conducted in August 1992 on two farms (n=49) after significant improvements were made to processing, including chlorine based alkaline scrubbing of the carcass post-slaughter, storage temperature decreased from 4°C to 2°C and the use of acetic acid to treat meat. The prevalence of *Salmonella* detection from the samples collected in 1991 was 48% (11/23) compared to 6% (3/49) of samples collected in 1992. No final meat product from the 1992 study yielded *Salmonella* (Rickard et al. 1995).

Internationally, two non-encapsulated *Trichinella* species have been identified in farmed and wild crocodiles. *T. zimbabwensis* was first detected in captive Nile crocodiles in Zimbabwe in 1995 and 40% (256/648) of farmed crocodiles tested were infected (Pozio et al. 2002). *T. zimbabwensis* has subsequently been identified in farmed and wild crocodiles in South Africa, Ethiopia and Mozambique (Pozio et al. 2007; La Grange et al. 2009; La Grange et al. 2012). A closely related species, *T. papuae*, has been isolated from 22.2% (16/72) of wild saltwater crocodiles (*Crocodylus porosus*) in Papua New Guinea (Pozio et al. 2004). The larvae of both *T. zimbabwensis* and *T. papuae* are destroyed by freezing (Pozio et al. 2002; Pozio et al. 2004). There is no current data to suggest that *Trichinella* spp. are present in any animal species on the Australian mainland, including wild and farmed crocodile populations.

3.5.2 Conclusion

Crocodiles are susceptible to salmonellosis but improvements to processing, including postslaughtering scrubbing with a sanitiser and dipping meat in an acetic acid solution greatly reduce the prevalence of contamination and reduce the level of contamination on final meat products.

There have been no cases of foodborne illness associated with consumption of crocodile meat reported in the published literature.

3.6 Kangaroo and wallaby

A comprehensive search of the literature found a limited number of articles describing the prevalence or level of contamination of microbiological hazards in kangaroos and wallabies or on final processed meat products in Australia.

Limited published literature was found describing an association between consumption of kangaroo meat and foodborne illness.

3.6.1 Summary

Microbiological evidence

Prevalence surveys of wild kangaroos have been conducted in Western Australia and Queensland. The review of literature did not identify pre-processing prevalence surveys of microbiological hazards in other Australian jurisdictions. The prevalence of *Salmonella* detection in faecal samples of commercially harvested western grey kangaroos from 10 locations in Western Australia was 3.6% (23/645), ranging from 0% to 9.8%. *Salmonella* was only detected in kangaroos from six locations and prevalence was significantly associated with increased rainfall in the 30 days prior to sample collection (Potter et al. 2011). The authors of this study did not report multivariable analysis and it was therefore not clear if the significant geographical differences in prevalences were due to variable rainfall patterns between the collection sites. All isolates were *S. enterica* and the most frequently isolated serovar was Muenchen (12/23), followed by Kiambu (6/23). Other serovars detected were Lindern, Champaign, Saintpaul, II 42:g,t:-, and Rubislaw (Potter et al. 2011).

A survey of Australian marsupials in southeast Queensland found 8.6% (13/151) of wild eastern grey kangaroos were infected with *E. coli* that were *stx* gene-positive by PCR. None of the detected isolates had an O serotype that was typically associated with human STEC (Rupan et al. 2012).

Several studies have assessed the microbiological quality of kangaroo carcasses at processing plants and kangaroo meat at retail premises, two in Queensland and two in South Australia. A survey in Queensland detected *Salmonella* in 25g meat samples in 0.84% (7/836) of kangaroo carcasses sampled from February 2003 to February 2006; *Salmonella*

was only detected on carcasses sampled in January and February. *E. coli* and aerobic bacteria were detected on 13.9% (116/836) and 68.7% (574/836) of carcasses, respectively. The mean bacterial count for *E. coli* and aerobic bacteria was 0.7 and 2.8 log cfu/g, respectively (Eglezos et al. 2007). In comparison, a smaller study reported in 1991 found 11% (9/81) of processed kangaroo carcasses were contaminated with *Salmonella* and 49% (40/81) were contaminated with coliforms with a mean count of 3.54 log coliforms/g and the mean total count of 5.2 log/g of muscle (Bensink et al. 1991).

In South Australia, a small survey of kangaroo meat purchased form retail outlets in Adelaide in 2002 found 31% (11/35) of steaks and 49% (17/35) of mince samples were contaminated with *Salmonella. Campylobacter* spp. was not isolated from kangaroo samples collected in this retail survey (Delroy et al. 2008). A survey of five processing plants in 2002 and 2004 in South Australia detected *Salmonella* on 1% (4/385) of carcasses. Eighteen per cent (9/50) of minced kangaroo meat samples in 2002 were found to be contaminated with *Salmonella*. Six of the contaminated minced meat samples came from a single processor. Seventy per cent (70/120) of minced meat samples collected in 2002 were contaminated with *E. coli* with a mean count of 2.1 log cfu/g (Holds et al. 2008).

It is not possible to make comparisons between the different studies due to the different sampling strategies and testing protocols used.

A serological survey of western grey kangaroos culled from seven sites around Perth found 15.5% (34/219) positive for *Toxoplasma gondii* antibodies; *T. gondii* DNA was detected by PCR from brain, tongue and heart muscle samples collected from nine seropositive kangaroos, DNA was not detected in the tissue samples of nine seronegative kangaroos (Parameswaran et al. 2009). A relatively small study of the genotypes circulating in Australian marsupials found kangaroos infected predominantly with atypical strains and a small number infected with archetypal genotypes I and II strains, all isolates were avirulent in mice. One atypical isolate from a Tasmanian wallaby caused neurologic disease in mice (Parameswaran et al. 2010).

Epidemiological evidence

The study by Rupan et al (2012) demonstrates that kangaroos are a potential carrier of pathogenic *E. coli*, but the public health importance of kangaroos with respect to the transmission of pathogenic *E. coli* to humans could not be determined. No outbreaks or cases of salmonellosis or pathogenic *E. coli* infection have been associated with the consumption of kangaroo meat.

No confirmed cases of human toxoplasmosis have been linked to the consumption of kangaroo or wallaby meat. A presumptive outbreak of toxoplasmosis was linked to consuming kangaroo meat in 1994 (Robson et al. 1995), however the study was unable to confirm kangaroo meat as a source of the outbreak only that it was "theoretically" the most likely.

