

Byron D. Chaves,^{1a} Siroj Pokharel,^{1b}
Jessie L. Vipham,^{1c} Alejandro Echeverry,¹
Markus F. Miller¹ and Mindy M. Brashears^{1*}

¹International Center for Food Industry Excellence, Dept. of Animal and Food Sciences, Texas Tech University, Lubbock, TX 79409, USA



Impact of Carcass Anatomical Location on the Microbiological Profile of Beef Trimmings

ABSTRACT

This study was conducted to determine the impact of carcass anatomical location on the microbiological profile of beef trimmings. A total of 375 chuck (24–30% fat), heel (5–10% fat), shank (5–10% fat), and sparse lean (> 70% fat) trim samples representing several carcass locations were collected at a large beef fabrication facility in the Midwestern U.S. on five non-consecutive days (morning, midday, and evenings production shifts) during the fall/winter season of 2015/2016. For each sample, aerobic (AC), coliform (CC), and *Escherichia coli* (EC) counts were estimated using 3M™ Petrifilms. AC were significantly higher ($P < 0.01$) on chuck trimmings ($2.00 \pm 0.75 \log_{10}$ CFU/cm²) than on heel, shank, or sparse lean trim (1.24 ± 0.74 , 1.23 ± 0.83 , and $1.43 \pm 0.75 \log_{10}$ CFU/cm², respectively). All CC and EC were under the limit of quantification (< 10 CFU/cm²). Production shift had no effect on aerobic bacteria counts, and surface fat content (used as a proxy for carcass location) was a poor predictor of AC on beef trim. These results indicate that

beef trimmings collected from different carcass locations with varying surface fat contents do not have significantly different microbiological profiles. The differences observed (0.57 – $0.77 \log_{10}$ CFU/cm²) in AC may not be of practical significance for food safety and quality.

INTRODUCTION

Beef manufacturing trimmings (beef trimmings or beef trim) are a precursor material consisting of portions of beef carcasses of different levels of lean, obtained during carcass boning and preparation of primal and subprimal cuts such as chucks, rounds, or shanks (9, 19). In the United States (U.S.), beef manufacturing trimmings are an example of an intact raw beef product that is intended to be used for non-intact products such as minced meat, ground beef, and hamburgers (19). Consequently, the microbiological status of the raw components is of paramount importance to ensure the safety and quality of the final products (5).

There is evidence that beef trim destined for ground beef production in the U.S. may carry a baseline load

^aPresent address: Dept. of Food Science and Technology, University of Nebraska–Lincoln

^bPresent address: Dept. of Food Science, The Pennsylvania State University

^cPresent address: Dept. of Animal Science and Industry, Kansas State University

*Author for correspondence: Phone: +1.806.742.2805; Fax: +1 806.742.4003; E-mail: mindy.brashears@ttu.edu

of pathogenic bacteria. Bosilevac et al. (3) estimated the prevalence of *Salmonella*, *Campylobacter*, *Listeria monocytogenes*, and Shiga toxin gene markers to be 0.8% (4/487), 1.3% (5/393), 5.0% (17/341), and 30% (147/487), respectively, in boneless beef trim collected in U.S. facilities, and Hill et al. (10) found *Salmonella* and *Escherichia coli* O157 in 1.6% (14,272/892,029) and 0.82% (7,315/892,029) of trim samples collected from 20 commercial beef processing facilities in the Midwestern U.S. between 2005 and 2008 (10). Additionally, routine verification testing programs from the U.S. Department of Agriculture, Food Safety and Inspection Service (USDA-FSIS) show that in 2015 and 2016, respectively, 0.06% (2/3,308) and 0.19% (7/3,779) of trim samples used as raw ground beef product components, i.e., beef trimmings, collected from federally inspected facilities were positive for *E. coli* O157:H7 (18, 20). Furthermore, non-O157 Shiga toxicogenic *E. coli* were present in 0.53% (12/2,264) of trim samples collected for verification activities in 2012 (18).

