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Evaluation of Two Thermal Processing Schedules at Low Relative Humidity for Elimination of *Escherichia coli* O157:H7 and *Salmonella* Serovars in Chopped and Formed Beef Jerky†

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ABSTRACT

Foodborne outbreaks have been linked to jerky produced under insufficient thermal processing schedules. Reduction of *Escherichia coli* O157:H7 and *Salmonella* serovars during thermal processing of chopped and formed beef jerky was evaluated under two processing schedules representative of those used by large-scale (LS) and small-scale (SS) jerky production facilities. Fresh chopped and formed all-beef jerky batter was inoculated with 5.8 to 7.3 log CFU of *E. coli* O157:H7 or *Salmonella* per g, extruded into strips, and thermally processed by LS or SS schedules. A ≥5.0-log CFU/g reduction of both pathogens occurred with <10% relative humidity and a cumulative process of 44 min at 55.6°C followed by 46 min at 77.8°C into the LS schedule. Additional drying at 77.8°C for 3.5 h was needed to achieve a water activity of 0.67 and a moisture-to-protein ratio (MPR) of 0.77. For the SS process, a ≥5.0-log CFU/g reduction of both pathogens occurred with 15 to 20% relative humidity and a cumulative process of 45 min at 52°C, 60 min at 57°C, 45 min at 60°C, 45 min at 63°C, 90 min at 68°C, and finishing with 30 min at 77°C. After processing for an additional 90 min at 77°C, water activity was 0.60 while the MPR was 0.82. The LS and SS processes for producing chopped and formed jerky provided ≥5.0 log lethality to control *E. coli* O157:H7 and *Salmonella*. However, both processes would require additional drying to achieve an MPR of 0.75 to be labeled as jerky.

The New Mexico Department of Health linked salmonellosis to beef jerky in 2003 after 26 individuals became ill; this prompted a recall of nearly 9,797 kg of product. *Salmonella enterica* serotype Kiambu, a rare *Salmonella* strain, was identified as the organism responsible for this outbreak *(15)*. In 2004, following this incident, the U.S. Department of Agriculture–Food Safety and Inspection Service (USDA/FSIS) instituted guidelines published in the *Compliance Guideline for Meat and Poultry Jerky Produced by Small and Very Small Plants (16),* which was then updated in 2007 with the *Quick Guide on Jerky Processing (17),* which addresses obtaining lethality and verifying drying conditions for jerky. The *Quick Guide* states that water activity (a_w) for jerky should be ≤0.85 for safety and the moisture-to-protein ratio (MPR) must be ≤0.75 to be labeled as jerky.

Appendix A of the USDA/FSIS *Compliance Guidelines for Meeting Lethality Performance Standards for Certain Meat and Poultry Products (13)* states that processors of meat and poultry products should meet a performance lethality of a ≥6.5-log CFU/g reduction for *Salmonella*. However, a letter of communication from a USDA/FSIS official stated that a ≥5.0-log CFU/g reduction of both *Salmonella* and *Escherichia coli* O157:H7 would be accepted as an indication of a ''safe'' process *(11)*. The 2004 and 2007 jerky compliance guidelines outline specific thermal processing parameters for relative humidity (RH) that should be used to achieve this reduction *(16, 17)*. Meat processing businesses producing jerky products must validate that their processes achieve a ≥5-log reduction of *E. coli* O157:H7 and *Salmonella* serovars *(3, 11)*.

Validation and challenge studies are used to determine if specific thermal processes are capable of producing safe products. In the case of whole-muscle and restructured jerky, validation studies have been conducted in home-style dehydrators and commercial smokehouses *(3–6)*. This information is used by the industry to establish scientifically based critical limits in hazard analysis and critical control point plans.