3.6.2 Conclusion

Published scientific literature indicates kangaroos and wallabies are susceptible to infections from the same pathogenic microorganisms as ruminants and other meat animals.

No confirmed cases of foodborne illness associated with consumption of kangaroo meat have been identified in the published literature.

3.7 Wild boar and feral pig

A comprehensive search of the literature found limited Australian data describing the prevalence or level of contamination of microbiological hazards of feral pigs. International literature provides comprehensive information on a range of foodborne pathogens and some associated foodborne illness. This has limited applicability to the Australian context, particularly with respect to trichinellosis and hepatitis E.

3.7.1 Summary

Microbiological evidence

The prevalence of *Salmonella* in wild boar or feral pig populations have been reported for a number of countries. In Switzerland, *Salmonella* was isolated from the tonsils of 19/153 (12%) wild boar but not from the faeces of the same animals; eight *Salmonella* serovars were identified amongst the 19 isolates, the most common being *S*. Enteriditis, *S*. Stourbridge and *S*. Veneziana (Wacheck et al. 2010). A small survey of the faeces of Swedish wild boar (n=66) was unable to detect *Salmonella* (Wahlstrom et al. 2003), whereas 22% (17/77) of wild boar in Northern Portugal (Vieira-Pinto et al. 2011) and 5% (8/161) of feral pigs in North Carolina, USA, were reported to be shedding *Salmonella* in faeces (Thakur et al. 2011). In Portugal, only *S*. Typhimurium and *S*. Rissen were detected in wild boar (Vieira-Pinto et al. 2011).

Pathogenic *E. coli* have been detected in the faeces of wild boar and feral pigs in a number of countries. An outbreak of human *E. coli* O157:H7 in 2006 was linked to the consumption of bagged spinach and resulted in many deaths. The outbreak strain was isolated from cattle grazing nearby and from feral pigs roaming in the vicinity of a spinach farm in California, USA, which was implicated in the spinach outbreak (Jay et al. 2007). In Spain, *E. coli* O157:H7 and non-O157 STEC were isolated from faeces of 3% (7/212) and 5% (11/212) of wild boar killed during the hunting season of 2007-2008 (Sanchez et al. 2010) and STEC were isolated from 8% (22/262) of wild boar killed during the hunting season of 2009-2010 (Mora et al. 2012).

Wild boars harbouring enteropathogenic *Y. enterocolitica* and *Y. pseudotuberculosis* have been reported from Japan and Switzerland (Hayashidani et al. 2002; Fredriksson-Ahomaa et al. 2009; Fredriksson-Ahomaa et al. 2011) and prevalence is higher in tonsils than in faeces (Fredriksson-Ahomaa et al. 2009).

Infections of wild boar with *L. monocytogenes* and *C. jejuni* have been reported from Japan (Hayashidani et al. 2002) and the USA (Jay-Russell et al. 2012), respectively.

Two published studies were identified that examine the microbiological quality of feral pig carcases at slaughter. A survey of feral pig carcasses processed at a Queensland game abattoir reported 1% (3/217) of carcasses contaminated with *Salmonella* (Eglezos et al. 2008) and a study of microbiological quality of wild boar carcasses from Italy did not detect *Salmonella* on 77 carcasses (Avagnina et al. 2012). *E. coli* were detected on 19% (42/217) of pig carcasses at the Queensland abattoir and the mean *E. coli* and APC counts were reported to be 1.9 and 4.7 log cfu/g, respectively. Five per cent and 1% of the pigs had an *E. coli* count greater than 2 and 3 log cfu/g, respectively (Eglezos et al. 2008).

Surveys for the detection of antibodies to *T. gondii* in wild boar have been reported from Japan, USA, France, Czech Republic, the Netherlands, Switzerland and Slovakia. Like that seen for deer, prevalence of *T. gondii* antibody detection in European and North American wild boar populations was high, ranging from 6.7% in Switzerland and 8% in the Slovakia to 18% in France, 26% in Czech Republic and 24% in the Netherlands; on Corsica, seroprevalence was reported as 0.6% in the summer of 2006-2007 and 0.3% in the summer of 2007-2008. In North Carolina, seroprevalence was reported to be 28% (Bartova et al. 2006; Antolova et al. 2007; Richomme et al. 2009; Richomme et al. 2010; Sandfoss et al.

2011; Opsteegh et al. 2011; Berger-Schoch et al. 2011). Two studies from Japan have reported seroprevalence of 6% and 1% (Shiibashi et al. 2004; Matsumoto et al. 2011).

In France, *T. gondii* cysts were isolated by mouse bioassay from 48% (21/44) of seropositive wild boar and only genotype II isolates were identified (Richomme et al. 2009).

Surveys of wild boar reported in the international literature indicate that at least three *Trichinella* species are endemic in the wild boar populations of Europe; *T. spiralis*, *T. britovi* and *T. pseudospiralis* (Nockler et al. 2006; Hurnikova and Dubinsky 2009; Garcia-Sanchez et al. 2009; Merialdi et al. 2011). *T. pseudospiralis* has been isolated from wild boar in the USA (Gamble et al. 2005); *T. spiralis* from wild boar in Argentina (Cohen et al. 2010) and a small survey in Canada was unable to detect *Trichinella* larvae in wild boar by either artificial digestion of muscle tissue or by serology (Gajadhar et al. 1997).

T. papuae has been detected in one Australian feral pig; larvae were isolated from one of 12 feral pigs sampled on two islands of the Torres Strait. In the same study, muscle samples were collected from 438 feral pigs in the Cape York Peninsula on the Australian mainland and no *Trichinella* larvae were detected (Cuttell et al. 2012).

Epidemiological evidence

Outbreaks of human trichinellosis associated with the consumption of wild boar meat have been reported from a number of European and Asian countries including Italy, France, Lithuania, Sweden, Spain, Turkey, Korea and Thailand (Frongillo et al. 1992; Jongwutiwes et al. 1998; Ranque et al. 2000; Heper et al. 2005; Gari-Toussaint et al. 2005; Gallardo et al. 2007; Khumjui et al. 2008; Bartuliene et al. 2009; Kusolsuk et al. 2010; Romano et al. 2011; Intapan et al. 2011; Kim et al. 2011a). In Thailand, outbreaks have been associated with wild boar infected with *T. pseudospiralis* and *T. papuae* (Jongwutiwes et al. 1998; Khumjui et al. 2010; Intapan et al. 2011) and with *T. spiralis* in Korea (Kim et al. 2018; Kusolsuk et al. 2010; Intapan et al. 2011) and with *T. spiralis* in Korea (Kim et al. 2011a). In France, Italy, Spain and Sweden outbreaks have been caused by *T. britovi* and *T. pseudospiralis* (Frongillo et al. 1992; Ranque et al. 2000).