Given that pathogenic bacteria may be present in beef trim destined for human consumption, there is a need to validate the in-plant sanitation conditions and antimicrobial interventions intended to prevent, reduce, and/or eliminate microbial hazards (6). This task may be performed by estimating the prevalence and/or concentration of the food safety hazards (6). However, the distribution of pathogens in live animals, carcasses, and raw meat products such as trimmings and ground beef is extremely variable, and this variability limits the degree of confidence with which a sampling plan can indicate the presence of a pathogen in a product lot (1, 15). In these cases, testing for indicator organisms, such as aerobic bacteria and generic *E. coli*, is the best approach to the validation and verification of a process control system that is designed to reduce microbial contamination. These organisms may be indicative of environmental and fecal contamination, and because their expected frequency is much higher than that of pathogens, they are more suitable as process control indicators (1, 15).

The greatest compositional variable in a beef carcass is the amount of fat (2, 12, 13). The fat content of the resulting cuts and ground beef greatly influences physicochemical, functional, and sensory properties, but the effect on microbiological characteristics is not clear (2, 12, 13). The subcutaneous fat layer comprises the major outer surface of the carcass, and it has been hypothesized that this tissue is most likely one of the first to be contaminated during slaughter and carcass dressing procedures (12), which may in turn impact the microbiological status of beef trim. Additionally, because primal and subprimal cuts differ in surface fat content, it has been suggested that the anatomical location of trimmings may influence bacterial counts (2). The objective of this study was to determine the impact of carcass anatomical location with varying

proportions of surface fat on the microbiological profile of beef trimmings destined for ground beef production.

MATERIALS AND METHODS

Sample collection

Samples of beef trimmings destined for human consumption were collected throughout the 2015/2016 fall and winter months at a large beef fabrication facility in the Midwestern U.S. Four different types of trimmings — chuck, heel, shank, and sparse lean — were sampled. Each set of trimmings represented different carcass locations and had distinct surface fat contents as visually determined in the plant as follows: Chuck (24–30% fat) — chuck area (shoulder); Heel (5–10% fat) — outside round; Shank (5–10% fat) — fore and hind shank; and Sparse lean (70% fat and higher) — various, but primarily navel, plate (ribs) and flank. Seventy-five trim samples were collected per replication throughout a production day, 25 per shift (morning, midday, and evening). Within a shift, five samples each of shank, heel, and chuck, as well as 10 samples of sparse lean, were collected. Sample collection was replicated five times on non-consecutive days, for a total of 375 beef trimming samples (75 shank, 75 heel, 75 chuck, and 150 sparse lean).

Trimmings were swabbed with sterile EZ™ Reach sponges pre-moistened with 25 ml of buffer peptone water (World BioProducts, Mundelein, IL, USA) using a 10 cm × 10 cm sterile cardboard template. All sponge samples were immediately chilled and shipped overnight to the Texas Tech University Food Safety Laboratories in insulated containers with ice packs.

Microbiological analyses

Upon arrival at the laboratory, sponge samples were stomached for 30 seconds at 230 rpm, using a countertop stomacher (Seward 400C Stomacher; England). One- and two-fold serial decimal dilutions were created for every sample in buffered peptone water (BPW; Becton Dickinson, Sparks, MD). A 1-ml aliquot of each dilution was plated onto duplicate Aerobic Count (AC) Petrifilms™ (3M™, St. Paul, MN) and *E. coli*/Coliforms (ECC) Count Petrifilms™ (3M™, St. Paul MN). Aerobic, coliform, and generic *E. coli* counts were estimated according to the manufacturer's instructions. Briefly, AC Petrifilms™ were incubated at 35 ± 1°C and red colonies were counted after 48 hours. ECC Petrifilms™ were incubated at 35 ± 1°C and coliforms (red colonies associated with gas) were counted after 24 hours, while *E. coli* (blue colonies associated with gas) were counted after 48 hours. Colonies were counted under a QCount® 530 colony counter (Advanced Instruments, Inc., Norwood, MA).

