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THE PRESENCE IN PIG CARCASS DEHAIRING EQUIPMENT OF *ESCHERICHIA COLI*, *CAMPYLOBACTER* AND SALMONELLA

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INTRODUCTION

The skins of scalded pig carcasses are contaminated with relatively small numbers of thermoduric bacteria (Gerats *et al.*, 1981; Nerbrink and Borch, 1989). The numbers of bacteria on carcasses increase after dehairing, decrease after singeing, and again increase after polishing (Dockerty *et al.*, 1970). The flora deposited on carcasses during dehairing is rich in psychrotrophic bacteria, and much of the flora survives the singeing operation (Gill and Bryant, 1992). The apparent increase in bacterial numbers as a result of the polishing operation may then reflect an even distribution of the flora that survives singeing, rather than contamination with bacteria originating from the polishing apparatus. It then seems that dehairing equipment is the major source of the numerous spoilage bacteria that contaminate polished pig carcasses (Gill and Bryant, 1992).

Despite the predominance of psychrotrophs in the flora on dehaired pig carcasses, the conditions within dehairing equipment would seem to be favourable for the survival and growth of mesophiles. If so, dehairing equipment could be a significant source of the mesophilic pathogens that contaminate pork (Snijders and Gerats, 1976; Duitschaever and Buteau, 1979; Stern, 1981). Therefore, pig dehairing equipment was examined for the presence of *escherichia coli*, *campylobacter* and *salmonella*.

MATERIALS AND METHODS

The dehairing equipment at two large plants for processing pigs (ca. 500 carcasses/hour) were examined. The machines used were similar at both plants, with carcasses being scraped by rotating flails while hot water is circulated over the carcasses and back to a tank. Two such machines in series are operated at plant A, but only one at plant B.

Samples of the hair and other detritus that collects on the machine frame, of water returning to the tank, and of water in the tank were collected on each of three days from each machine. Two samples of each type were collected on each of three days. Also, swab samples were collected from polished, uneviscerated carcasses, 10 carcasses being sampled on each of two occasions at each plant.
The samples of detritus and the swabs were each stomached with diluent. Suitable dilutions of each stomacher fluid and each water sample were prepared.

For the enumeration of total counts, 0.1ml portions of suitable dilutions of each sample were spread on duplicate plates of Plate Count Agar (Difco). The plates were incubated for two days at 25°C, and numbers determined from plates bearing 20 to 200 colonies.

For the enumeration of *E.coli*, duplicate 10ml portions from suitable dilutions of each sample were each filtered through a pre-filter and a hydrophobic grid membrane filter (QA Laboratories, Toronto, Canada). Each membrane filter was then removed from the filtration unit, and was placed on a plate of Lactose Monensin Gluconurate Agar (LMGA; QA Laboratories). The LMGA plates were incubated at 35°C for 24 hours. Each filter was then transferred to a plate of Buffered 4-Methylumbelliferyl-B-D-glucuronide Agar (BMA: QA Laboratories). The BMA plates were incubated at

35°C for two hours, then the filters were examined under magnification and long wave length ultraviolet light. Squares containing large blue-white fluorescent colonies were counted, and a Most Probable Number of *E.coli* was calculated from that count (Entis and Boleszczuk, 1990). The numbers at which *E.coli* would be detected were 1CFU/g of detritus, 1CFU/10ml of water, or 1CFU/100 cm^2 of skin.

For the enumeration of *campylobacter*, duplicate 0.1ml portions, from undiluted water samples and stomacher fluids and from all the dilutions of each, were spread on plates of Blood Agar Base (CM271:Oxoid, Basingstoke, U.K.) supplemented with Laked Horse Blood (SR 48:Oxoid), *campylobacter* Growth Supplement (SRO 84E:Oxoid), and *campylobacter* Selective Supplement (SRO 69E:Oxoid) as formulated by Skirrow (1977). The plates were incubated for two days at 42°C, under a microaerobic, CO_2-enriched atmosphere. Dark cream, smooth colonies, 1 to 3mm in diameter, that yielded cells showing typical *campylobacter* morphology and movement in wet slide preparations (Butzler and Skirrow, 1979) were considered to be *campylobacter*. The numbers at which *campylobacter* would be detected were 100CFU/g of detritus, 10CFU/ml of water, or 1CFU/cm^2 of skin.