Hepatitis E virus has been isolated from wild boar or consumption of contaminated meat for wild boar has caused human illness in Europe and North Asia. Several case reports linked to the consumption of raw liver or raw bile from wild boar have been reported from Japan and Korea without detection of virus in the boar meat (Matsuda et al. 2003; Kim et al. 2011b), in both cases genotype 4 HEV was recovered. Genotype 3 HEV RNA from a human case from Japan was found to have complete sequence homology over the entire ORF2 gene with HEV RNA isolated from wild boar meat that had been consumed by the case (Li et al. 2005). Furthermore, in Japan, genotype 3 HEV isolates from wild boar, deer and a human case that ate the deer meat had near-complete sequence homology over the ORF1, ORF2 and ORF3 portion of the genome demonstrating sylvatic transmission between wild game species in Japan (Takahashi et al. 2004). In this same survey, HEV RNA was isolated from three of seven wild boars (Takahashi et al. 2004). In Europe, HEV genotype 3 has been isolated from the livers, bile and serum of wild boar in Germany and France (Kaci et al. 2008; Adlhoch et al. 2009; Kaba et al. 2010); however the literature search did not reveal human cases linked to the consumption of HEV contaminated wild boar in Europe.

3.7.2 Conclusion

Published literature indicates wild boar and feral pigs are susceptible to infections from the same pathogenic microorganisms as domestic pigs.

International evidence exists to support an association between consumption of meat from wild boar and feral pigs with cases of foodborne illness due to *Trichinella* spp. and HEV. These have limited applicability to Australia since no evidence was found that *Trichinella* spp.

are prevalent in Australian feral pig populations that are harvested for human consumption and there is no data from Australia indicating that people are exposed to HEV through the consumption and handling of wild boar meat.

3.8 Ratites

A comprehensive search of the literature found no data describing the prevalence or level of contamination of microbiological hazards of ostriches and emus, either farmed or wild, on carcasses or on final processed meat products in Australia. Limited international literature provides data on a number of foodborne pathogens and microbiological quality of carcasses.

No articles were found describing foodborne illness associated with consumption of ratite meat.

3.8.1 Summary

Several international studies have examined the microbiological quality of ostrich carcasses during processing. A small Italian study of three abattoirs that also slaughter other domestic and farmed wild animals, found mean aerobic plate counts (APC) for ostriches immediately after skinning ranging from 0.98 – 1.34 log cfu/cm² and at the end of carcass dressing APCs ranged from 1.60 – 2.22 log cfu/cm² (Severini et al. 2003). In a small study (n=30) at a single South African export abattoir, mean APC values of slaughtered ostriches was 4.32 log cfu/cm² after skinning and 4.57 log cfu/cm² after chilling (Karama et al. 2003). A survey of ostriches in Zimbabwe for the presence of *Salmonella* by DNA probe, during processing and on processed meat products, found that 51% (61/120) of ostriches presenting for slaughter had feathers contaminated with *Salmonella*, 33% (40/120) of carcass wash waters were positive for *Salmonella*; none of the 120 meat fillets tested were positive for *Salmonella* (Gopo and Banda 1997).

In the USA, a relatively large study of ostrich carcasses from eight slaughterhouses in Ohio and one in Indiana detected *Salmonella* on 0.7% (1/152) of dressed carcasses and *E. coli* on 91% (116/128) of dressed carcasses. No isolates of *E. coli* O157:H7 were detected but the investigators did not look for other pathogenic *E. coli* strains. *Campylobacter* was detected on 10% (19/191) of dressed carcasses but the species was not determined. *E. coli* was isolated from the large intestine contents of 69% (149/217) of birds and *Campylobacter* was isolated from 3% (6/201) of ostrich large intestines; no *Salmonella* isolates were recovered from the large intestines of the ostriches (Ley et al. 2001).

Two studies have reported prevalence of antibodies to *T. gondii* in ostriches, one in Canada and one in Zimbabwe. The Canadian study detected antibodies in 3% (28/973) of farmed ostriches in six provinces (Dubey et al. 2000); the Zimbabwean study detected antibodies in 48% (24/50) of wild ostriches but were unable to isolate viable *T. gondii* cysts from the heart muscle of the seropositive birds (Hove and Mukaratirwa 2005).

3.8.2 Conclusion

No published literature was available describing the prevalence or concentration of microbiological hazards associated with ratites in Australia. However, international data indicate they are susceptible to infections from the same pathogenic microorganisms as ruminants and other meat animals. The limited evidence suggests they are unlikely to be a source of *T. gondii*.

There have been no cases of foodborne illness associated with consumption of ratite meat reported in the published literature.

3.9 Mutton birds

No published literature was found for the Tasmanian mutton bird using the search strategy described above.

4 Overall Conclusion

A comprehensive search of the literature found no published articles describing the prevalence or level of contamination of microbiological hazards in buffalo, deer, camel or ratites, either farmed or wild, on carcasses or on final processed meat products in Australia. Only internationally published data was available for these species.

Limited Australian data was available for microbiological hazards associated with kangaroos, and both international and Australian data was available for crocodiles, wild boar/feral pigs and rabbits. No data was identified that describes the pathogens associated with Tasmanian muttonbirds.

The minor and wild game species assessed during this review are susceptible to infections from the same pathogenic microorganisms as other meat animals commonly consumed in Australia.

Very little evidence was available from the published literature establishing consumption of meat from minor and wild game species as a cause of foodborne illness.

