



# final report

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Prepared by: <Name>  
Symbio Alliance

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## **E Coli in raw ground beef components**

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## 1. INTRODUCTION

Meat & Livestock Australia (MLA) has contracted Symbio Alliance to undertake a survey of the microbial safety and quality of raw ground beef components exported to the US. Although the microbiological quality of lean beef trim has been studied extensively (1, 2, 3) there is a dearth of information on all other components of raw ground beef (eg, head meat, cheek meat, oesophagus/weasand meat, organ meat and advanced meat recovery product).

The results of a telephone survey of all registered establishments exporting meat products to the US were provided to MLA in our report dated 22 November 2007. Following this report, 17 meat processing establishments were approached for their inclusion in a survey of the microbiological quality of raw ground beef components other than lean beef trim. Samples were subsequently received from 12 of those establishments.

The results of the microbiological survey are provided in this report.

## 2. METHODOLOGY

**Design of the study.** All meat samples were collected by respective staff at each of 12 meat processing establishments supplying raw ground beef components other than boneless beef trim to the US. Samples collected by product type and plant are provided in Table 1.

**Table 1: Sampling Plan**

Product	Establishment												Total
	1	2	3	5	6	7	9	10	11	12	13	14	
Primal/sub-primal													
- Sirloin/striploin				7						4	7		18
- Inside/knuckle	3			6	5		6	2			7	5	34
- Outside/silverside	6			3							6	4	19
- Blade/eye round	6											5	11
- Rump												4	4
- Topside cap	3												3
- Chuck												3	3
- Shank					5	5	5	3					18
- Bull F/H					5		5	2					12
Total Primal-subprimals													122
Head/cheek		3	3	4	4		7	6	4		6		37
Lips		13	13						10				36
Heart					9		10	3					22
Neck/tail/other					5		11		20				36
<b>Total</b>	<b>18</b>	<b>16</b>	<b>16</b>	<b>20</b>	<b>33</b>	<b>5</b>	<b>44</b>	<b>16</b>	<b>34</b>	<b>4</b>	<b>26</b>	<b>21</b>	<b>253</b>

**Sample collection.** Each sample of 400g comprised 60 sub-samples each of 6-7g. Every attempt was made to take the sub-samples from a range of cartons (12 max) but this was not always possible or practical. Samples were placed in individual sterile sealed bags and packed in insulated containers with chiller packs for overnight delivery to the Symbio Alliance laboratory. Upon arrival the temperature of each batch of samples was recorded. No samples exceeded 10°C.

**Laboratory analysis.** Upon arrival at the laboratory, 25g of each sample was processed for aerobic plate count (APC), coliforms and *E.coli*. The remaining 375g

(approximate) of each sample was frozen (-19°C) for later dispatch to the IEH Laboratory in the USA.

**Microbiological analysis of meat samples.** Ten grams of meat was added to 0.1% peptone water (90ml) and macerated in a Seward Stomacher BA 7021 (Seward, United Kingdom) for 2 minutes. Aliquots (1ml) were plated for APC, coliforms and generic *E. coli*. For APC, petrifilm plates were prepared according to the AOAC method 990:12 and incubated at 27°C for 96h at which time the colonies were counted and the count/g recorded. Generic *E. coli* were estimated by placing 1ml aliquots of appropriate dilutions onto *E. coli* Petrifilm (3M, Sydney, Australia) and incubating at 37°C for 48h. Colonies were counted as per the manufacturer's instructions and AOAC method 991.14. The limits of detection were 100 CFU/g for APC and 10 CFU/g for coliforms and *E.coli*.

### Detection of *Salmonella*, EHEC and STEC.

**Statistical analysis.** All data were analysed using MS Excel<sup>®</sup>. Logarithm base 10 transformation of all count data was performed to provide a convenient scale of interpretation. For TVC, a value of 1 was added to all counts such that non-detections were assigned a log value of '0'. For all other microorganisms, non-detections were assigned a missing value prior to calculation of the log<sub>10</sub> values.

## 3. RESULTS

Descriptive statistics are provided for all samples in Table 2 and for different product types in Tables 3 – 7.

**Table 2: Microbiological profile of raw ground beef components other than boneless beef trim (n=253)**

Microorganism	Prevalence (%)	Population (log CFU/g)			
		Mean	Median	SD	Maximum
Aerobic bacteria <sup>a</sup>	81.4	2.43	2.60	1.35	6.15
Coliforms <sup>b,c</sup>	57.7	1.78	1.70	0.66	3.92
<i>E. coli</i> <sup>b,c</sup>	9.1	1.43	1.30	0.55	3.34

<sup>a</sup> Limit of detection was 100 CFU/g.