Statistical analyses

All microbial counts were converted to log₁₀ CFU/cm². A single-factor analysis of variance was performed to compare

aerobic, coliform, and *E. coli* counts separately across trim type, using PROC GLM on the Statistical Analysis Software (SAS version 9.4; SAS Institute, Cary, NC). Means were separated with the LSD statement. Correlation coefficients between surface fat content and aerobic plate counts were estimated via PROC CORR on SAS. All differences were deemed significant at a 1% probability level.

RESULTS AND DISCUSSION

This study sought to determine the impact of carcass anatomical location on the microbiological profile of beef trimmings destined for ground beef production, as approximated by the load of bacterial indicators — aerobic plate counts (AC), coliform counts (CC), and generic *E. coli* counts (EC).

Overall, trimmings derived from the chuck (shoulder area of the carcass) and containing between 24 and 30% surface fat (determined visually by experienced plant personnel) had significantly higher AC than heel, shank, or sparse lean trimmings (Table 1). Regardless of the carcass location, the AC values estimated in this study were low, ranging from 1.23 to 2.00 log₁₀ CFU/cm², and are likely the result of hygienic and sanitary practices correctly designed and implemented in the fabrication facility (1, 15). Chuck trimmings had significantly higher AC than other trim types, by a difference of < 0.50 log₁₀ CFU/cm² (result from LSD mean separation test). Such differences may not have practical implications for food safety and quality (11, 14). These differences typically reflect the natural variability in the microbial concentration of the trimmings and the

inherent variations in the quantification method. Published results, such as those from the USDA-FSIS national survey of trim produced under federal inspection (17) show that the average aerobic plate counts for 1,707 samples was 4.71 log₁₀ CFU/g, while Bosilevac et al. (3) estimated a mean level of 2.5 log₁₀ CFU/g for 486 trim samples collected domestically. Although these values cannot be directly compared to ours because of methodological differences, the results of our study indicate that different carcass locations with varying surface fat levels do not negatively impact the aerobic bacteria counts on beef trimmings.

All CC and EC were under the limit of quantification for the detection assay, i.e., under 10 CFU/cm². Results from the USDA-FSIS national survey of trim produced under federal inspection (17) show that the average CC for 721 positive samples was 3.2 log₁₀ CFU/g, and Bosilevac et al. (3) reported a mean coliform count for 377 samples of domestic trim to be 1.6 CFU/g. The greatest application of coliform counts is for assessing the overall quality of the food and the hygienic conditions present during food production since coliform bacteria are not resistant to sanitizers (11). Generic *E. coli* (biotype I) is expected to be present to some degree in raw foods, because these organisms can grow in a variety of extra-intestinal niches, including the processing environment, and do not strictly reflect fecal contamination (11). National survey data showed an average of 1.9 log₁₀ CFU/g for 270 positive samples (17), and Bosilevac et al. (3) reported a mean concentration of 1.2 log₁₀ CFU/g for 377 positive samples collected domestically, demonstrating that beef trim carries

TABLE 1. Microbiological profile of beef trimmings collected at a large Midwestern U.S. fabrication facility over a five-month period

Type of trimming	Carcass location	Approximate surface fat content (%)	Concentration of microbiological indicators (Mean ± SD log ₁₀ CFU/cm ²) ¹		
			Aerobic counts	Coliform counts	<i>E. coli</i> counts
Chuck	Shoulders	24–30	2.00 ± 0.75 ^a	ND ²	ND
Heel	Outside Round	5–10	1.24 ± 0.74 ^b	ND	ND
Shank	Fore and hind shanks	5–10	1.23 ± 0.83 ^b	ND	ND
Sparse Lean	Navel, plate (ribs), and flank	> 70	1.43 ± 0.75 ^b	ND	ND

¹Average of five replications; SD represents the standard deviation of the mean.

^{a,b}Within columns, values with different letter superscripts are significantly different at a 1% probability level.