Appendix 2

E. coli and Salmonella Monitoring Program (ESAM) data 2008-2010

Acceptability of E. coli on minor and game meats in the export sector (ESAM

Table 1

Table 2Acceptability of Total Viable Count (TVC) on minor and game meats in the
export sector (ESAM 2008-2010)

	Number samples	Acceptable (%)	Marginal (%)	Unacceptable (%)	
		10,000-100,000 cfu/cm²	100,000-1000,000 cfu/cm²	>1,000,000 cfu/cm ²	
Camel	148	0	0	0	
Deer	13	0	0	0	
		≤ 10,000 cfu/cm ²	> 10,000 - ≤ 100,000 cfu/cm²	> 100,000 cfu/cm ²	
Kangaroo	3917	3766 (96.1%)	146 (3.7%)	5 (0.1%)	
Wild boar	894	886 (99.1%)	7 (0.8%)	1 (0.1%)	
		No performance criteria for TVC in Meat Notice 2005/06			
Emu 37 $34 \le 1,000 cfu$ (91.9%)		34 ≤ <i>1,000 cfu/</i> (91.9%)	cm² No cour	$ts > 10,000 cfu/cm^2$	
Ostrich	34	32 ≤ 1,000 cfu/ (94.1%)	, cfu/cm ² No counts > 10,000 cfu,)		

⁷ Performance criteria contained in: *Microbiological testing for process monitoring in the meat industry, Guidelines*, Meat Standards Committee (2002), for meat processed under AS4696; AQIS Meat Notice 2010/02 – *Microbiological testing of wild game carcases and products*; AQIS Meat Notice 2005/06- *ESAM sampling of ratites*

	2008	2009	2010
	Positive/total	Positive/total	Positive/total
	(%)	(%)	(%)
Camel	0/4	7/64	6/97
	(0%)	(10.9%)	(6.2%)
Kangaroo	10/2282	14/876	7/212
	(0.44%)	(1.6%)	(3.3%)
Deer	0/1	0/4	0/1
	(0%)	(0%)	(0%)
Emu	0/16	0/13	0/12
	(0%)	(0%)	(0%)
Wild boar	1/428	3/189	0/26
	(0.23%)	(1.65)	(0%)
Ostrich	0/12	1/12	0/12
	(0%)	(8.3%)	(0%)

Table 3Prevalence of Salmonella on minor and game meats in the export sector
(ESAM 2008-2010)

Table 4Salmonella serovars detected on minor and game meats in the export sector
(ESAM 2008-2010)

Serovar	Isolations	Species
S. Anatum	5	Camel (4), kangaroo (1)
S. Give	4	Wild boar (2), kangaroo (1), camel (1)
S. Infantis	3	Camel (2), kangaroo (1)
S. Fremantle	2	Kangaroo (2)
S. Saintpaul	2	Camel (1), kangaroo (1)
S. Virchow	2	Kangaroo (1), wild boar (1)
S. Havana	2	Camel (2)
S. Adelaide	2	Ostrich (1), kangaroo (1)
S. Meleagridis	1	Kangaroo
S. Chester	1	Kangaroo
S. Oranienburg	1	Camel
S. Orion	1	Kangaroo
S. Ohio	1	Camel
S. subs 1 ser 40:-:1,5	1	Kangaroo
S. subsp 1 ser 6,7:r:-	1	Kangaroo

Appendix 3

OzFoodNet Report





Foodborne outbreaks of gastrointestinal illness associated with minor meats, January 2001 to June 2011, Australia.

Prepared by: Timothy Sloan-Gardner Date: October 2011

Nature of report

This report summarises human illness due to foodborne outbreaks of gastrointestinal disease associated with minor meats in response to a data request from Michelle Robertson (FSANZ).

As per the request, minor meats were defined as: buffalo, antelope, camels, alpacas, llamas, deer, horses and donkeys (slaughtered other than in a wild state), rabbits, crocodile meat and ratites (ostrich/emu) – game animals (kangaroo, wallaby, wild boar, possum, mutton birds).

Data analysis

This analysis was carried out in the following manner:

- Reports of outbreaks were extracted from the OzFoodNet Outbreak Register. These were compared to those reported in the OzFoodNet Quarterly and Annual Reports. A full list of the search terms used to extract the data from the Outbreak Register is at Appendix A.
- Data were cleaned and recoded to provide consistent categories for data fields, including food vehicles.

Data dictionary

Year - Year of onset of the first case.

State - Where the outbreak occurred, or sometimes, where cases were resident.

Transmission - Description of the mode by which the outbreak was spread.

Setting - Where food was prepared.

Ill - Number of people meeting suspected and confirmed case definitions.

Hospitalised - Number of cases hospitalised during the outbreak.

Died - Number of cases who died during the period of the outbreak. The relative contribution of the infection to the deaths is not generally known.

Food vehicle mod - modified from another field "Food vehicle", but incorporating information from the field "Remarks" where relevant.

Comments - Explanatory information taken from a field "Remarks" that may aid interpretation.

Foodborne outbreaks of gastrointestinal illness associated with minor meats, January 2001 to June 2011, Australia.

Between January 2001 and June 2011 there were no foodborne or suspected foodborne outbreaks in which the food vehicle was identified, or suspected, as being a minor meat.

There were three foodborne or suspected foodborne outbreaks where a minor meat (kangaroo, roast rabbit and deer, respectively) was mentioned as being consumed however, these were not suspected as the source of infection for these outbreaks.

This summary is subject to some limitations given that it is often very difficult to identify the key vehicle causing outbreaks, or critical factors contributing to their occurrence.

Appendix A

Search terms used to identify minor meat-associated outbreaks in the OzFoodNet Outbreak Register:

- [Field: Year] = >"2000"
- [Field: Transmission=Foodborne/Suspected Foodborne]
- [Field: Food_Vehicle] Like "*buffa*" Or Like "*antel*" Or Like "*camel*" Or Like "*alpa*" Or Like "*llama*" Or Like "*deer*" Or Like "*horse*" Or Like "*donk*" Or Like "*wild*" Or Like "*rabbi*" Or Like "*croco*" Or Like "*rati*" Or Like "*ostri*" Or Like "*emu*" Or Like "*game*" Or Like "*kanga*" Or Like "*walla*" Or Like "*boar*" Or Like "*possum*" Or Like "*mutton*" Or Like "*bird*" Or Like "*hungi*"
- [Field: Remarks] Like "*buffa*" Or Like "*antel*" Or Like "*camel*" Or Like "*alpa*" Or Like "*llama*" Or Like "*deer*" Or Like "*horse*" Or Like "*donk*" Or Like "*wild*" Or Like "*rabbi*" Or Like "*croco*" Or Like "*rati*" Or Like "*ostri*" Or Like "*emu*" Or Like "*game*" Or Like "*kanga*" Or Like "*walla*" Or Like "*boar*" Or Like "*possum*" Or Like "*mutton*" Or Like "*bird*" Or Like "*hungi*"

Production practices

Information gained during a number of industry familiarisation visits has assisted in compiling the industry descriptions below. Data and information on the size of industry, production volumes, export markets and other industry statistics has been sourced from Proposal P1014 supporting documents⁸, compiled with the assistance of industry representatives and members of the Minor and Wild Game Working Group.