For the enumeration of *salmonella*, duplicate 0.1ml portions, from undiluted water samples and stomacher fluids and from all the dilutions of each, were spread on plates of Rambach Agar (Technogram, Paris, France). The plates were incubated for 24 hours at 37°C. Bright red colonies, 2-4mm in diameter, that gave typical *salmonella* reactions when inoculated into slants of Triple Sugar Iron Agar and Lysine Iron Agar were considered to be *salmonella* (ICMSF, 1988; Rambach, 1990). The numbers at which *salmonella* would be detected were 100CFU/g of detritus, 10CFU/ml of water, or 1CFU/cm^2 of skin.

At each time that waters were sampled, the temperature of the waters were determined, at each end and at the centre of the tank. The pH values of collected waters were determined using a glass electrode.

RESULTS AND DISCUSSION

The temperatures of the waters in the tanks of the first and second machine at plant A were respectively 44±2°C and 46±2°C. The pH of the waters in both tanks was 7.5±0.3. The temperature and pH of the water in the tank of the machine at plant B were 57±2°C and 7.3±0.2, respectively.

The samples of detritus from all three machines yielded bacteria at total numbers of about 10^8CFU/g (Table 1). *E.coli* and *campylobacter* were recovered from all samples, at numbers about 10^4CFU/g and between 10^3 and 10^6CFU/g, respectively. *Salmonella* were recovered from only half the samples, at numbers between 10^3 and 10^5CFU/g at plant A, but at 10^2CFU/g at plant B.

The bacteria recovered from the waters were at total numbers of 10^5/ml at plant A, but of 10^4/ml at plant B (Table 2). *E. coli* was recovered from all the water samples, at numbers about 10^3CFU/ml. *Campylobacter* was recovered from all plant A waters at numbers of 10^2CFU/ml. In most plant B water, *campylobacter* was recovered at numbers between 10 and 10^2CFU/ml. The organism was not recovered from two of the six samples of the water returning to the tank. *Salmonella* was recovered from half the plant A waters at numbers between 10 and 10^2CFU/ml, but from only one third of the plant B waters at numbers of 10CFU/ml.

The total numbers of bacteria recovered from polished carcasses were 10^3CFU/cm^2 at plant A, but 10^4CFU/cm^2 at plant B (Table 3). *E.coli* was recovered from most plant A carcasses at unit CFU/cm^2, but from most plant B carcasses at >10CFU/cm^2. *Campylobacter* was recovered from half the sampled carcasses at both plants at unit CFU/cm^2. *Salmonella* was not recovered from any carcass.

Faeces are often voided from carcasses during their passage through dehairing machines. The faeces of all pigs will contain *E.coli*, those from a majority of animals are likely to carry *campylobacter*, while a substantial minority of pigs will have faeces that contain *Salmonella* (Kotula, 1987). Thus, both the water that is circulated to spray the carcasses and the detritus that accumulates on the frames of dehairing machines will be repeatedly contaminated with those

organisms.

The flora of the detritus is rich in Gram-negative bacteria (acinetobacteria, moraxellae, pseudomonads, flavobacteria and enterobacteria) of the types associated with the spoilage of pork (unpublished results). That flora is evidently the source of the spoilage bacteria that contaminate cleaned pig carcasses (Gill and Bryant, 1992). The condition of the detritus would seem favourable for the growth of *E.coli* and *salmonella* as well as the spoilage bacteria. It is then likely that growth of *E.coli* and *salmonella* in the detritus increases the numbers of those organisms to which carcasses are exposed during dehairing.

