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ORIGINAL PAPER

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Bacterial population in counter flow and parallel flow water chilling of poultry meat

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Abstract In this study, a survey was carried out to determine the hygiene aspects of counter flow and parallel flow water chilling of poultry meat. Samples were taken in five sectors: in the sector subsequent to evisceration of the poultry, in the sector after water chilling, and in the sector after final washing. At the same time, the samples of water were taken from the pre-chilling sector and in the chilling sector. Bacterial detection of the inherence of various bacteria, their isolation, identification and determination was carried out. The results showed higher numbers of positive samples obtained from the section of water chilling in comparison to other sections, as well as a higher number of positive samples in the process of parallel flow water chilling in comparison to the results from counter flow chilling.

Keywords Poultry · Meat · Chilling · Bacteria · Hygiene

Introduction

The carcass chilling process is considered a critical step in poultry processing. Reduction of temperature inhibits or even stops the growth of bacteria, which prevents deterioration of the product and extends shelf life. The microbiological quality of poultry meat is directly dependant on the numbers and types of bacteria, particularly psychrotrophic spoilage bacteria, which are present on the final product [1, 2]. The process of chilling is generally divided into two stages: pre-chilling and final chilling or freezing. The pre-chilling process takes place immediately after evisceration and prior to any subsequent processing. Water immersion chilling can be carried out with two different technical and technological systems. One is counter flow water chilling where the flow of the chilling water runs opposite to the flow of spinning poultry carcasses, and the other is parallel water chilling. In the process of counter flow water chilling, the product, depending on the number of parameter settings, absorbs 4–8% of water. One of the disadvantages of this method is the need to manually rehang the carcasses after chilling.

Factors that contribute most to the bacterial contamination in the process of immersion chilling are bacterial contamination of carcasses before chilling, the amount of water overflowed and replaced per carcass and the ratio of carcasses to water in the chiller [2, 3]. It is also believed that commercial immersion chilling systems are a major source of cross-contamination of carcasses, with pathogenic microorganisms distributed by the water media during chilling [4, 5]. Allen et al. (2000) [6] have found that water immersion chilling reduces the microbiological load of carcasses, particularly coliforms and pseudomonads deposited on the skin in the first part of the process.

Much recent study has focused on the level of contamination on poultry during processing and the development of methodologies for the isolation and detection of pathogenic bacteria [7]. The psychrotrophic bacterial flora on freshly dressed broiler chicken carcasses are heterogeneous. *Flavobacteria*, *Shewanella putrefaciens*, *Acinetobacter* spp., *Corynebacteria* spp., *Moraxella* spp. and fluorescent pseudomonads are all common on aerobically stored, chilled poultry meats [8]. Poultry serves as a niche for wide variety of organisms, including the most prominent spoilage microorganisms, the psychrotrophic pseudomonads, and *Acinetobacter*, as well as the food-borne pathogens *Salmonella* spp. and *Campylobacter spp. Salmonella* and *Campylobacter* continue to be major food-borne pathogens and raw poultry is considered to be an important source of these bacteria [9, 10]. Although *Salmonella* spp. and *Campylobacter* spp. are more commonly found on poultry meat, *Escherichia coli* O157:H7, typically associated with ground beef, has also

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been isolated form the ceca of chickens. This presence in the intestinal tract of poultry is a source of possible contamination of the retail poultry meat product. Doyle and Schoeni (1987) [11] found that 1.5% of poultry samples taken from retail markets contained *E. coli* O157:H7. Considering the amount of poultry consumed in the world, this means that each day many people are at risk of becoming infected with the pathogen from poultry alone, if the product is not cooked and handled properly [12].

The objective of the current study was to determine the extension and identify potential bacteriological contaminants in two different immersion chilling processes. These results provide a baseline for evaluation of the hygienic justification for implementation of specific technology.

Materials and methods

This research was carried out in a slaughterhouse on two different processing lines in the summer period. Samples were taken in five sectors as follows: in the sector subsequent to evisceration of the poultry (48 samples), in the sector after water chilling (96 samples), and in the sector after final washing (32 samples). A swab was wiped at the surface of back of young fattened broilers of the Hybro line (Euribrid B.V., Boxmeer, Netherlands). A Latin square design was used. At the same time, samples of water were taken from the pre–chilling sector (16 samples) and the chilling sector (16 samples). Sterile bottles were used for collecting samples of water. Water samples were examined without further processing.

