A MICROBIOLOGICAL PROFILE OF DOMESTIC & IMPORTED BEEF RAW MATERIALS DESTINED FOR USE IN GROUND BEEF PRODUCTION

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Summary

In order to determine the level of contaminants in beef raw material and final ground beef products, samples of beef raw materials and final ground beef products were collected from 8 commercial beef grinding facilities representing fed cattle, culled-beef cows, culled-dairy cows and imported beef trimmings. Samples were collected from combo-bins (via core drilling and purge sampling) and final ground products, and subsequently analyzed for aerobic plate counts (APC), total coliform counts (TCC), generic *Escherichia coli* counts (ECC), *Staphylococcus aureus* counts and the presence or absence of *Salmonella* spp. and *Listeria monocytogenes.* As the fat content of trimmings increased, the APC also increased. Trimmings from fed cattle had higher ($P < .05$) APC and TCC counts than culled-beef cow, culled-dairy cow or imported beef trimmings. Purge sample APC were highly correlated to combo-bin core APC ($r = .80$), and overall, purge samples had higher numbers of bacteria than combo-bin core samples. *Listeria monocytogenes* and *Salmonella* spp. were found in 13.6% and 1.5% respectively in final ground beef products samples.

Introduction

In the U. S., bacterial pathogens cause 79% of the outbreaks and 90% of the total number of cases of foodborne illness, and beef was identified as the source of transmission in a total of 63 out of 2,085 cases between 1988 and 1992 (CDC, 1996a). Ground beef that was contaminated with *Escherichia coli* O157: H7 was identified as the source of a 1993 outbreak that affected over 500 people and ultimately lead to the death of four children (FDA, 1993). In order to proactively reduce and prevent the contamination of ground beef, the objectives of this research were to determine the frequency with which beef raw materials that are destined for use in raw ground beef are contaminated with pathogenic bacteria.

Material and Methods

Sample Collection. Samples were collected from eight commercial packing/grinding facilities located in diverse geographical regions. Raw materials sampled at these facilities originated from 19 different, individual slaughter/packing facilities. Samples were collected from domestic fed-beef trimmings(n = 113), domestic cull beef-cow trimmings (n = 56), domestic cull dairy-cow trimmings (n = 68) and imported trimmings (n = 65).

Combo-bin core (CC) samples (n = 302) were taken prior to combo-bin dumping into course grinders using a pneumatic core drill with a sterilized 91 cm x 5 cm stainless steel core attachment (Afeco, Model 6H117, Algona, IA). Each combo-bin was cored five times in a consistent pattern, and a random "grab" sample (~ 500 g) was taken with a sterile, gloved hand and deposited in a 10 x 20 cm Whirl-Pak® bag (Nasco, Fort Atkinson, WI).

Combo-bin purge (PG) samples (n = 108) were collected only from those bins of meat that were also core-sampled for analysis. These samples were collected following coring in sterile 50 ml tubes during the dumping process by slowly dumping the bin and collecting the drippings (~ 100 ml) as they ran from the combo-bin.

Final (FN) samples (n = 284) were aseptically collected as the final product was being ground and extruded from the final grinder. All samples were packed into insulated shipping containers with cooling packs and shipped overnight to IDEXX Food Safety Net laboratory, Richardson, TX for analysis.

Microbiological Analyses. Combo-bin core, PG and FN samples were analyzed to determine (1) Aerobic Plate Count (APC), (2) Total Coliform Count (TCC), (3) Generic *E. coli* count (ECC), (4) *Staphylococcus aureus* count, (5) the incidence of *Listeria monocytogenes* and (6) the incidence of *Salmonella* spa according to USDA-FSIS (1977).

Statistical Analyses. Bacteriological counts were transformed into base 10 logarithms before performing statistical analyses and all counts were reported as log CFU /g with exception to the frequency distributions which are reported in CFU/g. Data were analyzed using general linear models (GLM), regression and frequency procedures of SAS (SAS, 1988).

Results and Discussion

Combo-bin Core Samples. Combo-bin core samples were stratified by estimated fat content, trim type, plant of origin and grinding location. Within these categories, it was evident that trimmings from all types of cattle with a higher fat content had higher detectable levels of APC, with trimmings estimated at 30% fat having the highest ($P < .05$) detectable levels of APC (Table 1).

The trend of higher fat content trimmings to have higher bacterial counts were believed to be influenced by the physical characteristics, such as the location on the carcass of the trimmings (ventral thin meats compared to whole muscle cuts), particle size of the trimmings (whole muscle cuts compared to random trimmings) and the amount of particle surface area represented in the core sample, and not directly related to the fat content. Additionally, in some facilities, this type of trim was comprised largely of trimmings from steak fabrication which was extensively handled and exposed frequently to cross-contamination.

