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Changes in microbial contamination levels of porcine carcasses and fresh pork in slaughterhouses, processing lines, retail outlets, and local markets by commercial distribution

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ABSTRACT

The objective of this study was to evaluate the changes in microbial contamination levels of each porcine carcass and fresh pork in a general distribution process. A total of 100 commercial pigs were sampled (six sampling sites per individual, total 600 samples) at four sequential stages: slaughterhouse (after carcass grading and boning), processing line, retail outlet, and local market. No significant differences were observed in the contaminant percentages among sampling sites and sample collection years ($P > 0.05$) with the exception of *Bacillus cereus*. The contaminant percentage of *B. cereus* at 1st collection year was higher than these of 2nd collection year (28.31% vs. 12.26%, $P < 0.05$). *B. cereus* and *Listeria monocytogenes* were the most frequently detected pathogenic bacteria in the slaughterhouse and markets, respectively. On the other hand, *Escherichia coli* O157:H7 and *Yersinia enterocolitica* were not detected in carcasses or pork collected from any carcass sites and pork samples. However, the frequency of pathogenic bacteria in end-products at local markets was not highly related to the initial contamination of porcine carcasses in the slaughterhouse. Thus, the improvement of microbial safety for pork end-products requires hygienic control of porcine carcasses and meat cutting during all operations in the slaughterhouse, processing line, retail outlet, and local market.

1. Introduction

Foods originating from animals are important sources of infections with a variety of pathogenic bacteria. In recent years, concerns about meat and meat products carrying foodborne pathogenic microorganisms have increased, despite improved efforts in meat and processed meat hygiene (Bae et al., 2011; Choi et al., 2009). All fresh meat can have a level of microbial contamination present, but sometimes the contamination acts as a vector for pathogenic bacteria of animal and human origins (Cárdenas et al., 2008). Pork is one of the main products involved in foodborne infections, and the most important pathogenic bacteria associated with pork include *Salmonella* spp. (Borch et al., 1996; Korsak et al., 1998), *Campylobacter* (Epling et al., 1993; Malakauskas et al., 2006), *Listeria monocytogenes* (Borch et al., 1996), *Staphylococcus aureus* (Koutsoumanis and Sofos, 2004), and *Yersinia enterocolitica* (Bolton et al., 2002; Mataragas et al., 2008).

A variety of sources contribute to microbial contamination when porcine carcasses or meat cuts are exposed to the environment (Koutsoumanis and Sofos, 2004). Livestock slaughter, in particular, is an open process providing many opportunities for contamination of the carcass with potentially pathogenic bacteria (Borch et al., 1996). Major sources of contamination during slaughter are the animal hide, equipment, water, and utensils (Bolton et al., 2002). Many studies have concentrated on the carcasses and environmental factors during slaughter when trying to improve or analyze the microbial quality of meat (Bae et al., 2011; Mataragas et al., 2008; Pearce et al., 2006; Stopforth et al., 2003). However, meat can be further contaminated or cross-contaminated by various pathogenic bacteria after the slaughter process during chilling, cutting, deboning, and slicing (Berends et al., 1998; Duffy et al., 2001). Thus, all processing conditions are important factors affecting microbiological quality. To improve the safety of final meat products, more information is needed on the point where porcine carcasses or meat cuts are contaminated with foodborne pathogens, and which pathogens are associated with carcasses or meat at further processing stage. However, the association between the initial contamination extent of carcasses and the contamination extent of final meat products has not been

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extensively studied. Therefore, the purpose of this study was to investigate the frequency of nonpathogenic *Escherichia coli* and major pathogens (*Bacillus cereus*, *E. coli* O157:H7, *L. monocytogenes*, *Salmonella* spp., *S. aureus*, and *Y. enterocolitica*) in pigs in general distribution process (slaughterhouse to local market), to improve the management of microbial hazards.

2. Materials and methods

2.1. Sample collection

A total of 100 commercial pigs were evaluated, and each stepwise sample was collected for analysis of microorganisms from the slaughter line, processing step, retail outlets, and local markets (three slaughterhouses, three retail outlets, and six local markets; six sampling sites per individual; total = 600 samples; Fig. 1). Three slaughterhouses were located at three administrative regions in Korea (Gyonggi, Kangwon, and Chungchong), while three retail outlets and six local markets were selected based on their regional distribution and location in metropolitan areas within Korea (Seoul in Gyonggi region, Wonju in Kangwon region, and Daejeon in Chungchong region). The treatment conditions for all pigs were the same before and after slaughter, and all treatment conditions were approved by the Ministry for Food, Agriculture, Forestry, and Fisheries of South Korea. Pigs were transported to the slaughterhouses under the same conditions and they were handled in six batches (16–17 pigs per slaughter batch). Sampling was conducted in the months of July and August in two years (2009 and 2010; three batches per year; 50 pigs per year). Pigs were slaughtered following standard procedures under the supervision of the Korean Animal Products Grading Service. The slaughter plants used electrical stunning and a traditional scalding process. After slaughter, each labeled porcine carcass was placed in a 1 ± 2 °C cold room for 24 h. After a carcass grading step in the cold room, each porcine carcass was swabbed three times at each sampling point (rump, midline, and brisket) using a sterile swab (Difco Laboratories, Detroit, MI, USA) with peptone water and a sterile template (10 × 10 cm). Sterile moistened sponge swabs were used to collect all samples.