1 Farmed animals (intensive/extensive/harvested) slaughtered under AS4696:2007

1.1 Buffalo

Feral buffalo populations are spread across the top end of the Northern Territory (NT) with an estimated population of around 150,000 head. A small herd of buffalo are farmed in every state of Australia for milk and dairy production, live export and a limited amount of meat production. The total farmed buffalo population is estimated to be 15,000 head.

Meat production is primarily derived from wild caught buffalo from the NT with a small proportion derived from farmed animals culled from the buffalo dairy industry.

Buffalo Primary Production and Processing

Free roaming feral buffalo typically graze on native and introduced weed grasses in the tropical northern part of the NT. Buffalo are susceptible to diseases and conditions similar to cattle and other large ruminants, however, feral buffalo populations do not receive veterinary inputs.

After capture, buffalo are typically held for several days and undergo ante mortem inspection. Feed is generally withheld for 24 hours prior to slaughter.

Processing of buffalo meat is similar to cattle and in accordance with the Australian Standard for the Hygienic Production and Transportation of Meat and Meat Products for Human Consumption (AS 4696:2007). Captive bolt stunning is not suitable for adult buffalo and a high calibre rifle is used to kill the buffalo prior to hanging and bleeding. Inspection protocols are similar to those of cattle and other ruminants and all viscera are disposed of after inspection for liver fluke, Taenia saginata, cysticerci and lymph node lesions.

Carcasses are typically broken down into primal cuts, vacuum packaged and chilled for distribution into the supply chain.

The major production and processing stages are shown in Figure 1

⁸ http://www.foodstandards.gov.au/foodstandards/proposals/proposalp1014primary5331.cfm



Figure 1 Buffalo production and primary processing

1.2 Camel

Feral camels are scattered throughout the arid and semi-arid interior of Australia with a population currently estimated at between 500 thousand and 1 million head. Approximately half of the feral camel population are estimated to be in Western Australia (WA), a quarter in the NT and the remaining spread across western Queensland and northern South Australia (SA).

The Australian camel meat industry is based largely on the harvesting of feral camels in the arid central regions with a small proportion of camels (1-2%) sourced from commercial farms. The majority of Australian camel meat is exported, with a limited amount entering the domestic market.

Camel Primary Production and Processing

Feral camels wander extensively according to conditions and may cover up to 70 kilometres in a single day. The feral camel population can utilise most habitats in the arid and semi-arid areas of Australia, depending on availability of food, water and summer shade. Free-ranging camels browse trees and select a wide variety of plants, eating up to 80% of available plant species in a given location. They tend to select the freshest first but always mix intake. Camels prefer plants with a high moisture and mineral content and prefer the leaves of trees, shrubs and herbs or forbs over grass. Grass is mainly eaten after rain and before herbs and forbs are available. As a consequence of grazing a wide variety of plants, camels may be exposed to many poisonous plants found in desert areas and are especially at risk if feed is limited. When forage is green and moist, feral camels gain all the water they need from their food and do not require drinking water. In the summer months, camels will drink regularly if water is available.

Vaccination against clostridial diseases is recommended for farmed camels.

Camel production is conducted according to the *Model Code of Practice for the Welfare of Animals: The Camel* which addresses camel management for all types of enterprises, including watering and feeding, mustering, transport, reproduction and health.

Processing of camel meat is similar to cattle and is in accordance with the Australian Standard for the Hygienic Production and Transportation of Meat and Meat Products for Human Consumption (AS 4696:2007). The hump of the camel (fat tissue) is removed prior to carcass splitting and retained for human consumption. The neck of the camel is excised at the shoulder to prevent contact of cut surfaces on the floor of the processing facility. Carcasses are typically fabricated into primal cuts, edible offal and trimmings, packed into cardboard boxes, labelled and frozen for distribution into the supply chain.

The major production and processing stages are shown in Figure 2



Figure 2 Camel production and primary processing

1.3 Deer

Production of deer meat in Australia is concentrated in the south-eastern states with some production occurring in Queensland and WA. The predominant farmed species is Red deer followed by Fallow then Elk deer. Other breeds include the tropical breeds Rusa and Chital, Sambar (found in the Victorian alps) and Sika deer, although these make up only a very small proportion of the total farmed deer population in Australia.

The Australian deer industry produced an estimated 288 tonnes of venison in 2010 with over 65% of meat exported, predominantly to the European Union and Southeast Asia. The remaining 35% of product enters the domestic restaurant and speciality butcher market.

Deer Primary Production and Processing

Deer are extensively grazed on improved pastures with supplementary feeding (grains like barley and corn, and silage) provided when necessary.

Deer are less able to maintain body temperature therefore paddocks have shelter and wind breaks in place to minimise cold stress. Handling practices are also such to keep stress to the animal at a minimum.

Most diseases and health issues are related to stress but deer are also susceptible to diseases of other ruminants such as clostridial enterotoxaemia. Deer are also susceptible to yersiniosis and cryptosporidiosis and when cold stressed; pasteurellosis. Vaccinations may be used for treatment against clostridial diseases (ie: with a 5 in 1 commercial vaccine) but this is becoming less common. Treatments for parasite control are also used.

Animals are transported directly to the abattoir on specialty deer transport trucks or modified cattle trucks to ensure animals are in semi-darkness and as unstressed as possible. Feed is withheld for 12-24 hours before transport, although not always necessary as transport time can be sufficient to ensure stomach emptying before slaughter. Water is provided in the trucks and in hot weather conditions, deer may be hosed prior to and during transport to reduce any heat-related stress.

Requirements for the transport of deer are contained in the Australian Animal Welfare Standards and Guidelines – Land Transport of Livestock.