The main objective of our validation study was to determine the reduction of *E. coli* O157:H7 and *Salmonella* serovars during thermal processing of chopped and formed beef jerky under two processing schedules representative of those used by large-scale (LS) and small-scale (SS) jerky production facilities. It was hypothesized that an LS processing facility may be more effective at controlling pathogens than an SS processing facility because small and very small processors may not have the equipment capable of achieving the specific high-humidity levels recommended by FSIS *(1, 8)*. A secondary objective was to determine

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TABLE 1. *Strains of microorganisms used for large- and small-scale jerky processing*

Bacterium	ID code or ATCC number	Source
E. coli O157:H7	43890[a,b]	Human infection
E. coli O157:H7	43894[a,b]	Human with hemorrhagic colitis
E. coli O157:H7	43895[a,b]	Ground beef associated with hemorrhagic colitis
E. coli O157:H7	KSU-01[a]	Human infection
E. coli O157:H7	KSU-02[a]	Human infection
E. coli O157:H7	43889[b]	Human with hemolytic uremic syndrome
E. coli O157:H7	35150[b]	Human infection
Salmonella Enteritidis	4931[a]	Human experiencing salmonellosis
Salmonella Enteritidis	13076[a]	Human experiencing salmonellosis
Salmonella Enteritidis	USDA 15060[a]	Human experiencing salmonellosis
Salmonella Enteritidis	BAA-710[b]	Clinical specimen
Salmonella Enteritidis	6962[b]	Foodborne illness fatality in England
Salmonella Enteritidis	13314[b]	Laboratory strain
Salmonella Abaetebua	9263[b]	Laboratory strain
Salmonella Abaetebua	35640[a]	Obtained from creek in Argentina
Salmonella Typhimurium	13311[a,b]	Human experiencing salmonellosis

[a] Used in LS thermal processing cycle.
[b] Used in SS thermal processing cycle.

whether xylose lysine desoxycholate (XLD) alone or a thin agar layer (TAL) method using XLD with a thin top layer of tryptic soy agar (TSA) would provide better detection of injured *Salmonella* cells during LS jerky processing.

MATERIALS AND METHODS

Experimental design. This study validated commercial thermal processing schedules representative of those used by LS and SS commercial processing facilities. The LS schedule was obtained from a large commercial jerky processor, while the SS schedule was derived from survey results of processors from small Midwestern meat processing businesses *(8)*. For LS and SS, two treatments were analyzed: an *E. coli* O157:H7–inoculated and a *Salmonella*-inoculated batch of chopped and formed beef jerky. Noninoculated jerky control batches also were prepared. A replication consisted of both inoculated batches and the control batch placed in the smokehouse simultaneously. Three replications were completed for LS and SS.

***E. coli* O157:H7 and *Salmonella* serovar cultures.** *E. coli* O157:H7 and *Salmonella* serovar cultures were obtained from the American Type Culture Collection (Rockville, MD), the Centers for Disease Control and Prevention (Atlanta, GA), and the USDA–Agricultural Research Service (Athens, GA) (Table 1). Some different strains were used due to culture availability for LS and SS trials; however, strains for LS and SS are representative of clinical isolates and no statistical comparisons are made between LS and SS.

Preparation of inoculum. Five-strain inocula of *E. coli* O157:H7 and *Salmonella* serovars were prepared. One loopful of each culture was transferred into 9 ml of tryptic soy broth (TSB; Difco, Becton Dickinson, Sparks, MD) and incubated at 35°C for 18 to 24 h. Next, 6 ml of each culture suspension was transferred to a sterile bottle (Nalgene, Rochester, NY), resulting in two separate bottles: one containing 30 ml of *E. coli* O157:H7 culture, and one containing 30 ml of *Salmonella* culture The cell densities of the final *E. coli* O157:H7 and *Salmonella* inocula were approximately 9.2 log CFU/ml and 8.3 log CFU/g for LS and SS, respectively.

Meat batter preparation and inoculation. Frozen (−5°C), vacuum-packaged, chopped and formed all-beef jerky batter containing 83% lean beef, dextrose, flavorings, beef stock, salt, soy, corn protein, smoke flavoring, and cure was obtained from a commercial processor, immediately stored (−15 ± 2°C) for up to 2 weeks, and then tempered overnight at 4°C for use the following day. The batter was split into three 1.8-kg batches.

To inoculate batter with *E. coli* O157:H7 or *Salmonella,* a 29-ml inoculum was intermittently pipetted drop-wise over the batter surface and massaged into the batter with gloved hands for approximately 3 min until thoroughly mixed. The noninoculated control was prepared by hand mixing with 29 ml of sterile deionized water. All batters were stored less than 2 h at 4°C until sampled for raw *E. coli* O157:H7, *Salmonella,* or total plate count and then extruded.