The different temperatures of the circulating waters apparently had no effect upon the microbiological condition of the detritus, or on the numbers of *E.coli* and *salmonella* in the water. However, the total numbers of bacteria and the numbers of *campylobacter* were lower in the circulating water of the machine at plant B than in the cooler waters of the machines at plant A. At the temperature of the water in the machine at plant B, the decimal reduction time for *campylobacter* would be <1min (Blankenship and Craven, 1982). Similar decimal reduction times for *E.coli* and *salmonella* could be expected only with temperatures of 63°C or more (Goodfellow and Brown, 1978; Doyle and Schoeni, 1984). Unfortunately, such high temperatures for the water in dehairing equipment may well be impracticable, because the flaccid skin of over-warm carcasses is prone to being torn by the dehairing flails.

Despite the lower numbers of *campylobacter* in the dehairing equipment water at plant B, the numbers of *campylobacter* on polished carcasses were not lower at plant B then at plant A. Moreover, numbers of *E.coli* were higher on the polished carcasses at plant B. That indicates the post-dehairing treatments, of washing carcasses with clean water and singeing, at plant A are more effective in removing or destroying contaminating bacteria than is the singeing treatment at plant B.

Evidently, all pig carcasses passing through dehairing equipment of the type used at large plants will be contaminated with faecal bacteria. The treatment of carcasses immediately after dehairing will affect the numbers of enteric pathogens surviving on carcasses presented for evisceration. However, reductions of pathogen numbers by washing and singeing are likely to be moderate at best. Some other treatment that reliably destroys the pathogens on uneviscerated pig carcasses would seem to be required to eliminate the hygienic hazards that arise from existing dehairing equipment.

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Table 1. The ranges of total bacteria and of the numbers of *E.coli*, *campylobacter* and *salmonella* in samples of detritus from pig carcass dehairing equipment.

	Machine		
	1A	2A	B
Total counts (log CFU/g)	8.26 - 8.88	8.72 - 8.97	7.93 - 8.51
E.coli[a] (log CFU/g)	4.75 - 5.05	4.28 - 4.67	4.53 - 4.91
Campylobacter[a] (log CFU/g)	3.42 - 6.04	4.45 - 5.87	3.72 - 5.59
Salmonella (+ve samples)	4/6	3/6	3/6
(log CFU/g)	3.94 - 5.57	3.48 - 4.93	2.00[b]

[a] all samples +ve
[b] limit of detection

Table 2. The ranges of total bacteria and of the numbers of *E.coli*, *campylobacter* and *salmonella* in samples of water from pig carcass dehairing equipment.

	Machine					
	1A		2A		B	
	Tank	Return	Tank	Return	Tank	Return
Total counts (log CFU/g)	5.23-5.43	5.43-5.85	5.52-6.11	5.78-6.08	4.54-5.11	4.15-4.90
E.coli[a] (log CFU/g)	3.26-3.74	3.34-3.58	3.04-3.46	3.28-3.40	3.15-3.72	2.98-3.66
Campylobacter[a] (+ve samples)	6/6	6/6	6/6	6/6	6/6	4/6
(log CFU/g)	1.90-2.80	2.60-3.21	1.65-2.56	2.00-2.92	1.30-2.72	1.00[b]-1.30
Salmonella (+ve samples)	4/6	2/9	3/6	3/6	1/6	2/6
(log CFU/g)	1.70-2.74	1.00[b]	1.00[b]-1.85	1.00[b]-1.48	1.00[b]	1.00[b]

[a] all samples +ve
[b] limit of detection

Table 3. The ranges of total bacteria and of the numbers of *E.coli*, *campylobacter* and *salmonella* recovered from polished carcasses of pigs.

	Plant A	Plant B
Total counts (log CFU/cm^2)	3.08 - 3.34	4.45 - 4.74
E.coli (+ve samples) (log CFU/cm^2)	10/12 0.00 - 0.78	12/12 0.78 - 1.40
Campylobacter (+ve samples) (log CFU/cm^2)	6/12 0.00 - 0.30	7/12 0.00 - 0.74