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ORIGINAL ARTICLE

The microbiological conditions of the carcasses of six species after dressing at a small abattoir

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At a small abattoir, samples were collected from carcasses of cattle, pigs, deer, bison, ostriches and emus at the ends of the dressing processes. A single sample was collected from each of 50 or 25 carcasses of each species, by swabbing a randomly selected area of 100 cm^2. Total aerobes, coliforms and Escherichia coli *were enumerated in each sample. The microbiological conditions of the carcasses were assessed by reference to the log mean numbers of total aerobes, coliforms and* E. coli *estimated from sets of counts recovered from 25 samples, or to the log total numbers of coliforms and* E. coli *recovered from each set of 25 samples. The log mean numbers of total aerobes on beef carcasses were about 2·5 log cfu cm^{-2}. The log mean numbers of aerobes on deer carcasses were similar, but the log mean numbers on other types of carcass were 0·5–1 log unit more. The coliforms recovered from carcasses were largely* E. coli*, except for pig carcasses where* E. coli *were only about 10% of the coliforms recovered.* Escherichia coli *were recovered from the majority of samples from beef and pig carcasses, at log mean numbers about 1·5 and 2·5 log cfu 100 cm^{-2}, respectively, and log total numbers recovered $>$ 3 log cfu 2500 cm^{-2}.* Escherichia coli *were recovered from minorities of samples from deer, buffalo, ostrich and emu carcasses at log total numbers about 2 log cfu 2500 cm^{-2}. The findings indicate that when carcasses of different species are dressed at an abattoir, similar microbiological contamination of the various types of carcass cannot be assumed.*

Introduction

Studies of the hygienic performances of beef carcass dressing processes have shown that there are wide variations between processes in the extents to which carcasses are contaminated with bacteria (Roberts et al. 1984, Jericho et al. 1994). Despite this, it appears that the performance of an individual process for dressing beef carcasses will tend to be consistent with respect to the numbers of aerobes, coliforms and *Escherichia coli* deposited on the carcasses, with the numbers of each remaining much the same irrespective of the season of the year or whether carcasses are from feedlotted cattle or culled cows (Jericho et al. 1996, Gill et al. 1998a).

Individual processes for dressing the carcasses of other species may be similarly consistent (Bell and Hathaway 1996, Gill and Jones 1997). However, studies of the hygienic performances of dressing processes have generally involved consideration of the dressing of only one species at any plant. Most larger packing plants will indeed slaughter and dress only

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one species, but smaller plants may process several. In fact, the range of species processed at some plants is increasing as the farming of game and exotic meat animals becomes more prevalent (Deeming 1994, Galbraith et al. 1998).

If the hygienic quality of the carcasses produced at such plants is to be properly controlled, it is necessary to know whether the dressing of all species can be regarded as a single process or if the dressing of each species must be regarded as a distinct process with unique hygienic characteristics. Therefore, the microbiological conditions of the carcasses of six species at the completion of dressing at a small packing plant were assessed.

Materials and Methods

Carcass dressing process

The plant involved in the study is part of a meat research facility. It is inspected by the national authority responsible for meat inspection, and much of the meat produced is dispatched for normal commercial uses. Typically, the plant is operated on 2 or 3 days each week, with 20 to 30 animals of a single species being slaughtered on each day. Cattle and pigs are regularly slaughtered at the plant, but occasional batches of white tailed deer, bison, ostriches and emus have also been slaughtered.

After stunning by a captive bolt, each animal is shackled, raised to the processing rail and stuck. After bleeding out, carcasses of cattle, deer and bison are moved to the first work station. The carcasses of birds are not scalded, but they are plucked before they are moved to the first work station. After bleeding, pig carcasses are scalded by immersion in water of about 65°C for about 3 min and then are dehaired in an open cradle dehairing machine. The dehaired carcasses are singed with a hand-held torch and subjected to both further mechanical flailing and manual scraping to polish each while it is still on the cradle of the dehairing machine. Subsequently, the polished pig carcasses are also moved to the first work station.

At that first work station, the throat is opened, the head and neck are dressed, the oesophagus of mammals is tied, and the head is removed. The front hooves of mammals or the wings of birds are also removed.

The carcass is then moved to a second work station where, except for pigs, the hindquarters are skinned. The tail and rear hooves are removed from the carcasses of mammals, and the feet from the carcasses of birds. The hind legs of all carcasses are each attached to a hook dependant from a trolley on the rail. The bung or vent is freed, enclosed securely in a plastic bag, and pushed into the body cavity. All carcasses except those of pigs are then moved to a third work station where the forequarters of each carcass are skinned, and the front hocks are cut from the carcasses of mammals.