All samples were analysed as described by Baumgart (1997) [13]. Analysis was based on the following indicators: *Acinetobacter calcoaceticus, Alcaligenes faecalis, Sarcina, Enterococcus faecalis, Salmonella spp., Escherichia coli, Escherichia* O26:B6, *Bacillus cereus, Clostridium perfringens, Proteus vulgaris, Proteus mirabilis, Morganella morganii, Providencia rettgeri, Staphylococcus spp., Campylobacter jejuni, Yersinia enterocolitica, Citrobacter freundii, Pantoea agglomerans, Enterobacter cloacae, Klebsiella pneumoniae, Serratia marcescens, Pseudomonas spp.,* and *Shewanella putrefaciens.*

Results and discussion

Results of the bacteriological analysis of poultry carcasses and water samples are shown in Table 1 and Table 2.

In the section of pre washing after evisceration the difference in bacteriological contamination is not marked, and one could say that the contamination is higher in the counter flow than in the parallel flow. *Enterococcus faecalis* was found in four samples in counter flow in comparison to only one positive sample for parallel flow. Similar results were found for *Salmonella* spp., *E. coli*, *Clostridium perfringens*, *Proteus* spp., *Staphylococcus* spp., *Campylobacter jejuni* and *Pseudomonas* spp. From previous studies by other authors it is clear that the number of pseudomonads on freshly slaughtered broilers can vary substantially, and that the initial flora contained 45% and 35% pseudomonads, respectively [8].

The results of the section of counter flow and parallel flow water chilling evidenced lower levels of contamination in the counter flow process. Samples from counter flow showed more positive findings for *Enterococcus faecalis, Proteus vulgaris, Klebsiella pneumoniae, Serratia marcescens* and *Shewanella putrefaciens.* Other bac-

Table 1 Number of positive findings of bacteria species in samples taken from different stages of technological processing by the method of parallel flow water-chilling

Bacteria species	Evisceration and pre washing	Parallel flow water chilling	Final washing	Cold water	Ice water
Total samples	48	96	32	16	16
Acinetobacter calcoaceticus	4	8	1	6	2
Alcaligenes faecalis	2	8	1	4	–
Sarcina	–	–	–	–	2
Enterococcus faecalis	1	4	–	–	–
Salmonella spp.	8	15	–	10	2
Escherichia coli	11	27	5	7	3
Escherichia O26:B6	1	6	–	2	–
Bacillus cereus	3	2	1	1	–
Clostridium perfringens	2	4	1	2	–
Proteus vulgaris	4	3	–	3	1
Proteus mirabilis	3	1	1	–	1
Morganella morganii	1	6	–	1	2
Providencia rettgeri	1	1	1	2	–
Staphylococcus spp.	4	10	1	6	1
Campylobacter jejuni	3	12	2	2	1
Yersinia enterocolitica	1	6	1	1	1
Citrobacter freundii	–	–	–	––	–
Pantoea agglomerans	1	3	–	1	1
Enterobacter cloaceae	1	3	1	1	–
Klebsiella pneumoniae	1	–	1	–	–
Serratia marcescens	–	–	–	1	2
Pseudomonas spp.	2	8	–	6	–
Shewanella putrefaciens	–	1	–	–	–

Table 2 Number of positive findings of bacteria species in samples taken from different stages of technological processing by the method of counter flow water-chilling

Bacteria species	Evisceration and pre washing	Counter flow water chilling	Final washing	Cold water	Ice water
Total samples	48	96	32	16	16
Acinetobacter calcoaceticus	1	3	–	–	–
Alcaligenes faecalis	–	–	–	4	–
Sarcina	1	–	–	1	2
Enterococcus faecalis	4	6	–	–	–
Salmonella spp.	8	11	–	6	–
Escherichia coli	12	20	4	6	2
Escherichia O26:B6	1	3	–	–	–
Bacillus cereus	–	1	–	1	–
Clostridium perfringens	3	3	1	–	–
Proteus vulgaris	3	7	–	1	–
Proteus mirabilis	4	1	–	1	–
Morganella morganii	2	3	–	–	–
Providencia rettgeri	–	–	–	–	–
Staphylococcus spp.	2	6	3	1	1
Campylobacter jejuni	3	9	1	2	1
Yersinia enterocolitica	1	5	2	2	–
Citrobacter freundii	–	1	–	2	–
Pantoea agglomerans	–	1	–	–	–
Enterobacter cloaceae	–	1	3	2	–
Klebsiella pneumoniae	–	1	–	2	–
Serratia marcescens	–	2	–	–	–
Pseudomonas spp.	4	5	–	6	1
Shewanella putrefaciens	–	2	–	–	–

teria species were found more frequently in samples obtained from the parallel flow method.