Raw jerky batter was transferred to manual jerky strip dispensers (model H6253, Grizzly Industrial, Inc., Springfield, MO) with jerky nozzles (2.54 by 0.64 cm; model LEM468D, Allied Kenco, Houston, TX) and extruded into strips placed on polyscreen sheets (Excalibur, Sacramento, CA) with eight strips per sheet. Each strip was approximately 15.24 by 2.54 by 0.64 cm. Treatments were loaded into a smokehouse (Alkar Model 450-UA, Alkar, Lodi, WI) following the schematic of Roberts *(10)* to prevent cross-contamination and processed following LS (Table 2) or SS (Table 3) processing schedules.

***E. coli* O157:H7 and *Salmonella* serovar inoculum enumeration.** For LS processing, serial dilutions of each inoculum were prepared with 0.1% peptone water (Difco, Becton Dickinson). *E. coli* O157:H7 and *Salmonella* were enumerated in duplicate by spread plating 0.1 ml on phenol red sorbitol agar (PRSA; Remel, Lenexa, KS), or XLD (Difco, Becton Dickinson) and TAL-XLD (Difco, Becton Dickinson), respectively. TAL-XLD consisted of 25 ml of XLD with a 14-ml top layer of TSA for recovery of injured cells *(19)*. All plates were incubated at 37°C for 24 h and then enumerated. For SS, *Salmonella* inoculum was plated only on XLD because LS results indicated no significant difference ($P > 0.05$) between XLD and TAL-XLD.

***E. coli* O157:H7 and *Salmonella* serovar jerky enumeration.** For LS and SS, samples were collected at six different times

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TABLE 2. *Large-scale commercial thermal processing schedule for chopped and formed beef jerky and sample collection times for enumeration and enrichment*[a]

Stage	DB temp (°C)	Stage time	Blower speed[b]	Collection time		Cumulative times and temps at each sampling time
				Enumeration	Enrichment	
0[c]						Raw
1	55.6	14 min	Medium			
2	55.6	16 min	Medium			
3	55.6	14 min	Medium			
4	77.8	16 min	Medium			
5	77.8	14 min	Medium			
6	77.8	16 min	Medium	End of stage		44 min at 55.6°C and 46 min at 77.8°C
7	77.8	14 min	High	End of stage		44 min at 55.6°C and 1 h at 77.8°C
8	77.8	16 min	High	End of stage		44 min at 55.6°C and 1 h 16 min at 77.8°C
9	77.8	14 min	High			
10	77.8	16 min	High	End of stage		44 min at 55.6°C and 1 h 46 min at 77.8°C
11	77.8	14 min	High			
12	77.8	5 h	High	1.5 h into stage	1.5 h into stage	44 min at 55.6°C and 3 h 30 min at 77.8°C
End				End of stage	End of stage	44 min at 55.6°C and 7 h at 77.8°C

[a] The smokehouse has an automated damper system and the ability to inject steam humidity as needed to control humidity. Percent RH remained at <10% throughout the entire smokehouse cycle. The exhaust fan was activated during the entire cycle.
[b] Medium speed, 240.4 ± 16.1 m/min; high speed, 347.9 ± 34.1 m/min.
[c] Stage 0, raw meat batter.

throughout thermal processing (Tables 2 and 3). At each sampling time, two jerky strips were collected to form a composite sample from each treatment. All sampling was done in duplicate.

Two strips from each sampling time were aseptically cut into small pieces and combined. A 25-g subsample was placed into a filtered stomacher bag (Fisher Scientific, Pittsburgh, PA) containing 50 ml of peptone water and stomached (Stomacher Mix 1 Lab Blender, Microbiology International, Frederick, MD) for 1 min. Serial dilutions were prepared.

For LS, 0.1 ml was spread plated in duplicate onto PRSA for *E. coli* O157:H7–inoculated samples and onto XLD and TAL-XLD for *Salmonella*-inoculated samples. However, for SS all samples were spiral plated, and *Salmonella* enumeration was done using XLD only. Control samples for LS were spread plated on TSA, while SS controls were spiral plated on TSA, PRSA, and XLD. All plates were incubated at 37°C for 24 h and then enumerated.