At a fourth work station, the sternum of each mammalian carcass is split, using a reciprocating saw. The abdomen is opened and first the abdominal and then the thoracic viscera are removed. With the carcasses of birds, the neck is cut off. Then, the rib cage with the contained viscera is cut from the carcass. After that, the abdomen is opened along its length and the abdominal viscera are removed. After evisceration the body cavity is stripped of fat and trimmed. The carcasses of cattle, pigs and bison are split, using a counterweighted band saw, at a fifth work station. Then, each side or carcass is trimmed, before being washed for about 5 min with water of about 50°C applied from a hand-held spray nozzle.

Sampling of carcasses

A single sample was collected from each carcass, approximately 5 min after it had been washed, by swabbing with a moistened gauze swab an undelimited area of approximately 100 cm^2, as previously described (Gill and Jones 1998, Gill et al. 1996). For each species, samples were collected from 25 or 50 carcasses over 2, 3 or 4 days, with each consecutive carcass being sampled until the required number of samples had been obtained. The site to be sampled on each carcass was selected at random using a random number generating program and with reference to a grid specific for each species which divided one side of a carcass into areas each of about 100 cm^2 (Gill et al. 1996, Gill and Jones 1997).

Microbiological analysis

The total counts recovered from each sample were enumerated by a spread plate procedure with a detection level of 1 cfu cm^{-2}, and coliforms and *E. coli* were enumerated by a hydrophobic grid membrane filter procedure with a detection level of 1 cfu 100 cm^{-2}, as previously described (Gill et al. 1996).

The bacterial counts of each type from each type of carcass were grouped into sets of 25 consecutive counts. All counts were transformed to log values. When counts were recovered from 20 or more of 25 samples, values for the mean log ($\bar{x}$) and standard deviation (s.d.) of a set of 25 bacterial counts were calculated on the assumption of a log normal distribution of counts (Brown and Baird-Parker 1982). In the calculation of $\bar{x}$ and s.d. for sets of *E. coli* or coliform counts, log value of $-0{\cdot}5$ 100 cm^{-2} were assumed for samples in which *E. coli* and/or coliforms were not detected at the level of 1 *E. coli* or coliform cfu 100 cm^{-2}. When values for $\bar{x}$ and s.d. were calculated for a set of counts, a value for the log mean (log A) was also calculated for the set, from the formula $\log A = \bar{x} + \ln 10\ s^2/2$ (Kilsby and Pugh 1981). A value for the log of the total number of bacteria recovered (N) was calculated for each set of counts by summing the counts in each set and obtaining the log of the sum. The microbiological conditions of carcasses were preferably compared by reference to log A values, but were compared by reference to values for N when the numbers of bacteria-positive samples were too few for estimation of log A values. All calculations were performed with Microsoft Excel Version 4, statistical functions (Microsoft Corp. Redmond, Washington, USA).

Results

Total aerobic counts were recovered from all, and coliforms that were largely *E. coli* from most samples from 50 beef carcasses (Table 1). Estimated log mean numbers of total aerobes, coliforms and *E. coli* on dressed beef carcasses were about 2·5 log cfu cm^{-2}, 2·0 log cfu 100 cm^{-2}, and 1·5 log cfu 100 cm^{-2}, respectively.

Total aerobic counts were recovered from all, and coliforms and *E. coli* from most samples from pig carcasses also (Table 2). However, the log mean numbers of total aerobes, coliforms and *E. coli* estimated for pig carcasses were, respectively, about 1, 2 and 1 log units greater than the corresponding values estimated for beef carcasses.

Total aerobic counts were recovered from all samples from carcasses of deer and buffalo (Table 3). The log mean numbers of total aerobes estimated for deer carcasses were similar to those estimated for beef carcasses, but the corresponding value estimated for buffalo carcasses was about one log unit greater. Coliforms that were largely *E. coli* were recovered from a minority of deer carcasses and a small

Table 1. Statistics for sets of 25 total aerobic counts (cfu cm^{-2}), coliform counts (cfu 100 cm^{-2}) or *E. coli* counts (cfu 100 cm^{-2}) obtained from randomly selected sites on beef carcasses leaving the dressing process at a small abattoir

Count	Set	Statistics				
		$\bar{x}$	s.d.	no	log A	N
Total aerobes	1	1·93	0·62	0	2·37	3·60[a]
	2	2·09	0·63	0	2·55	3·83[a]
Coliforms	1	0·93	0·93	3	1·93	3·33[b]
	2	0·85	1·01	4	2·01	3·08[b]
E. coli	1	0·55	0·94	6	1·56	3·20[b]
	2	0·54	1·01	7	1·72	3·07[b]

$\bar{x}$ = mean log.
s.d. = standard deviation.
no = number of samples from which bacteria were not recovered.
log A = estimated log of the arithmetic mean.
N = log of the total number recovered from [a]25 cm^2 or [b]2500 cm^2.