Processing of deer is similar to other small ruminants and is in accordance with the *Australian Standard for the Hygienic Production and Transportation of Meat and Meat Products for Human Consumption (AS 4696:2007).* Venison is typically vacuum packaged and frozen for distribution into the supply chain.

The major production and processing stages are shown in Figure 3



Figure 3 Deer production and primary processing

2 Farmed animals (intensive/extensive/harvested) slaughtered under Australian Standards AS 4466:1998, AS4467:1998 and AS5010:2010

2.1 Rabbit

Rabbits were first introduced to Australia with the First Fleet in 1788 but numbers remained relatively contained until the European rabbit was introduced into Victoria in 1859, resulting in an explosive increase in the population. Rabbits have been harvested from the wild in large numbers since the mid-1800's, however, due to the pest status of wild rabbits, commercial farming was prohibited throughout Australia until 1987. All jurisdictions, with the exception of Queensland and the NT, now allow commercial rabbit farming.

Commercial rabbit farming became established after the introduction of calcivirus in 1996. Rabbits for human consumption are now produced predominantly on intensive feedlot farms with limited supply of wild rabbits by professional game harvesters. The number of harvested wild rabbits dropped from approximately 2.7 million per year in 1990, to about 100,000 per year in 1999 (NSW Department of Primary Industries 2006). Since the commercial industry was first established there has been a trend for intensification of production. The majority of commercial rabbits are produced in New South Wales, particularly in the north-west and central regions.

Rabbit Primary Production and Processing

Rabbits are produced in accordance with the *Model Code of Practice for the Welfare of Animals: Intensive Husbandry of Rabbits (SCARM Report 33).* Disease control is a critical component of rabbitry management and important infectious diseases include pasturellosis, coccidiosis, myxomatosis and rabbit calcivirus disease (all of which pose no threat to human health). Rabbits are able to be vaccinated against rabbit calcivirus but it is an offence to vaccinate rabbits against myxomatosis in all Australian jurisdictions. Feed is commercially available as pellets and cereal grains to provide protein. Commercial feed is supplied premixed with 'off-label' veterinary pharmaceuticals to control bacterial scours and coccidiosis. Pre-mixes are specific for breeding stock, weaners, growers and finishers. Lucerne and oaten hay may also be provided to weaners up to 8 weeks of age to provide roughage.

Several slaughter methods are currently used across the industry. Slaughter practices may include guillotine or high speed blade decapitation and stunning methods, if used, include gas or electric shock. Rabbits are currently processed according the existing *Australian Standard for the Hygienic Production of Rabbit Meat for Human Consumption (AS 4466:1998)*.

The major production and processing stages are shown in Figure 4.

On-farm inputs and



- manufactured feed supplemented with broad spectrum antibiotics and coccidiostats Water
- Agricultural and veterinary chemicals
- Stress Pathogen stability in animals and the environment

activities:

conditions:

equipment Workers



Bucks

Inputs/activity:

Breeding and pre-weaning

Figure 4 Farmed rabbit production and processing

2.2 Crocodile

Commercial crocodile farming began in Australia in the 1980s. Presently the industry comprises 14 commercial farms situated in the NT, Queensland and WA. Farming is centred on the production of high-value skins from the saltwater crocodile (*Crocodylus porosus*) with meat for human consumption produced as a by-product.

It is estimated 100 tonnes of meat is processed annually with 60% exported to Japan, Malaysia, Hong Kong and Taiwan. The remaining 40% is consumed domestically through restaurants and caterers with very little retailed through supermarkets.

The *Australia New Zealand Food Standards Code* only permits crocodile meat for human consumption to be derived from farmed animals.

Crocodile Primary Production and Processing

The Code of Practice on the Humane Treatment of Wild and Farmed Australian Crocodiles applies to crocodiles farmed for meat production, while slaughtering is in accordance with the Australian Standard for the Hygienic Production of Crocodile Meat for Human Consumption (AS 4467:1998).

Australian crocodile farms operate captive breeding programs with breeding animals often originally sourced from the wild. More recently, farms are keeping juvenile crocodiles as replacement breeding stock. Western Australia and the NT also permit collection of eggs and juveniles directly from the wild for stocking farms.

Crocodile eggs are collected from the nest within 24 hours of oviposition to minimise embryo mortality. They are marked to indicate "upright" position, as rotation causes death of any embryo, then washed and "candled" to determine presence of an embryo. Eggs are then placed into trays, tagged to record nesting information, and incubated under constant humidity at 32°C; producing higher embryo survival and majority male sex (~86%). At 32°C, hatching occurs after 80 days.

Once hatched, crocodiles are placed into specifically designed hatchling pens. These are environmentally-controlled with water maintained at a constant 32°C. Hatchlings are fed a diet of fine minced red meat, kangaroo or chicken meat fortified with vitamins and minerals. After the first year, the hatchlings are moved into yearling pens where they are fed a coarser meat mince. During the third year, crocodiles are moved into grow-out pens and weaned onto chicken heads until they reach harvest size. Stocking densities are continually monitored and modified as animals grow.

Water is sourced from town supply or rain water and stored in on-site tanks. Salt water can be used in outdoor billabongs and grow out ponds. Water can also be re-used following filtration and chlorination steps. Raw meat is sourced in frozen blocks but may be left at ambient temperatures for extended time prior to feeding.

Harvest of crocodiles occurs when their belly skins measure between 35 and 45 cm; corresponding to a total length of around 1.5-1.9 meters. This equates to an average age of 3 years, although can be between 2-5 years.

Animals are inspected to determine acceptability for skin size and quality requirements. Any diseased or injured animals are rejected. Selected animals are then transferred to individual holding pens to reduce stress and disturbance from fellow pen-mates and preserve skin quality. Food is withheld for up to a week prior to slaughter which minimises potential for ingesta spillage during processing.

Crocodiles are first stunned (to assess skin quality) then killed either by a bullet to the brain or insertion of a knife to sever the spinal cord and pith⁹ the brain. If shot, they are then also immediately pithed. Carcases are then hung by the tail, washed and bled. After bleeding, the entire carcass is scrubbed with a sanitiser (hypochlorite solution or acetic acid) and hung by the tail in the cool room overnight at 0°C (carcass temperature maintained below 4°C). The bung and throat may also be plugged (or bagged) to prevent leakage of gut content. An additional chlorinated bath wash may also be undertaken prior to carcasses being placed in the chiller. Feet and tail tips may also be removed.