A 1:3 dilution allowed for a 1.5-log CFU/g detection limit for jerky collected at the end of stages 6, 7, 8, and 10 and 1.5 h into stage 12 for LS and at the end of stages 1, 2, and 3 for SS. To enhance the detection limit down to 0.5 log CFU/g, 0.25 ml of a 1:3 dilution was spread plated onto four plates in duplicate for LS and SS jerky taken at the end of both cycles.

***E. coli* O157:H7 and *Salmonella* serovar enrichment.** Samples were collected (Tables 2 and 3) in duplicate and enriched by adding 225 ml of modified *E. coli* medium (Difco, Becton Dickinson) containing 0.1% sodium novobiocin (Sigma Chemical Co., St. Louis, MO) to 25 g of *E. coli* O157:H7–inoculated sample or by adding 225 ml of Preuss broth (Preuss; Difco, Becton Dickinson) to 25 g of *Salmonella*-inoculated sample. After stomaching for 1 min, samples were incubated at 37°C for 24 h. Diluent from the enriched samples was streaked onto PRSA for *E. coli* O157:H7–inoculated samples and XLD and TAL-XLD (LS only) for *Salmonella*-inoculated samples. Plates were incubated at 37°C for 24 h and observed for typical colonies.

Confirmation. *E. coli* O157:H7 and *Salmonella* strains and presumptive colonies were confirmed using Enterotubes (Becton Dickinson, Franklin Lakes, NJ) for LS and API 20E biochemical identification test strips (bioMerieux Vitek, Inc., Hazelwood, MO) for LS and SS processing schedules.

pH and a_w. For LS, pH was measured on duplicate raw and heat-treated control samples by weighing 25 g of jerky into a filtered stomacher bag containing 50 ml of peptone water and stomaching for 1 min. A pH meter and temperature compensating probe (model 530 pH meter, Corning Pinnacle, Corning, NY) was used to measure pH.

a_w was measured on duplicate LS and SS raw and heat-treated control jerky by using a calibrated a_w meter (model CX2, Aqualab, Pullman, WA). Strips of LS jerky were diced into square pieces (1 by 1 cm) for analysis, while intact pieces or undiced pieces were used for SS jerky.

Proximate analysis. Samples were taken from the noninoculated control batch prior to putting in the smokehouse (raw), 90 min into stage 12, and at the end of stage 12 for the LS process and prior to putting into the smokehouse (raw), 60 and 90 min into stage 6, and at the end of stage 6 for the SS process. Two 25-g samples of raw batter and two jerky strips from the designated sampling times were vacuum packaged and placed in frozen storage at −80°C prior to analysis. For each sample, duplicate measurements were obtained. Samples were frozen in liquid nitrogen and pulverized in a blender (Waring Laboratory Science, Torrington, CT). Following AOAC methods *(2),* moisture (AOAC 985.14) and fat (AOAC 985.15) were analyzed using a rapid microwave solvent method (CEM, Matthews, NC). Protein was

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TABLE 3. *Small-scale commercial thermal processing schedule for chopped and formed beef jerky and sample collection times for enumeration and enrichment*[a]

Stage	DB temp (°C)	RH (%)	Stage time (min)	Blower speed[b]	Collection time		Cumulative times and temps at each sampling time
					Enumeration	Enrichment	
0[c]					Raw		
1	52	20	45	Medium			45 min at 52°C
2	57	20	60	Medium	End of stage		45 min at 52°C 60 min at 57°C
3	60	23	45	High	End of stage		45 min at 52°C 60 min at 57°C 45 min at 60°C
4	63	22	45	High	End of stage		45 min at 52°C 60 min at 57°C 45 min at 60°C 45 min at 63°C
5	68		90	High	End of stage	End of stage	45 min at 52°C 60 min at 57°C 45 min at 60°C 45 min at 63°C 90 min at 68°C
6	77	15	120	High	30 and 60 min into stage	30 and 60 min into stage	45 min at 52°C 60 min at 57°C 45 min at 60°C 45 min at 63°C 90 min at 68°C 120 min at 77°C

[a] The smokehouse has an automated damper system and the ability to inject steam humidity as needed to control humidity. The exhaust fan was activated during the entire cycle.
[b] Medium speed, 240.4 ± 16.1 m/min; high speed, 347.9 ± 34.1 m/min.
[c] Stage 0, raw meat batter.

determined by the LECO method (AOAC 990.03), and salt was analyzed by a volumetric method (AOAC 935.47).