<sup>b</sup> Limit of detection was 10 CFU/g.

<sup>c</sup> Counts are log CFU/g for positive samples only.

There was one detection of *Salmonella* (0.4%) in a primal sample (knuckle), 28 detections (11.1%) of STEC and 3 (1.2%) EHEC detections. All EHEC detections recorded positive STEC detections.

The highest mean log counts of APC were recorded in the head, cheek meat and lip samples (Tables 3-7) as was the prevalence of both coliforms and *E. coli*.

Two of the EHEC detections were from lip samples from the same establishment and received by the laboratory on the same day. The third EHEC detection was recorded from a heart meat sample from another establishment.

Of the 28 STEC detections, 12 (42.9%) were recorded from primal/subprimal samples collected at 5 of the 9 establishments from which these sample types were obtained. Eight (28.6%) were recorded from lip samples across each of the establishments from which these

sample types were obtained. Four (14.3%) STEC detections were recorded from each of the heart meat and head/cheek meat samples, however, while all 3 establishments from which heart meat samples were collected recorded at least one detection, only 37.5% (3) of the establishments from which head/cheek meat samples were taken recorded at least one STEC detection.

**Table 3: Microbiological profile of raw ground beef components – primals/subprimals (n=122)**

Microorganism	Prevalence (%)	Population (log CFU/g)			
		Mean	Median	SD	Maximum
Aerobic bacteria <sup>a</sup>	78.7	2.09	2.48	1.20	4.20
Coliforms <sup>b,c</sup>	41.0	1.68	1.60	0.64	3.64
<i>E. coli</i> <sup>b,c</sup>	2.5	1.30	1.00	0.52	1.90

<sup>a</sup> Limit of detection was 100 CFU/g.

<sup>b</sup> Limit of detection was 10 CFU/g.

<sup>c</sup> Counts are log CFU/g for positive samples only.

**Table 4: Microbiological profile of raw ground beef components –head/cheek meat (n=37)**

Microorganism	Prevalence (%)	Population (log CFU/g)			
		Mean	Median	SD	Maximum
Aerobic bacteria <sup>a</sup>	94.6	3.34	3.60	1.12	6.15
Coliforms <sup>b,c</sup>	78.4	2.29	2.38	0.68	3.92
<i>E. coli</i> <sup>b,c</sup>	27.0	1.50	1.30	0.73	3.34

<sup>a</sup> Limit of detection was 100 CFU/g.

<sup>b</sup> Limit of detection was 10 CFU/g.

<sup>c</sup> Counts are log CFU/g for positive samples only.

**Table 5: Microbiological profile of raw ground beef components – lips (n=36)**

Microorganism	Prevalence (%)	Population (log CFU/g)			
		Mean	Median	SD	Maximum
Aerobic bacteria <sup>a</sup>	100	3.79	3.68	0.47	5.32
Coliforms <sup>b,c</sup>	72.2	1.88	1.81	0.68	3.34
<i>E. coli</i> <sup>b,c</sup>	16.7	1.51	1.65	0.42	2.00

<sup>a</sup> Limit of detection was 100 CFU/g.

<sup>b</sup> Limit of detection was 10 CFU/g.

<sup>c</sup> Counts are log CFU/g for positive samples only.

**Table 6: Microbiological profile of raw ground beef components – heart meat (n=22)**

Microorganism	Prevalence (%)	Population (log CFU/g)			
		Mean	Median	SD	Maximum
Aerobic bacteria <sup>a</sup>	68.2	1.71	2.30	1.25	3.46
Coliforms <sup>b,c</sup>	50.0	1.36	1.48	0.36	1.85
<i>E. coli</i> <sup>b,c</sup>	1.5	1.24	1.24	0.34	2.48

<sup>a</sup> Limit of detection was 100 CFU/g.

<sup>b</sup> Limit of detection was 10 CFU/g.

<sup>c</sup> Counts are log CFU/g for positive samples only.

**Table 7: Microbiological profile of raw ground beef components – other (n=36)**

Microorganism	Prevalence (%)	Population (log CFU/g)			
		Mean	Median	SD	Maximum
Aerobic bacteria <sup>a</sup>	66.7	1.77	2.30	1.34	3.94
Coliforms <sup>b,c</sup>	83.3	1.49	1.39	0.40	2.68
<i>E. coli</i> <sup>b,c</sup>	5.6	1.15	1.15	0.21	1.30

<sup>a</sup> Limit of detection was 100 CFU/g.

<sup>b</sup> Limit of detection was 10 CFU/g.

<sup>c</sup> Counts are log CFU/g for positive samples only.

#### **4. REFERENCES**

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