Skinning is done either while hanging from a chain or on a table. Opening lines, or first cuts, depend on the style of skin required with the majority along the animal's back. The key requirements in the skinning process are: to avoid cutting or nicking the skin; and to avoid contact between the carcass meat and the outer surface of the skin.

Once the skin is removed, carcasses are broken up into various portions. This can occur with or without the carcass first being eviscerated (depending on market requirements and abattoir practices). Meat portions are dipped in an antimicrobial solution such as 0.15% glacial acetic acid, chlorine solution or 1.3% acetic acid, prior to being vacuum packed and frozen. Some processing of crocodile meat into value-added products like marinated or minced product is also undertaken.

The major production and processing stages are shown in Figure 5.

⁹ Spinal cord and blood vessels severed behind the skull.





2.3 Ratites

The ratite industry in Australia produces meat for human consumption from farmed ostrich and emu for supply into the export and domestic markets.

No wild harvest of emus is permitted therefore commercial farms maintain breeding birds, or occasionally, introduce fertilised eggs to the flock. To maintain and replenish ostrich flocks, producers have their own on-farm breeding programs or introduce fertilised eggs to hatch, or 12-week old birds to grow out.

Commercial farming of emus is undertaken throughout Australia with emu oil being the commercially important product and meat produced as a by-product. In 2012, the size of the industry was estimated at 50 licensed farms; 3500 birds were slaughtered producing 38 tonne of meat and 19,600 litres of oil. While 90% of the oil produced enters the domestic market, less than half of the meat is distributed nationally.

The main commercial products of farmed ostriches are meat and leather, and to a lesser extent, oil and feathers. In 2012, the Australian ostrich industry consisted of 4-5 commercial farms, approximately 10,000 birds and produced around 30 tonnes of meat. The majority of this is exported to premium markets in the United States, Canada, Japan and at times, the European Union (EU).

To satisfy EU market access requirements, farms adhere to the *Australian Ratite Industry On-Farm Surveillance Plan* which incorporates, among other things, traceability and biosecurity measures in relation to Newcastle Disease (ND).

Processing of ratites is in accordance with the Australian Standard for the *Hygienic Production of Ratite (Emu/Ostrich) Meat for Human Consumption* (AS 5010: 2001).

Ratite Primary Production and Processing

Ratites are reared using semi-intensive production practices, grazing on improved pastures with supplementary feeding provided when necessary. Eggs laid in field nests are collected and incubated. Ostrich eggs may be cleaned with disinfectant and stored at <18°C to halt embryo development. Chicks are reared in indoor/outdoor runs with artificial heating, before being transferred to outdoor runs for grow out. The diet of chicks consists of home-mixed cereal mixes or commercial pellets. Additionally, ostrich chicks are fed bacterial cultures such as yoghurt, as well as having early contact with 'clean' soil and pasture to promote bacterial colonisation of the gut.

Emus are considered hardy to disease but may be affected by Erysipelas (*Erysipelothrix rhusiopathiae*). *E. rhyusiopathiae* is not a zoonotic organism and treatment includes vaccination (Eryvac) as well as antibiotics such as penicillin, oxytetracycline or chlortetracycline. Use of antibiotics (e.g. amoxicillin) to treat gastrointestinal infections and clostridia is common in ostrich chicks, while ostriches of all ages are susceptible to respiratory aspergillosis.

Slaughter of ratites occurs when birds reach 10-14 months of age for ostrich and 15-16 months for emu. Birds are transported directly from farms to the abattoir on purpose built trucks. Feed is withheld from ostrich for 12-24 hours prior to transport but not from emu (as oil is the main product). Upon receipt at lairage facilities, birds are inspected and any suspect birds quarantined.

For slaughter, birds are first electrically stunned, hung, an incision made in the neck and the head removed. After bleed-out, feathers are manually removed followed by removal of the lower legs at the knee joint and re-hanging. Any remaining feathers and skin is then removed. Particular care is taken with removal of skin from ostrich due to its high commercial value.

As only the hind legs and pelvic cradle are used for meat, evisceration involves removal of the entire neck, wing, chest and abdominal sac as a single unit. This minimises the risk of contaminating the carcass from spilled ingesta.

Carcass cradles are then loaded into the chiller (achieving a deep muscle temperature of 2-3°C within 24 hrs) prior to being portioned, packed and frozen for distribution into the supply chain.

The major production and processing stages are shown in Figure 6.



Figure 6 Ratite production and primary processing

3 Wild game animals slaughtered under AS4464:2007

3.1 Muttonbird

Muttonbirds, also known as short-tailed shearwaters, are a migratory bird harvested for a 3-4 week period each year in Tasmania. Around 100,000 birds are commercially harvested annually from an estimated population of over 20 million. Quota limits are applied through issue of recreational permits and commercial leases by Tasmanian Parks, Wildlife and Heritage. Granting of commercial leases is restricted to three islands: Trefoil Island, Big Dog Island and Babel Island which are managed by the Aboriginal Land Council of Tasmania.

Approximately 85-90% of product is marketed through speciality butcher shops in Tasmania. The remainder of product is distributed interstate with no product exported in 2012.

Muttonbird Harvest and Processing

The harvesting and processing of muttonbirds complies with requirements of the Australian Standard for Hygienic production of wild game meat for human consumption (AS 4464:2007) and the Australian Standard for Hygienic production of poultry meat for human consumption (AS 4465:2006).

Processing of muttonbirds occurs in small purpose built facilities situated in close proximity to the island's muttonbird rookery. Final product may include skin-off or clean (plucked) carcasses marketed as fresh, frozen or salted product.

Harvesting of muttonbirds involves the bird being manually retrieved from burrows in the rookery, humanely killed then transported to the onsite processing facilities. Where gurry (the oily gut content) is collected, carcasses are placed onto a spit passed through the lower beak for transport. This keeps the birds upright and prevents gurry leakage onto feathers. Alternatively, gurry can be removed in the field prior to transport.