Statistical analysis. The experimental design was a strip-split plot, and data were analyzed by using PROC MIXED in SAS (version 9.0, SAS Institute, Cary, NC). Fixed effects were medium types, sampling time, and bacterium types, along with all combinations of these effects. Random effects were replication, replication by sampling time by bacterium type, replication by sampling time, and replication by bacterium type. Significant interactions ($P < 0.05$) were sampling time by bacterium type and medium type (LS only). Least squared means were used to compare sampling times by bacterium type for LS and SS and medium types for LS only. Least significant differences were used to compare least squared means of sampling time, bacterium type, and media.

Duplicate plate counts were assigned a log CFU per gram value of 0.8 for LS when no colonies were present throughout the process and for positive enrichment. This assumed that the actual value was between zero and the detection limit, 1.5 log CFU/g. This was similar for samples collected at the end of the smokehouse cycle for LS and SS processes; however, this assumed that the actual value was between zero and the detection limit, 0.5 log CFU/g. In the case of a negative enrichment, a zero value was used. However, for determining logarithmic reductions, only the detection limit was used as a value.

TABLE 4. E. coli *O157:H7 and* Salmonella *reductions during production of chopped and formed beef jerky under a large-scale commercial thermal processing schedule*[a]

Stage/sampling time	Medium:		
	PRSA	XLD	TAL-XLD
Stage 6	5.0 ± 0.4 E	5.4 ± 0.1 EX	5.4 ± 0.3 EX
Stage 7	5.3 ± 0.3 F	5.5 ± 0.2 EX	5.4 ± 0.2 EX
Stage 8	5.5 ± 0.2 G	5.5 ± 0.2 EX	5.5 ± 0.2 EX
Stage 10	5.9 ± 0.3 H	5.7 ± 0.3 EX	5.6 ± 0.1 EX
Stage 12 (1.5 h into stage)	6.6 ± 0.0 H	6.4 ± 0.1 FX	6.6 ± 0.1 FX
End of stage 12	7.1 ± 0.0 I	6.9 ± 0.1 GX	7.1 ± 0.1 GX

[a] Values are means ± standard deviations (log CFU per gram) of six samples per sampling time. Letters following values indicate significant differences as follows: E through I, significant differences in a column within the heating process; X and Y, significant differences between XLD and TAL-XLD counts for that sampling period.

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TABLE 5. E. coli *O157:H7 and* Salmonella *reductions during production of chopped and formed beef jerky under a small-scale commercial thermal processing schedule*[a]

Stage (sampling time)	Medium: PRSA	Medium: XLD
Stage 2	2.0 ± 0.8 D	3.3 ± 0.6 D
Stage 3	3.1 ± 1.1 DE	5.1 ± 0.5 E
Stage 4	3.6 ± 0.6 E	5.8 ± 0.1 F
Stage 5	4.7 ± 0.6 EF	>5.8 ± 0.1[b] G
Stage 6 (30 min in)	5.0 ± 0.3 F	>5.8 ± 0.1[b] G
Stage 6 (60 min in)	4.7 ± 0.5 EF	>5.8 ± 0.1[b] G

[a] Values are means ± standard deviations of six samples (log CFU per gram) per sampling time. Letters following values indicate significant differences in a column within the heating process.
[b] Reported as >5.8 due to negative for enrichment.