All raw materials sampled were classified into one of four types of trimmings, those from culled-beef-cows, culled-dairy-cows, fed-cattle trimmings and imported trimmings. Across these trim types, fed beef trimmings had the highest ($P < .05$) detectable levels of APC, whereas the detectable levels of TCC, ECC and *S. aureus* were not different ($P > .05$) between the trim types and throughout the study, the levels of TCC, ECC and *S. aureus* were relatively low, and often below the detection limits (10 CFU/g) of the microbiological analyses. Trimmings from fed beef

Table 1. Mean ± SD (log CFU/g) for aerobic plate counts (APC), total coliform counts (TCC), generic *E. coli* counts (ECC) and *S. aureus* counts for combo-bin core samples stratified by fat percentage and trim source

Effect	APC	TCC	ECC	*S. aureus*
Fat Content				
10%[a] (n = 112)	2.6 ± 1.1[z]	1.1 ± .4	1.1 ± .3	1.0 ± .1
20% (n = 50)	3.2 ± 1.1[y]	1.3 ± .5	1.1 ± .3	1.0 ± .0
30% (n = 53)	4.0 ± 1.8[x]	1.1 ± .3	1.0 ± .2	1.0 ± .1
50% (N = 82)	3.3 ± 1.3[y]	1.3 ± .6	1.2 ± .4	1.1 ± .1
Trim Source				
Beef Cow (n = 56)	2.6 ± .9[z]	1.2 ± .5	1.2 ± .4	1.0 ± .1
Dairy Cow (n = 68)	2.8 ± 1.3[z]	1.3 ± .5	1.2 ± .4	1.0 ± .0
Fed Beef (n = 113)	3.6 ± 1.6[y]	1.2 ± .5	1.1 ± .3	1.0 ± .1
Imported (n = 65)	3.0 ± 1.1[z]	1.1 ± .3	1.0 ± .2	1.0 ± .0

[a] Fat percentages are based upon visual estimates of the raw materials.

[xyz] Means, within column and effect, lacking common superscript letters differ ($P < .05$).

cattle were most often utilized as a source of fat in ground beef formulations and were generated largely from thin meats or external trimmings that contained a large quantity of subcutaneous fat. Also, the particle size of fed-beef trimmings was smaller than other trim types, much like above, and therefore a single sample reflects a greater amount of surface area.

All combo-bin core samples were analyzed for the presence or absence of *Listeria monocytogenes* and *Salmonella* spp. within the type of trim and the estimated fat composition of the raw materials. *Salmonella* was found in 1.9% of the core samples collected, well below the performance standards for percent positive *Salmonella* (7.5%) in ground beef (USDA, 1996). *Listeria monocytogenes* was found in 3.3% of the core samples evaluated.

Table 3. Mean ± SD (log CFU/g) for aerobic plate counts (APC), total coliform counts (TCC), generic *E. coli* counts (ECC) and *S. aureus* counts for combo-bin purge samples stratified by fat percentage and trim source

Effect	APC	TCC	ECC	*S. aureus*
Fat Content				
10% (n = 48)	3.7 ± .9	2.1 ± .8	1.9 ± .8	1.0 ± .1
20% (n = 5)	4.6 ± 1.4	1.8 ± .6	1.2 ± .4	1.0 ± .0
30% (n = 45)	4.4 ± 1.6	1.6 ± .5	1.2 ± .3	1.0 ± .1
50% (N = 10)	4.6 ± 1.1	2.1 ± .9	1.6 ± .5	1.0 ± .0
Trim Source				
Beef Cow (n = 42)	3.9 ± .8[z]	2.1 ± .8[y]	1.9 ± .8[y]	1.0 ± .1
Fed Beef (n = 66)	4.5 ± 1.5[y]	1.7 ± .6[z]	1.3 ± .4[z]	1.0 ± .1

[y,z] Means, within column and effect, lacking common superscript letters differ ($P < .05$).

Combo-bin Purge Samples. Combo-bin purge samples were stratified by fat content of the combo-bin and type of trim (Table 3). There were no differences in APC, TCC, ECC or *S. aureus* counts across fat percentages of combo-bin. Purge obtained from combo-bins of fed beef trimmings had higher ($P < .05$) APC and lower ($P < .05$) TCC and ECC counts than purge collected from culled-beef-cow trimmings (Table 5). This again could be related to the particle size of the trim and the greater amount of total surface area within the combo-bins of fed beef trimmings compared to the culled-beef-cow trim that was primarily comprised of wholesale cuts. The APC, TCC and ECC were consistently higher for the purge samples than core samples; however, among the purge samples, the mean APC, TCC, ECC and *S. aureus* were not different across fat percentages. It was found that combo-bin core sample APC counts were highly related to purge sample APC (Figure 1). These results are consistent with those of Dorsa and

