Innovative Cloth Sampling Mitt to Improve Pathogen Detection for Turkey Carcasses

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I. INTRODUCTION

Sampling for detection of foodborne pathogens is a key component of food safety plans for turkey processors. We have developed a more robust and representative sampling device using a spunbond polymer cloth and validated it for various approaches to sampling beef trimmings for pathogen detection [1, 2, 3]. We further have validated an improved version of the sampling cloth by configuring it as a Mitt that fits on one hand to improve the ease of sampling beef trimmings [4]. In the current experiments the application of the sampling Mitt for use on turkey carcasses was evaluated. The objective was to determine whether Mitt sampling was at least as effective as currently used methods for monitoring food safety processes.

II. MATERIALS AND METHODS

Carcass sampling at rehang and post-chill locations in the process line was evaluated by comparing matched samples of standard cellulose sponge sampling (100^2cm x 2 locations) to a Mitt sample of a half carcass (left: 1 Mitt for *Salmonella* and right: 1 Mitt for *Campylobacter*). Mitt sampling included vigorous rubbing for 30 sec for each side of the Mitt for rehang or 30 sec on outside and 30 sec on inside for post-chill. On each of 3 days at 3 different plants, 12 rehang and 11 post-chill matched samples were collected for a total of 108 rehang and 99 post-chill observations per sampling method.

Samples were transported on cold packs overnight to the lab where 200 mL mEHEC broth (MilliporeSigma, Burlington, MA) prewarmed to 42°C was added to the mitt samples. ~~Combine~~ 30 mL of rinsates were combined with 30 mL nBPW warmed to 42°C and mixed well. Samples were homogenized by stomaching for 30 sec on speed setting 7 with a BagMixer 400 (Interscience, Woburn, MA) then 2.5 mL of homogenate was removed from each sample for aerobic plate count (APC) analyses. Samples were then incubated for 12 h at 42°C and then held at 4°C until analysis. Analyses performed on enrichment broths were prevalence by PCR for the pathogen *Salmonella*: PCR for *inv*A gene found in *Salmonella*-like organisms, and PCR for pathogen index targets representative of STEC-like and *Salmonella* like organisms (Hemolysin, intimin, heme receptor [*chu*A], adhesion siderophore [*iha*A], H7, *tet*A and *tet*B genes, O group: data were obtained from three individual, non-STEC-specific, *E. coli* O serogroups: O113, O117, and O146, and generic *E. coli*. The pathogen index targets were chosen to be representative of pathogenic bacteria without being specific for any pathogen. These targets allowed for more relevant data collection as opposed to indicator counts, but ~~do~~ did not convey any regulatory significance. For *Camplylobacter* ~~add~~ 25 mL Hunt Broth was added to the sponge samples and 100 ml to the Mitt. ~~Enrich~~ Samples were enriched at 42°C for 24h under microaerophilic conditions and ~~use~~ 3M MDA used to detect (3M, St. Paul, MN).

Enumeration data were calculated on a per-sample basis and reported as log CFU/sample. APC data were analyzed using a t test with the probability level at $P \leq 0.05$ (Prism, GraphPad Software, La Jolla, CA). Prevalence data were tallied as positive or negative for the specific PCR pathogen

index targets and reported as the proportion of positive samples. Prevalence data were analyzed with a two-sided Fisher's exact test using Prism 10 (La Jolla, CA).

III. RESULTS AND DISCUSSION

At rehang and post-chill, the Mitt had higher ($P < 0.05$) recoveries of aerobic plate counts than the cellulose sponge method (Table 1). The Mitt had higher ($P \leq 0.05$) recoveries of *Campylobacter* at rehang and post-chill than the cellulose sponge method (Table 1). For *Salmonella* recovery at rehang, the Mitt had a higher ($P \leq 0.05$) prevalence than the cellulose sponge method. *Salmonella* was detected in only one sample post-chill, hence no analyses could be performed. At rehang, the prevalence of most of the pathogen index targets exceeded 80% lowering their utility in comparative analyses (20-80% provides best range for comparisons). However, the trends were similar to the results of the indicator counts and pathogen prevalence where the Mitt had higher ($P \leq 0.05$) recovery than the cellulose sponge method for tet resistance and H7 genes. The results of the O serogroup assay were within the 20% to 80% prevalence range preferred for analysis and while the Mitt had the higher numerical prevalence, it was not different statistically ($P > 0.05$) from the cellulose sponge method (Table 1). At post-chill, the Mitt had consistently higher ($p \leq 0.05$) target recoveries than the cellulose sponge (Table 1).

Table 1 – Comparison of cellulose sponge and Mitt for sampling turkey carcasses for pathogen detection.

Sample	APC CFU/sample	*Campylobacter* %	*Salmonella* %	*E. coli* %	Vir %	Tet %	O groups %	H7 %
Rehang								
Sponge	5.7[b]	44.9[b]	13.9[b]	94.4[a]	99.9[a]	93.8[b]	39.8[a]	76.9[b]
Mitt	6.7[a]	89.3[a]	28.7[a]	99.1[a]	100[a]	100[a]	52.8[a]	94.4[a]
Post-chill								
Sponge	3.1[b]	8.1[b]	0.0	56.6[b]	40.4[b]	46.6[b]	10.1[a]	5.1[b]
Mitt	3.7[a]	23.4[a]	1.9	96.0[a]	90.9[a]	89.8[a]	17.2[a]	45.5[a]

IV. CONCLUSION

These data demonstrate that Mitt sample collection would provide at least as good if not better performance for recovering bacteria and detecting pathogen contamination for turkey carcasses as the existing sponge method. The Mitt method samples more surface area and provides a more robust, representative sample when compared with the sponge sampling method. Furthermore, the flexibility of the Mitt provides opportunities to design sampling strategies to enhance process control monitoring by sampling multiple carcasses with one Mitt and to use the Mitt for sampling turkey parts such as wings or parts destined for ground product.

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