RESULTS AND DISCUSSION

***E. coli* O157:H7 and *Salmonella* serovar enumeration and enrichment.** Initial levels of *E. coli* O157:H7 and *Salmonella* populations in raw, inoculated batter for LS were approximately 7.3 log CFU/g ($P > 0.05$). For LS, processing at dry-bulb (DB) temperatures as high as 55.6°C for 45 min followed by 77.8°C DB for 46 min with RH levels at <10% achieved reductions of ≥5.0 log CFU/g of *E. coli* O157:H7 and *Salmonella* on XLD and TAL-XLD by the end of stage 6 (Table 4), meeting the lethality guidelines suggested by USDA/FSIS *(11)*. At all sampling times, internal product temperatures were similar to DB temperatures, meeting the USDA/FSIS recommendation of heating jerky to an internal temperature of 71.1°C *(17)*. From stages 6 to 12, *E. coli* O157:H7 consistently decreased ($P < 0.05$). Recovery levels of *Salmonella* were similar ($P > 0.05$) on XLD and TAL-XLD. Although these results do not support the supposition that the TAL method recovers a greater portion of heat-injured cells than selective media alone, Wu and Fung *(18)* found that TAL significantly recovered 0.8 log CFU/g more *Salmonella* Typhimurium than selective media alone.

No populations were recovered for either pathogen by 1.5 h into stage 12, with populations reported as <1.5 log CFU/g (detection limit). At the end of the cycle, jerky microbial populations were consistently <0.5 log CFU/g (detection limit) on all medium types, resulting in final reductions of ≥6.5 log CFU/g for *E. coli* O157:H7 and *Salmonella* (Table 4). All 24 jerky samples taken 1.5 h into stage 12 and at the end of the cycle were negative for both pathogens after enrichment, indicating that the pathogens were dead as opposed to heat injured. This suggests an even greater reduction of approximately 7.2 log CFU/g for both pathogens. Although the recommended logarithmic reductions and a_w of ≤0.85 were achieved by the end of stage 6, the product was dried further in order to meet the USDA/FSIS requirement of an MPR of ≤0.75. Lethality performance standards in Appendix A of the USDA/FSIS *Compliance Guidelines for Meeting Lethality Performance Standards for Certain Meat and Poultry Products* for *E. coli* O157:H7 and *Salmonella (13)* were met by using this thermal process, and this would provide processors with a safe jerky product *(11, 14)*.

For the SS process, *Salmonella* serovars were reduced by ≥5.0 log CFU/g by the end of stage 3, while *E. coli* O157:H7 was reduced by 5.0 log CFU/g 30 min into stage 6 of thermal processing (Table 5). All enriched *Salmonella* samples were negative at the end of stages 5 and 6, whereas *E. coli* O157:H7 populations above the detection limit were obtained from nonenriched samples.

Results indicate that high humidity, such as the ≥90% RH stated in the FSIS jerky compliance guideline *(17),* may not be necessary to achieve a ≥5.0-log reduction for *Salmonella* and *E. coli* O157:H7 depending on the thermal processing parameters used. This is important because many small and very small processors do not have equipment capable of achieving the specified high-humidity levels *(1)*.

Faith et al. *(4)* evaluated the reduction of *E. coli* Ol57:H7 in restructured jerky processed in a home dehydrator with no added humidity. They achieved 5.0-log CFU/g reductions at 52°C when processed for 8 to 10 h or at 68°C for 4 to 6 h. Other studies *(5, 6)* found similar results when using a home-style dehydrator with *E. coli* O157:H7, *Salmonella,* and *Listeria monocytogenes* in beef jerky production; however, jerky was preheated to 71°C and then placed in a dehydrator and dried at 60°C for 6 h.

Buege and others *(3, 7)* conducted a validation study using a commercial smokehouse to process whole-muscle beef jerky inoculated with *Salmonella* and *E. coli* O157:H7. They found ≥5.0-log CFU/g reductions of both pathogens

TABLE 6. *pH, water activity, and proximate analysis of the control chopped and formed beef jerky made under a large-scale commercial thermal processing schedule*[a]

Stage or sampling time	pH	a_w	% moisture	% protein	MPR	% fat	% salt
Raw	6.1 ± 0.1	0.94 ± 0.016	53.7 ± 1.4	16.5 ± 0.4	3.25:1	17.4 ± 1.8	2.2 ± 0.0
End of stage 6	6.0 ± 0.0	0.85 ± 0.013					
End of stage 7	6.0 ± 0.1	0.83 ± 0.024					
End of stage 8	6.0 ± 0.0	0.84 ± 0.021					
End of stage 10	6.0 ± 0.1	0.82 ± 0.017					
90 min into stage 12	5.7 ± 0.1	0.67 ± 0.032	24.8 ± 1.5	32.0 ± 0.9	0.77:1	24.5 ± 1.4	4.3 ± 0.3
End of stage 12	5.2 ± 0.1	0.59 ± 0.020	16.8 ± 2.2	36.2 ± 1.4	0.46:1	25.6 ± 1.4	4.5 ± 0.5

[a] Values are means of six samples per sampling time ± standard deviations for all columns except MPR.