Upon receipt at the processing facilities, birds are placed into a waterbath. The head, wings and feet are removed, then, depending on operator practices, birds may be processed as either skin-off or clean carcasses. For skin-off, the skin (with feathers intact) is manually removed by initially tearing or cutting down the centre line of the breast and then pulling the skin down over the tail. Plucked birds undergo an initial rough pluck, followed by immersion in a scald tank, then a final pluck and brush down to remove all feathers and remaining down. Plucked carcasses are placed into the cold room for approximately 3 hours to facilitate evisceration and further processing. Skin-off birds undergo a wash step before and after evisceration before being placed into a cool room to drain and chill. Once chilled, birds are packaged, chilled or frozen, and distributed to storage or retail facilities.

Salted birds are only produced from cleaned birds. Following evisceration, cleaned birds are rubbed and covered with dry rock salt (food grade) before being packed into clean plastic barrels (usually 50 per barrel). After 24 hours, the barrels are topped up with a brine solution and the product is distributed. Refrigerated storage is not required for salted muttonbird product.

Untreated sea water is used for processing operations including in waterbaths, scald tanks and for washing carcasses and cleaning equipment and facilities. Waste, including head, feet, wings, feathers, viscera and rejected carcasses is collected and disposed of into the ocean.

The major production and processing stages are shown in Figure 7.



Figure 7 Muttonbird harvest and primary processing

3.2 Kangaroo

Four species of kangaroo are commercially harvested on the Australian mainland and two species of wallaby are commercially harvested in Tasmania:

- Red kangaroo (*Macropus rufus*), harvested in NSW, Qld, SA, WA
- Eastern grey kangaroo (*M. giganteus*), harvested in NSW, Qld
- Western grey kangaroo (*M. fuliginosus*), harvested in NSW, SA, WA
- Common wallaroo or euro (*M. robustus*), harvested in NSW, Qld, SA, WA
- Bennett's wallaby (*M. rufogriseus rufogriseus*), harvested in Tasmania,
- Tasmanian pademelon (a species of wallaby) (*Thylogale billardierii*), harvested in Tasmania.

Kangaroos commercially harvested for human consumption are widely dispersed across Australia and share habitat with a wide array of other wildlife and in the pastoral grazing areas of Australia, they co-exist with domestic livestock; sheep, cattle and other ruminant species.

Kangaroo Primary Production and Processing

Kangaroos are harvested from areas designated in each jurisdiction's kangaroo management plan. Requirements exist for harvesters to be licenced, hold approved qualifications in firearms proficiency and marksmanship, and have approved qualifications in hygienic field dressing of kangaroos. Vehicles used to harvest kangaroos are fitted out for field processing and are registered and approved by the controlling jurisdictions food safety authority and maintained in a hygienic and mechanically sound state. To comply with animal welfare requirements, all kangaroos and wallabies must be taken in accordance with the *National Code of Practice for the Humane Shooting of Kangaroos and Wallabies for Commercial Purposes*.

Shot kangaroos are bled, eviscerated and hung on the vehicle according to the requirements of the Australian Standard *AS4464:2007 - Hygienic production of wild game meat for human consumption.* Only kangaroos with a single head shot can be accepted for processing. The head and hind-feet are removed in the field as well as the tail for all species except red kangaroo. Harvested kangaroos are tagged with each jurisdiction's National Parks and Wildlife tags to monitor harvest quotas, and processor tags for traceability and the harvester's food safety declaration.

Kangaroo carcasses are transported to the processor by refrigerated truck with air and deep muscle temperature monitored. In accordance with AQIS Meat Notice 2009/04, carcasses must be processed within 14 days of field dressing. Carcasses are skinned, trimmed and inspected, including the attached heart, liver, kidneys and lungs, for abnormalities and lesions. Meat for human consumption is produced as primal cuts or further processed product (ie: sausages, burgers, mince). A metal detection step (ferrous and non-ferrous) may be applied before and after packaging depending on the facility.

Harvested kangaroo meat is used for human consumption and pet supplies and is sold both domestically and internationally. The majority of kangaroo meat sold for human consumption in Australia is processed at export certified establishments.

The major harvest and processing stages are shown in Figure 8.



Figure 8 Kangaroo harvest and processing

3.3 Wild boar

Feral pig (*Sus scrofa*) populations became established in Australia soon after European settlement from pig stocks imported from Europe and Asia that were allowed to roam or escaped. The current feral pig population of up to 23.5 million head are spread across approximately half of the Australian continent, from western Victoria, through New South Wales into Queensland and parts of South Australia, and across northern Australia. Isolated populations can also be found in Tasmania and a few offshore islands.

Australian feral pig meat, which is marketed as "wild boar" has been commercially harvested for export since 1980. The major markets for Australian wild boar are EU countries where wild boar meat is traditionally consumed.

Wild boar Primary Production and Processing

Wild game harvesters who are licenced to commercially harvest kangaroo are also licenced to commercially harvest feral pigs and other wild game for human consumption. The game harvester is required to have qualifications in firearm proficiency and marksmanship and the hygienic field dressing of wild game and have a vehicle fitted out for field dressing that is registered and approved by the controlling jurisdiction's food safety authority and maintained in a hygienic and mechanically sound state. There is, however, no quota system for feral pigs as they are considered a pest species in every Australian jurisdiction. Game processors receiving feral pigs require pigs to be tagged for traceability purposes and for providing the harvester's signed food safety declaration as per the kangaroo harvest. As with kangaroo harvest, feral pigs are hung, bled and eviscerated according to the requirements of AS 4464. The legs, head and heart, liver, kidneys and lungs are left attached to the carcass for inspection. Time and temperature requirements, from being shot to being placed in the chiller, and deep muscle temperature reaching 7°C, are the same as for kangaroos. Harvested feral pigs are transported to processors as per kangaroos. Upon receival, the head is removed, bagged and attached to the carcass for traceability and inspection purposes. The carcasses are skinned, trimmed and inspected, including the heart, liver, kidneys and lungs, for abnormalities and lesions. The diaphragm muscle is excised and tested for trichinellosis in a DAFF Biosecurity approved/accredited laboratory using a validated test protocol for meat intended to be exported to the EU. Skun carcasses then undergo a hot water wash to remove contaminating hair and, depending on the client, are either cut six ways and boxed whole, or boned out and processed as primal cuts and manufactured meat products.

The major field harvest and processing stages are shown in Figure 9.

Harvest and processing steps for other wild game are comparable to both kangaroo and wild boar according to AS 4464-2007 *Hygienic production of wild game meat for human consumption*.





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