²ND: under quantification limit of 10 CFU/cm².

a baseline load of generic *E. coli*. In a study by Gill & McGuinnis (8), the authors reported that only about 50% of the coliforms identified in beef trim samples collected at a Canadian abattoir were identified as *E. coli*, an indication that a large proportion of coliforms in beef products may not be of fecal origin but rather be indicative of poor environmental sanitation practices. Adequate sanitary practices were likely responsible for the extremely low CC and EC values observed in this study.

The impact of carcass anatomical location on microbial counts has not been extensively studied and, consequently, making comparisons to our results is questionable. In a survey of the microbial levels of incoming raw beef ingredients, Eisel et al. (7) found that the brisket and skirt areas of the carcass were more heavily contaminated with aerobic bacteria (6.9 and 6.6 log CFU/g, respectively) than the round and flank areas (4.7 and 4.0 log CFU/g, respectively), presumably because the animal is hung by the hind legs, which in turn may promote contamination of anterior parts of the carcass caused by splashing (7). In the

same study, the authors reported that surface contamination with APC for carcass beef ranged from 2.0 to 2.5 log CFU/cm², values similar to those found in our study for chuck trimming surface contamination, but much higher than for the other trim types.

Kotula et al. (12) hypothesized that a higher fat content may influence the microbiological profile of beef products. However, Prasai et al. (13), who evaluated the effect of removing surface fat on the microbial contamination of beef carcasses, reported a non-significant effect of removing surface fat on the microbial contamination of beef carcasses, reported a non-significant effect of removing subcutaneous and kidney-pelvic-heart fat on aerobic bacteria counts on beef carcasses. With and without the presence of fat, aerobic bacteria were around 2.75 log₁₀CFU/cm², a value in the same order of magnitude as that found for chuck trimmings in our study. The authors concluded that their proposed hot-fat trimming protocol did not significantly improve the microbiological quality of beef carcasses or resultant subprimal cuts, indicating that surface fat may not be a relevant factor affecting the microbiological profile of beef carcasses. Under