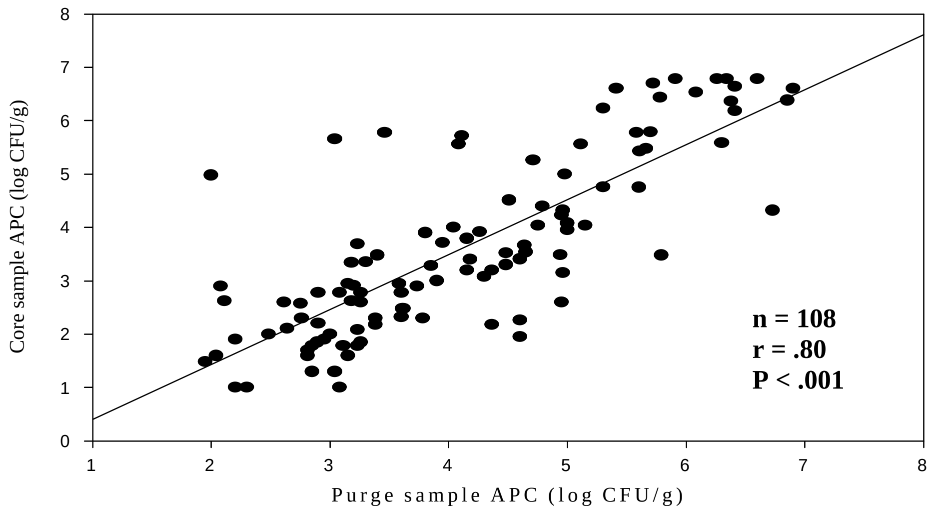

Figure 1. Scatterplot for aerobic plate counts (log CFU/g) obtained from combo-bin core samples compared to samples obtained from combo-bin purge

Siragusa (1998) who also concluded that purge had elevated APC counts presumably due to a concentration effect. It is, however, difficult to conclude from these results whether purge sampling is a more accurate measure of the actual contamination within a combo-bin, as purge sampling could remove the effects of surface area in the combo-bin, but it is probable that bacteria became concentrated in the purge and perhaps enjoyed a more favorable growing environment than organisms located on the surfaces of trimmings. Therefore, it is unclear which method (core sampling or purge sampling) more accurately enumerates actual levels of contamination, but it is clear that greater numbers of APC, TCC, ECC and *S. aureus* are enumerated using the purge sampling technique. The incidence of *L. monocytogenes* and *Salmonella* spp. in combo-bin purge samples were found to be 1.9 % and 3.7%, respectively.

Final Product Samples. At each of the eight facilities sampled, the final product generated was determined to be the product that was blended to a final fat percentage and ground to the smallest particle size. All samples were taken before patty formation, bulk packaging (chubs) or further processing (i.e. cooking). Final product was categorized into groups according to the specified fat content of the finished product. Final products with a higher fat content again had higher detectable levels of APC; but it should be noted that the majority of final product sampled containing over 25% fat was being further (heat) processed (Table 5). Aside from those fat blends, there was no consistent pattern of bacterial detection based upon fat percentage of final blends.

Listeria monocytogenes was detected only in final products that contained at least 20% fat, and *Salmonella* spp. was detected in those final product blends that were at least 25% fat. The levels of *Salmonella* spp. (1.5%) that were detected were again below those levels reported by USDA-FSIS (USDA, 1996), however the incidence of *Listeria monocytogenes* (13.6), was more frequent and, due to the nature of this organism, indicates a need for improved equipment and facility sanitation.

Conclusions

This work confirmed that contamination of beef trimmings increases as the product progresses through the grinding and comminuting process. This is due to several factors, including increased surface area, increased product temperature, product homogenization and greater exposure to contamination. The final bacterial populations of these products are, however, related to the initial contamination on the raw materials and single sources of heavy contamination can cross-contaminate numerous final product batches of ground beef. In order to minimize the contamination of final ground beef products, it is important to utilize raw materials that have been handled properly and are used promptly and any raw materials suspected or tested to be microbiologically challenged should be redistributed and used in a fully-cooked product, or destroyed in order to maintain the microbiological integrity and safety of raw ground beef products.

Table 5. Mean ± SD (log CFU/g) for aerobic plate counts (APC), total coliform counts (TCC), generic *E. coli* counts (ECC) and *S. aureus* counts final product samples stratified by fat percentage

Effect	APC	TCC	ECC	*S. aureus*
Fat Content				
5% (n = 10)	3.5 ± 1.5^{xy}	$1.8 \pm .7^{yz}$	$1.7 \pm .7^{y}$	1.1 ± .3
10% (n = 48)	$2.7 \pm .7^{z}$	$1.3 \pm .3^{z}$	$1.1 \pm .3^{z}$	1.0 ± .1
15% (n = 37)	$2.8 \pm .6^{z}$	$1.2 \pm .4^{z}$	$1.1 \pm .3^{z}$	1.0 ± .0
20% (n = 5)	$4.0 \pm .9^{y}$	$1.5 \pm .6^{yz}$	$1.3 \pm .5^{z}$	1.0 ± .1
25% (n = 43)	3.7 ± 1.0^{y}	$1.4 \pm .6^{z}$	$1.1 \pm .3^{z}$	1.1 ± .2
35% (n = 28)	$6.0 \pm .6^{x}$	$2.0 \pm .7^{y}$	$1.2 \pm .4^{z}$	1.0 ± .0
50% (n = 8)	$5.0 \pm .6^{x}$	$1.5 \pm .4^{yz}$	$1.4 \pm .4^{yz}$	1.0 ± .0

^{x,y,z} Means, within column lacking common superscript letters differ (P < .05).

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