Table 2. Statistics for sets of 25 total aerobic counts (cfu cm^{-2}), coliform counts (cfu 100 cm^{-2}) or *Escherichia coli* counts (cfu 100 cm^{-2}) obtained from randomly selected sites on pig carcasses leaving the dressing process at a small abattoir

Count	Set	Statistics				
		$\bar{x}$	s.d.	no	log A	N
Total aerobes	1	2·28	0·87	0	3·16	4·68[a]
	2	2·60	0·87	0	3·47	4·89[a]
Coliforms	1	2·56	1·22	0	4·27	4·97[b]
	2	2·30	1·03	1	3·51	4·31[b]
E. coli	1	1·37	1·05	2	2·64	4·04[b]
	2	1·33	1·15	5	2·86	3·21[b]

$\bar{x}$ = mean log.
s.d. = standard deviation.
no = number of samples from which bacteria were not recovered.
log A = estimated log of the arithmetic mean.
N = log of the total number recovered from [a]25 cm^2 or [b]2500 cm^2.

Table 3. Statistics for sets of 25 total aerobic counts (cfu cm^{-2}), coliform counts (cfu 100 cm^{-2}) or *Escherichia coli* counts (cfu 100 cm^{-2}) obtained from randomly selected sites on carcasses of white tailed deer or buffalo leaving the dressing processes at a small abattoir

Species	Count	Set	Statistics				
			$\bar{x}$	s.d.	no	log A	N
Deer	Total aerobes	1	1·51	0·74	0	2·15	3·65[a]
		2	1·79	0·66	0	2·28	3·50[a]
	Coliforms	1	–	–	20	–	2·36[b]
		2	–	–	16	–	2·69[b]
	E. coli	1	–	–	20	–	2·00[b]
		2	–	–	17	–	2·64[b]
Buffalo	Total aerobes	1	2·46	0·90	0	3·39	4·63[a]
	Coliforms	1	–	–	11	–	1·78[b]
	E. coli	1	–	–	14	–	1·45[b]

$\bar{x}$ = mean log.
s.d. = standard deviation.
no = number of samples from which bacteria were not recovered.
log A = estimated log of the arithmetic mean.
N = log of the total number recovered from [a]25 cm^2 or [b]2500 cm^2.
– = insufficient data for calculation of the statistic.

majority of buffalo carcasses at log total numbers about one log unit less than the corresponding values for beef carcasses.

Total aerobic counts were recovered from all samples from ostrich and emu carcasses (Table 4). The log mean numbers of total aerobes estimated for those carcasses were somewhat greater than the corresponding values estimated for beef carcasses. Coliforms that were largely *E. coli* were recovered from a minority or small majority of the samples at log total numbers about one log unit less than the corresponding values for beef carcasses.

Discussion

In a study of beef carcasses leaving the dressing processes at ten commercial abattoirs, large differences in the microbiological conditions of the carcasses produced at different abattoirs were observed (Gill et al. 1998a). Log mean numbers of total aerobes, coliforms and *E. coli* estimated for carcasses from each of the processes ranged from about 2 to 5 log cfu cm^{-2}, about 0–3 log cfu 100 cm^{-2} and about 0–2 log cfu 100 cm^{-2}, respectively. There was no consistent relationships between the

Table 4. Statistics for sets of 25 total aerobic counts (cfu cm^{-2}), coliform counts(cfu 100 cm^{-2}) or *Escherichia coli* counts (cfu 100 cm^{-2}) obtained from randomly selected sites on carcasses of ostriches or emus leaving the dressing processes at a small abattoir

Species	Count	Statistics				
		$\bar{x}$	s.d.	no	log A	N
Ostrich	Total aerobes	2·15	0·85	0	2·98	4·41[a]
	Coliforms	–	–	15	–	1·83[b]
	E. coli	–	–	18	–	1·54[b]
Emu	Total aerobes	2·82	0·59	0	3·22	4·33[a]
	Coliforms	–	–	12	–	1·77[b]
	E. coli	–	–	16	–	1·31[b]

$\bar{x}$ = mean log.
s.d. = standard deviation.
no = number of samples from which bacteria were not recovered.
log A = estimated log of the arithmetic mean.
N = log of the total number recovered from [a]25 cm^2 or [b]2500 cm^2.
– = insufficient data for calculation of the statistic.

numbers of the three groups of organisms, as at some plants relatively low numbers of total aerobes were accompanied by relatively large numbers of coliforms and/or *E. coli*; and at some the coliforms recovered were largely *E. coli* while at others *E. coli* were only about 10% of the coliforms.