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TABLE 7. *Phase 2 water activity and moisture-to-protein ratio of the control chopped and formed beef jerky made under a small-scale commercial thermal processing schedule*[a]

Time of sampling	a_w	% moisture	% protein	MPR
End of stage 5	0.73 ± 0.004	36.7 ± 0.9	23.5 ± 0.6	1.27:1
30 min into stage 6	0.66 ± 0.026			
60 min into stage 6	0.64 ± 0.035			
90 min into stage 6	0.63 ± 0.031			
End of stage 6	0.60 ± 0.020	19.6 ± 0.8	24.1 ± 0.8	0.82:1

[a] Values are means of six samples per sampling time ± standard deviations for all columns except MPR.

by ensuring that high wet-bulb temperatures were reached and maintained early in the process followed by drying at 76.7°C. However, they also found that if jerky is initially heated at a DB temperature of 51.7°C for a short time, and if the jerky a_w is 0.86 or greater before the drying phase begins, the product could be subsequently dried at 76.7°C DB to achieve a ≥5.0-log CFU/g reduction for both pathogens. The authors did caution that this process provided a lower safety margin than others discussed in their study.

Total plate count enumeration. Initial total plate count of background flora in raw, noninoculated batter averaged 3.7 and 5.4 log CFU/g for LS and SS, respectively. Background flora populations for LS were 1.9 to 2.5 log CFU/g in stages 6 to 12, indicating the survival of background flora. For SS, TPC decreased ($P < 0.05$) from 3.6 log CFU/g at stage 2 to 1.5 log CFU/g 60 min into stage 6. For LS and SS, there were no detectable *E. coli* O157:H7 or *Salmonella* counts in raw, noninoculated batter samples (detection limit of <1.5 log CFU/g).

pH and a_w. Raw batter and finished product pH values for LS were 6.1 and 5.2, respectively (Table 6). a_w declined from 0.85 at the end of stage 6 to 0.59 for the finished product. USDA/FSIS recommends that jerky have an a_w of ≤0.85 to inhibit pathogen growth *(17)*. Water activity was also below 0.85 for SS by the end of stage 5 of thermal processing (Table 7). By the end of stage 6 for SS, a_w was 0.60.

Proximate analysis. For LS, the moisture content was 53.7% for raw noninoculated batter and 16.8% for the finished jerky (Table 6). The final product moisture content was below the typical 28 to 30% moisture content for jerky *(9)*. The protein contents were 16.5 and 36.2% for raw noninoculated batter and finished jerky, respectively. For a product to be labeled as jerky, USDA requires that it meet the MPR standard of identity of ≤0.75 *(12)*. The MPR of noninoculated jerky was 0.46 at the end of stage 12, meeting the USDA standard of identity for jerky. Salt content was typical for jerky *(8)* at 2.2 and 4.5% for raw noninoculated batter and finished jerky, respectively (Table 6).

Although jerky collected at the end of stage 12 of LS processing met the requirements typical of shelf-stable jerky, the product at this point was very dry for jerky. To achieve a more acceptable product, jerky should be removed from thermal processing somewhere between 90 min into stage 12 and the end of stage 12. By keeping the MPR closer to 0.75 and the a_w near 0.70, a processor would have lower costs, as water is an inexpensive ingredient. Jerky produced with these parameters meet USDA guidelines for safety and the standard of identity.

Jerky produced by SS thermal processing had moisture and protein contents of 19.6 and 24.1%, respectively, at the end of stage 6, resulting in an MPR of 0.82 (Table 7). Because the MPR exceeded the USDA jerky standard of identity, the product would require additional drying to be labeled as beef jerky. However, this product could be labeled as kippered beef, which requires an MPR of ≤2.03.

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