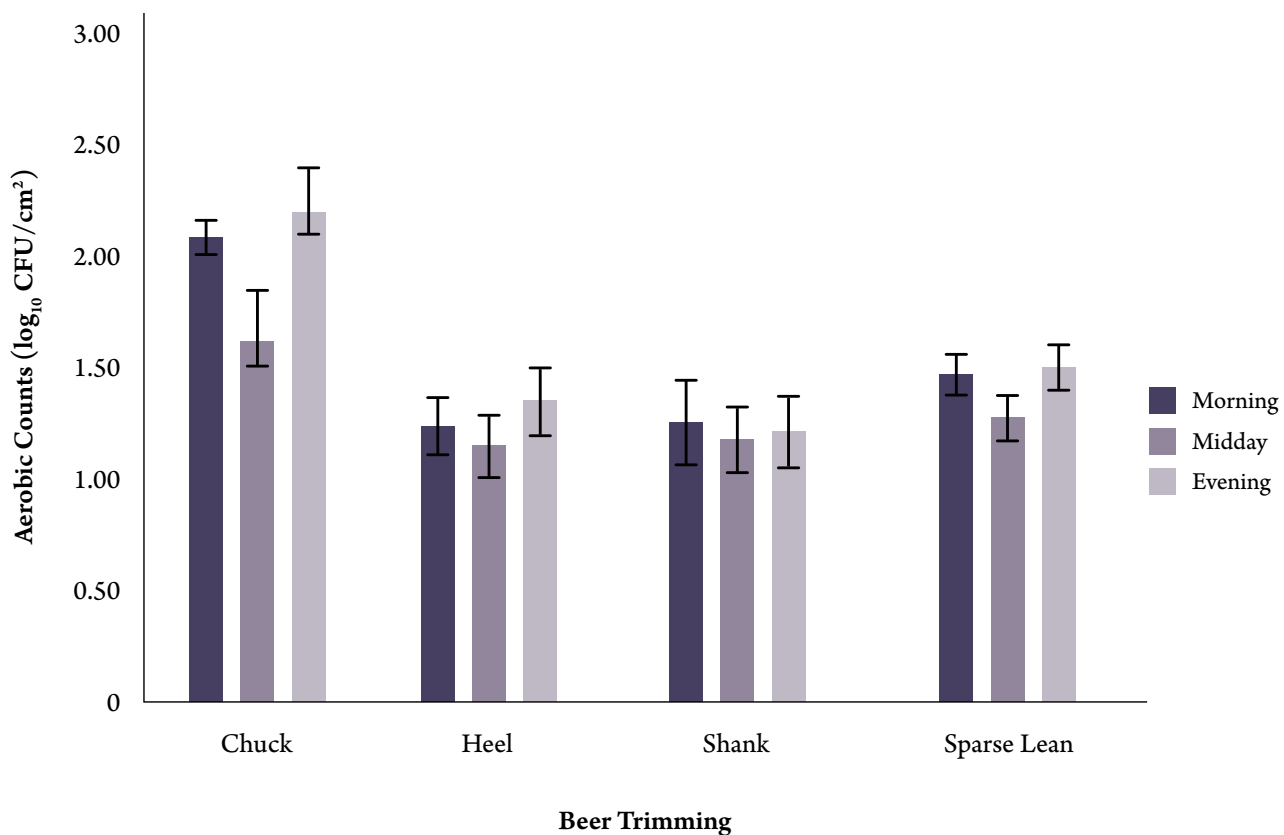


FIGURE 1. Distribution of aerobic counts in beef trimmings collected throughout three production shifts at a large Midwestern U.S. beef fabrication facility over a five-month period. Bars represent standard error of the mean, with n = 25, 25, 25, 25, 25, 25, 25, 25, 25, 50, 49, and 48, respectively, from left to right. Within trim type, none of the means were different at a 1% level of significance.

the same hypothesis as Kotula et al. (12), Scanga et al. (16) reported that as the fat content of beef trimmings increased, the aerobic counts also increased, with 30% fat trimmings having the highest aerobic bacteria counts, compared with 10, 20, or 50%; however, there were no significant differences in total coliform, generic *E. coli*, or *Staphylococcus aureus* counts across fat percentages. When the samples were collected via a combo-bin purge, there were no significant differences among microbial indicator counts across any values for fat content of the samples.

The concentration of background organisms in trim may vary because of the effectiveness of sanitary hide removal, processing interventions, and adequate cold chain management (4). In this study, production shift — morning, midday, or evening — did not significantly affect the load and distribution of aerobic counts (Fig. 1). This demonstrates highly consistent hygienic practices during production, and/or may indicate that the microbiological quality of the incoming carcasses used for fabrication is consistent. Although non-significant, there was a slight tendency for numbers of aerobic bacteria to be lower during the midday shift. There was no clear tendency for the distribution of CC and EC, and given that all counts were under the limit of quantification, it would be impossible to make inferences about those values.

Finally, we attempted to determine the linear relationship between the visually estimated surface fat content (min-

imum and maximum values of the range for chuck, heel, and shank, and a set value of 70% for sparse lean) and the concentration of aerobic plate counts. The correlation coefficients ranged from 0.044 to 0.057, indicating that surface fat content may be an extremely poor predictor of the load of aerobic bacteria on beef trimmings, if a linear relationship between the two variables is assumed.

CONCLUSIONS

The carcass anatomical location does not significantly affect the surface microbiological profiles of beef trimmings destined for ground beef production, as indicated by the load of aerobic bacteria, coliforms, and generic *E. coli*. The overall differences observed in this study, even when statistically significant, are too small to be likely to have an impact on food safety or quality. Not surprisingly, surface fat content (used as a proxy for carcass location) was found to be an extremely poor predictor of the concentration of aerobic bacteria on beef trimmings. In establishments with adequate and strict sanitation, cold chain, and fabrication practices in place, and with adequate standards of the hygienic status of incoming carcasses, the location of the trimmings, even with varying surface fat contents, does not influence their microbiological status and should not negatively impact the safety or quality of the resulting ground beef and ground beef products.

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