At the abattoir involved in this study, the log mean numbers of aerobes on beef carcasses were at the lower end and log mean numbers of *E. coli* were at the upper end of the ranges for those organisms on beef carcasses from other abattoirs. As the coliforms were largely *E. coli*, the log mean numbers of coliforms were about the centre of the range of values for those organisms on beef carcasses. Those findings indicate that, at the abattoir involved in the study, beef carcasses are generally dressed by procedures which minimize the depositing of bacteria on carcasses, but suggest that poorer control of, probably, one or two skinning operations results in some avoidable contamination of the meat with *E. coli* (Gill et al. 1998b).

The pig carcasses carried larger loads of bacteria of all three types than the beef carcasses. Although all three types of bacteria can be deposited on the carcass during operations on the head and for removing the viscera (Gill and Jones 1997), it is unlikely that the majority of the bacteria were deposited on the skin at those stages of the dressing process. Instead, the scalded carcass was probably recontaminated during the dehairing and polishing operations.

Although bacteria are numerous on the skins of pigs at the time of slaughter, their numbers are greatly reduced by scalding treatments, with the remaining bacteria being mainly thermoduric, Gram-positive types (Nickels et al. 1976). The scalded carcasses are then dehaired using equipment in which the carcass rotates while being struck with rubber flails. During that operation, saliva and faeces are likely to flow from a carcass and be spread over that and subsequent carcasses by the flails. Additionally, the dehairing equipment is not well designed for cleaning and so is likely to harbour persisting detritus and associated bacteria that can also spread to carcasses that enter it. Consequently, the loads of bacteria on the skins of scalded pig carcasses are greatly increased by the dehairing operation (Gill and Bryant 1992). The numbers are reduced by singeing, but are again increased during polishing of the singed carcass, by brushing or flailing in apparatus specifically designed for the purpose at large plants but by further flailing in the dehairing apparatus at the plant involved in this study. The final microbiological condition of the dressed carcass is then largely determined by the state of the polished carcass, before evisceration or any operation on the head (Gill et al. 1997). The relatively poor microbiological condition of the pig as opposed to the beef carcasses at the abattoir involved in this study therefore likely reflects the effects of operations on the pig carcasses for which there

are no corresponding operations in the dressing of beef carcasses.

The carcasses of the other four species were subjected to dressing operations comparable with those for beef carcasses. However, the differences between the carcasses and the workers' unfamiliarity with skinning other than beef carcasses could be expected to result in other carcasses being more contaminated than the beef. With respect to the numbers of aerobic bacteria, buffalo, ostrich and emu carcasses did indeed appear to be more contaminated than the beef carcasses, but the numbers on deer carcasses were no more than on beef. That latter finding, and reports of lengthy storage stability of chilled venison (Seman et al. 1988), suggest that dressing of deer carcasses to a good general standard of hygiene is relatively easily accomplished by application of non-specific good manufacturing practices during the dressing process. Similar performance in the dressing of other carcasses may require detailed knowledge, from experience, of how best to carry out particular operations that are difficult to perform because of species-specific peculiarities.

As with the beef carcasses, the coliforms on the other skinned carcasses were largely *E. coli*. Despite the similar or larger numbers of aerobic bacteria on the other skinned carcasses than on the beef carcasses, the numbers of *E. coli* on all types of the former were less than on the beef carcasses. That may arise from the game animals and exotic birds being raised under free range conditions at all times instead of, like the cattle, being reared intensively during the 2 or 3 months before slaughter. Because of the greater and continuous crowding of animals during intensive rearing, their hides are likely to carry larger amounts of faecal material, and therefore greater numbers of faecal organisms than the hides of free ranging animals (Van Donkersgoed et al. 1997). As most of the bacteria on skinned carcasses are derived directly or indirectly from the hide (Gill 1998), fewer *E. coli* on the hides of free range than of feedlotted animals would tend to result in smaller numbers of that organism being deposited on the carcasses of the former animals during dressing. Thus, the findings indicate that even when comparable procedures are used for dressing carcasses of different species at a slaughtering plant, similar bacterial contamination of the various types of carcass cannot be assumed. Therefore, it seems that the dressing of each species should be regarded as a unique process, unless microbiological data are available to establish the similar hygienic performance of the dressing of different species.

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