The results of bacteriological testing of samples of cold water from the spin chiller showed contamination with *Acinetobacter calcoaceticus, Alcaligenes faecalis*, *Salmonella* spp. as well with *E. coli*, *Staphylococcus* spp. and *Pseudomonas* spp. Bacteriological analysis of ice water showed contamination with *Acinetobacter calcoaceticus, Salmonella spp., E. coli, Morganella morganii* and *Serratia marcescens*. High contamination of samples taken in the sectors of counter flow and parallel flow water chilling are similar to results of cold-water testing, particularly considering contamination with *Salmonella spp., E. coli* and *Pseudomonas spp*. The high proportions of *E. coli* isolated indicated a high prevalence of faecal contamination. The high incidence of faecal contamination was not unexpected because rupturing of viscera during the evisceration process probably resulted in faecal contamination of carcasses and further contamination of water in the spin chillers [14]. The samples were also positive in higher numbers for *Acinetobacter calcoaceticus, Staphylococcus* and *Campylobacter jejuni*, both in samples of cold water and samples from the section of parallel and counter flow. It can be presumed that this section presents high cross contamination risk in the process of water immersion chilling.

Samples taken in the final wash sector showed high contamination with *E. coli*, *Staphylococcus spp*. *Campylobacter jejuni*, *Yersinia enterocolitica*, and *Enterobacter cloaceae*. The contamination in the process of parallel flow in the final wash sector showed more positive findings of different bacteria in comparison to the final wash of the counter flow process, where most positive findings were of *E. coli, Clostridium perfringens, Staphylococcus spp., Campylobacter jejuni, Yersinia enterocolitica* and *Enterobacter cloaceae*.

All in all, the number of positive findings was low throughout the sections of the process, but there are still some indications that there is a possibility of cross contamination in the final wash processes, where there were some positive findings of bacteria species that were not present in samples of ice-water, and this leads to the presumption that even one contaminated carcass could lead to overall contamination.

References

1. Geornaras I, de Jesus AE, van Zyl E, von Holy A (1996) Food Microbiol:13:457–465
2. Petrak T, Kalođera Z, Novković P, Gumhalter Karolyi L (1999) Meat Sci 53:269–271
3. Bailey JS, Homson JE, Cox NA (1983) Poult Sci 62:193–211
4. Hamilton MAE, Ahmad MH (1994) Lett Appl Microbiol 18:21
5. Jones FT, Axtell RC, Rives DV, Scheideler SE, Tarver Jr FR, Walker RL, Wineland MJ (1991) J Food Prot 54: 259–262
6. Allen VM, Corry JEL, Burton CH, Whyte RT, Mead GC (2000) Int J Food Microbiol 58:39–48
7. Kotula K, Pandya Y (1995) J Food Prot 58:1326–1329
8. Arnaut–Rollier I, De Zutter L, Van Hoof J (1999) Int J Food Microbiol 48:87–96
9. Jørgensen F, Bailey R, Williams S, Henderson P, Wareing D RA, Bolton FJ Frost, JA Ward, LT, Humphrey J (2002) Int J Food Microbiol 76:151–164

10. Sackey BA, Mensah P, Collison E, Sakyi–Dawson E (2001) Int J Food Microbiol 71:21–28
11. Doyle MP, JL Schoeni (1987) Appl Environ Microbiol 53:2394–2396
12. Beery JT, Doyle MP, JL Schoeni (1985) Appl Environ Microb 49:310–315
13. Baumgart J (1997) Mikrobiologische Untersuchungen von Lebensmitteln Behr's Verlag, Robert Seeman GmbH&Co, Hamburg
14. Mead GC (1989) Hygiene problems and control of process contamination. In: Mead GC (ed) Processing of poultry. Chapman & Hall, London