

TRANSLOCATION OF NATURAL MICROFLORA FROM MUSCLE SURFACE TO INTERIOR BY BLADE TENDERIZATION

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Summary

The effect of blade tenderization on translocation of natural microflora from the surface to the interior of *longissimus dorsi* steaks aged for 7, 14, and 21 days was evaluated. Samples from the exterior and interior of steaks from blade-tenderized (BT) and non-blade-tenderized (N-BT) strip loins were analyzed for aerobic plate, coliform, and *Escherichia coli* counts. Results showed that BT translocated microorganisms (aerobic plate counts) from the exterior to the interior of muscle. Microorganism numbers increased with extended storage ($P < .05$). Counts of coliforms and *Escherichia coli* recovered from BT steaks were comparable to those from N-BT steaks because of very low exterior counts, showing the importance of good hygiene.

(Key Words: Blade Tenderization, Beef Steaks, Microflora Translocation.)

Introduction

The meat industry utilizes several tenderization techniques including aging, application of proteolytic enzymes, marination, electrical stimulation, flaking and forming, and mechanical or blade tenderization. Blade tenderization improves tenderness of meat, especially low grade or cheaper cuts, without changing other sensory or quality attributes. Other tenderization techniques can affect sensory and textural characteristics of products.

Blade tenderization disrupts the muscle structure by cutting through muscle tissues, fibers, and connective tissue with sharp-

edged blades. This penetrating action can increase tenderness, especially for meat high in connective tissue and improve overall product uniformity. More passes or larger blade size may increase tenderness without adverse sensory or bacteriological effects. Product life of vacuum-packaged or frozen, blade-tenderized (BT) meat has been comparable to that of non-blade-tenderized (N-BT) meat when high hygienic standards were maintained. Microbiological aspects of blade tenderization need further investigation, because it violates the surface of intact muscle, and contamination may be carried from the surface to the interior of cuts. This experiment examined the effects of blade tenderization on translocation of natural microflora from the surface to the interior of *longissimus dorsi* steaks.

Experimental Procedures

Strip loins (IMPS 180; NAMP, 1997) conforming to Certified Angus Beef™ (CAB) specifications were purchased from a commercial beef packing facility. The loins (n=27) were separated into three groups of nine and aged for 7, 14, or 21 days at 34°F. After aging, loins from each group were divided randomly into three sets of three. One set of loins was BT using a Ross™ tenderizer (model T7001, Ross Industries Inc., Midland, VA) by passing each of the loins one time (1X) through the tenderizer, another set was passed two times (2X), and the third served as the N-BT control (0X; no blade passes). The tenderizer gave an average penetration density of 32-36 punctures per square inch per blade pass. Following treatment, the loins were crust frozen for 30-40 min at -35°F in a spiral freezer. Loins were fabricated into 1-inch-thick steaks using

an automatic spiral slicer. Steaks were vacuum-packaged individually and stored at -20°F until microbial analyses.

Longissimus dorsi (LD) steaks were thawed at 40°F for 12 hours prior to microbiological analyses. Each steak was removed aseptically from its package, and a 1-inch-thick sample at a cutting angle perpendicular to the muscle grain was removed using a sterile stainless steel coring device (2-in. diameter). The sample was cut horizontally into three equal portions (each 1/3-in. thick); top, mid, and bottom. The top and bottom portions represented the upper and lower exterior surfaces of the steak that had been exposed to the packaging material. The middle portion represented muscle interior that was not exposed to the outside environment until removed for microbial analyses. Each sample was homogenized in 50 ml of 0.1% peptone water for 2 min using a stomacher. Serial dilutions were made using 9 ml of 0.1% peptone water. Aerobic plate counts were determined using 3M Petrifilm™ Aerobic Count Plates (3M, St. Paul, MN) incubated at 95°F for 48 hrs. Coliforms and *E. coli* were determined using 3M Petrifilm™ *E. coli* Count Plates incubated at 95°F for 24 hrs.

A split plot experimental design was used to select for treatments in which storage time

and number of blade passes represented the whole plot, and sampling location was the split plot. Data were analyzed using PROC GLM and MIXED of the Statistical Analysis System. Differences among least square means were determined at $P<.05$. All experiments were replicated three times.

Results and Discussion

Aerobic plate (APC), coliform, and *E. coli* counts increased ($P<.05$) with aging time (Table 1). Also, APC, coliform, and *E. coli* counts from the exterior (upper plus lower) of muscle were higher ($P<.05$) than those from the interior, but very low. Counts of *E. coli* and coliforms recovered from BT steaks (1X and 2X) at 7, 14, or 21 d of aging were comparable ($P<.05$) to counts recovered from non-tenderized (0X; N-BT) steaks. Total APC indicated some translocation of microorganisms from the exterior to the interior ($P<.05$), and this translocation was more pronounced with longer aging. No interactions ($P>.05$) were found among storage time, treatment (tenderization), and sampling location. Sanitation, proper handling, and good hygiene practices, which result in low surface microbial counts and clean tenderizer blades, are important to avoid translocation of bacteria during blade tenderization.

Table 1. Average Microbial Counts (\log_{10} CFU/cm²) for Blade Tenderized (1X, 2X) and Non-Tenderized (0X) *longissimus dorsi* Steaks^{1,2}

Aging (Days)	Blade Passes	APC		<i>E. coli</i>		Coliforms	
		Exterior	Interior	Exterior	Interior	Exterior	Interior
7	0x	1.36 ±1.92	0.82 ±1.15	NG	NG	0.29 ±0.0	0.58 ±0.35
	1x	1.54 ±0.41	0.48 ±0.03	0.15 ±0.21	0.12 ±0.16	0.36 ±0.51	0.21 ±0.30
	2x	1.80 ±1.57	1.21 ±1.25	NG	NG	NG	0.24 ±0.34
14	0x	1.21 ±0.23	0.67 ±0.02	NG	NG	NG	0.13 ±0.0
	1x	1.88 ±0.07	1.03 ±0.33	0.18 ±0.18	NG	0.15 ±0.21	NG
	2x	2.36 ±0.34	1.32 ±0.27	NG	NG	0.07 ±0.09	NG
21	0x	2.65 ±0.17	0.92 ±0.42	0.18 ±0.25	NG	0.12 ±0.16	NG
	1x	2.17 ±0.78	0.89 ±0.33	NG	NG	0.18 ±0.26	NG
	2x	2.67 ±0.08	1.74 ±0.54	NG	NG	0.35 ±0.30	NG
Standard Error (STD)		0.60	0.45	0.09	0.14	0.14	0.14

¹ = Microbial counts reported are means ± standard deviations (n=3).

² = NG: No Growth.