Each pork sample was collected from each labeled porcine carcass at the general distribution process (processing line, retail outlets, and local markets). After meat cutting and boning in the processing line, 200 g samples were taken for isolation and identification of nonpathogenic *E. coli* and pathogenic bacteria, including *B. cereus*, *E. coli* O157:H7, *L. monocytogenes*, *Salmonella* spp., *S. aureus*, and *Y. enterocolitica*. Samples were taken from each prelabeled boneless pork loin, before the remainder of the pork loin was overwrapped with polyvinyl chloride film. Samples were labeled with the same number as the carcass sampled. Pork loins were transported to retail outlets. Two-hundred gram samples were taken from each prelabeled pork loin after opening the package, before the remainder of the pork loins were sliced and placed on pre-labeled styrofoam trays at retail outlets. Trays were vacuum-packaged with multilayer polyolefin and polyvinylidene chloride film. In local markets, sliced pork loins were stored under market display conditions (4 °C, deluxe warm white fluorescent lighting) for 24 h. Sliced pork samples were transported to the laboratory where 200 g samples were taken after opening the package. All pork samples were trimmed using a stainless steel knife, which had been sterilized with alcohol and flaming. All samples were immediately transferred to the laboratory after checking that the labels matched.

2.2. B. cereus isolation and identification

Twenty-five grams of each sample were enriched in 225 ml of trypticase soy-polymyxin broth (Difco), homogenized using a stomacher (Seward, Stomacher 400, UK) for 2 min, and incubated at 30 °C for 24 h. The enriched cultures were streaked onto mannitol-egg yolk-polymyxin (MYP; Difco) agar, and incubated for 30 °C for 24 h. Typical pink colonies surrounded with a precipitation zone were transferred to tryptic soy agar and *B. cereus* identification was confirmed by performing a sequence of morphological and physiological tests, and miniaturized biochemical tests with API 50CHB and API 20E galleries (BioMerieux, Marcy l'Etoile, France).

2.3. E. coli and E. coli O157:H7 isolation and identification

Twenty-five grams of each sample were homogenized with 225 ml of EC broth (Difco) using a stomacher for 2 min. The mixture was incubated at 37 °C for 24 h. The enriched cultures were streaked onto eosin–methylene blue agar (Difco), and incubated at 37 °C for 18 h. Plates were inspected for presumptive colonies

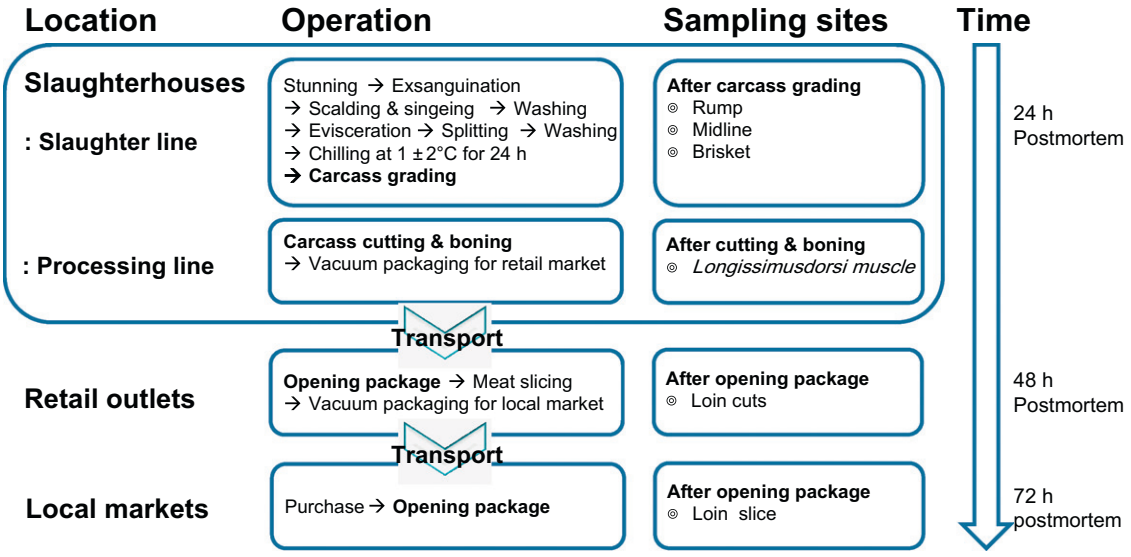

Fig. 1. Stepwise sampling sites of porcine carcasses and fresh pork loins at the slaughterhouses, retail outlets, and local markets.