RESEARCH REPORT
PORK SAFETY

**Title**: Model for the reduction of Salmonella on swine carcasses in slaughter facilities. I. Location of probable sources and sites of contamination
**NPB# 00-102**

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**Abstract**: Carcass swabs, carcass cavity swabs, head meat and trim samples were analyzed for populations of coliforms, *Escherichia coli* Biotype I, and the presence of salmonellae. Approximately 560 samples were analyzed over a 12 month period. Only 5 samples (2 carcass cavity and three head meat) tested positive for the presence of salmonellae. For all 5 samples, the corresponding populations of either coliforms or *Escherichia coli* Biotype I were below a statistically calculated value of "mean + 2 standard deviations", and in 4 of the 5 samples, the populations of both indicator bacteria were actually below the calculated mean for the sample set. There were insufficient salmonellae positive samples to draw any statistical valid conclusions. However, populations of neither coliforms nor *Escherichia coli* Biotype I were predictors of the presence or absence of salmonellae.

Recent studies have identified places in pork slaughter where contamination of swine carcasses can occur (2-4). Most of the *Salmonella* contamination occurs as a result of fecal contamination of the carcasses (3). Proposed sites of fecal contamination appear to be the scalding tank, polishing equipment, evisceration, removal of pluck, carcass splitting, and the trimming area (4). Potential places for the measurement of product contamination include cheek meat, head meat, and tongue (14).

Potential interventions for the reduction of *Salmonella* include:

1. adequate heating of the scald tank to a temperature greater than 62° Celcius (4, 10)
2. bagging and knotting the anus during bung removal (4, 9)
3. improved evisceration practices (4)
4. environmental contamination (6)
5. the slaughter of pigs with low prevalence of *Salmonella* (4).

Continuous process improvement methods have been described for the purpose of affecting quality of manufacturing products (7, 8, 12, 13). The goal of continuous

improvement is to affect improved average product quality and reduced product variation (5). This is accomplished by the objective evaluation of production processes rather than process outcomes (5).

**Literature Cited**


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**Objectives**: To develop a process model which describes the methods and steps for developing a strategy for the reduction of the *Salmonella* contamination of swine carcasses and pork products within one slaughter house.

**Procedures**:

Samples: Samples were obtained from a modern pork slaughter establishment on a regular basis, typically weekly or every other week. Typically, six samples of each type were collected on a given sampling date, and then sent chilled (<5$^{o}$C) to the laboratory, usually arriving the two days after sampling. The samples consisted of swabs and tissue samples. Carcass swabs were taken according to standard USDA-FSIS procedures. Briefly, three, 100 cm$^{2}$ areas (ham, belly, and jowls) were swabbed per carcass with a sterile sponge moistened in 10 mls of buffered peptone water (BPW). The sponge was placed in a sterile bag and an additional 10 mls BPW was added to the bag. A similar swabbing procedure was followed for the carcass cavity swabs, except that the entire pleural and peritoneal cavity were swabbed on each carcass. Head meat and special trim (72% lean from the fabrication operation) typically arrived as 150 – 250 gram tissue samples. Over the course of twelve months, approximately 200 of each of the two types of swab samples, approximately 100 head meat samples and approximately 80 special trim samples (total 560 samples) were analyzed.

Microbiological methods:

Coliforms and *Escherichia coli* Biotype I: Swab samples were serially in BPW as necessary. Tissue samples were homogenized for 2 min in a 1:10 dilution with BPW in a Tekmar Stomacher 400 Mark II, and serially diluted in BPW. The bacterial populations were enumerated using the PetriFilm *E. coli* plates (3-M, Minneapolis, MN), following the manufacturers instructions provided with the kit.

Salmonella: Salmonellae were determined using a presence/absence method. Samples were pre-enriched for 24 hr at 37$^{o}$C in a in buffered peptone water, followed by selective enrichment for 24 hr at 37$^{o}$C in Tetrathionate broth. Presumptive positive salmonellae were determined using the BioControl 1-2 test (BioControl Systems, Inc., Bellevue, WA), following the manufacturers instructions provided with the kit. Presumptive positive samples were streaked from the selective enrichment for isolation on XLD agar (Difco, Detroit MI), and colonies exhibiting typical reactions for salmonellae were further evaluated using triple sugar iron agar and lysine iron agar slants (Difco). Cultures which demonstrated typical reactions in these tests were confirmed a more extensive set of biochemical reactions (BBL Crystal System, Enteric/Non-fermenter, Becton Dickinson Microbiology Systems, Cockeysville MD).

Results: The original objective was to identify points in the process where salmonellae contamination might occur. However, after analyzing approximately 560 samples, only 5 salmonellae samples were identified (two carcass cavity swabs and three head meat samples, Figures 2 and 3). While it was encouraging to find that the incidence of salmonellae positive samples was approximately 1%, it did result in a change of the analysis of the data.

Applying the principles of statistical process control, the arithmetic means and standard deviations of the populations of coliforms and *Escherichia coli* Biotype I were calculated. The sample data were then graphed in comparison to the means and an upper control limit, arbitrarily defined as the mean + 2 standard deviations. For carcass

and cavity swabs (figs. 1 and 2) , there was no correlation of samples where the populations of coliforms and *Escherichia coli* Biotype I exceeded the upper control limit. That is, a sample which exceeded the “mean + 2 standard deviations” limit for one population did not necessarily exceed the limit with the other populations. In the case of the carcass cavity swabs, salmonella was detected in samples which were actually below the mean population for coliforms. This suggests that in the case of swabs, the presence of salmonellae was not accompanied by an increase in either coliform or *Escherichia coli* Biotype I populations.

Similar trends were seen with the tissue samples, although there were some differences with head meat samples (Fig. 3). While all three of the salmonellae positive head meat samples fell below the upper control limit of “mean + 2 standard deviations”, in one case the *Escherichia coli* Biotype I population would have exceeded a limit of “mean + **1** standard deviation”. This may provide a reference for further study, However, it should be noted that in the case of the other two salmonellae positive samples, the populations of the two indicator bacteria were in fact below the mean population for the sample set.

In summary, there were insufficient salmonellae positive samples to draw any statistical valid conclusions. However, since these were actual production samples, it is worth noting that in every case, populations of neither coliforms nor *Escherichia coli* Biotype I were predictors of the presence or absence of salmonellae.

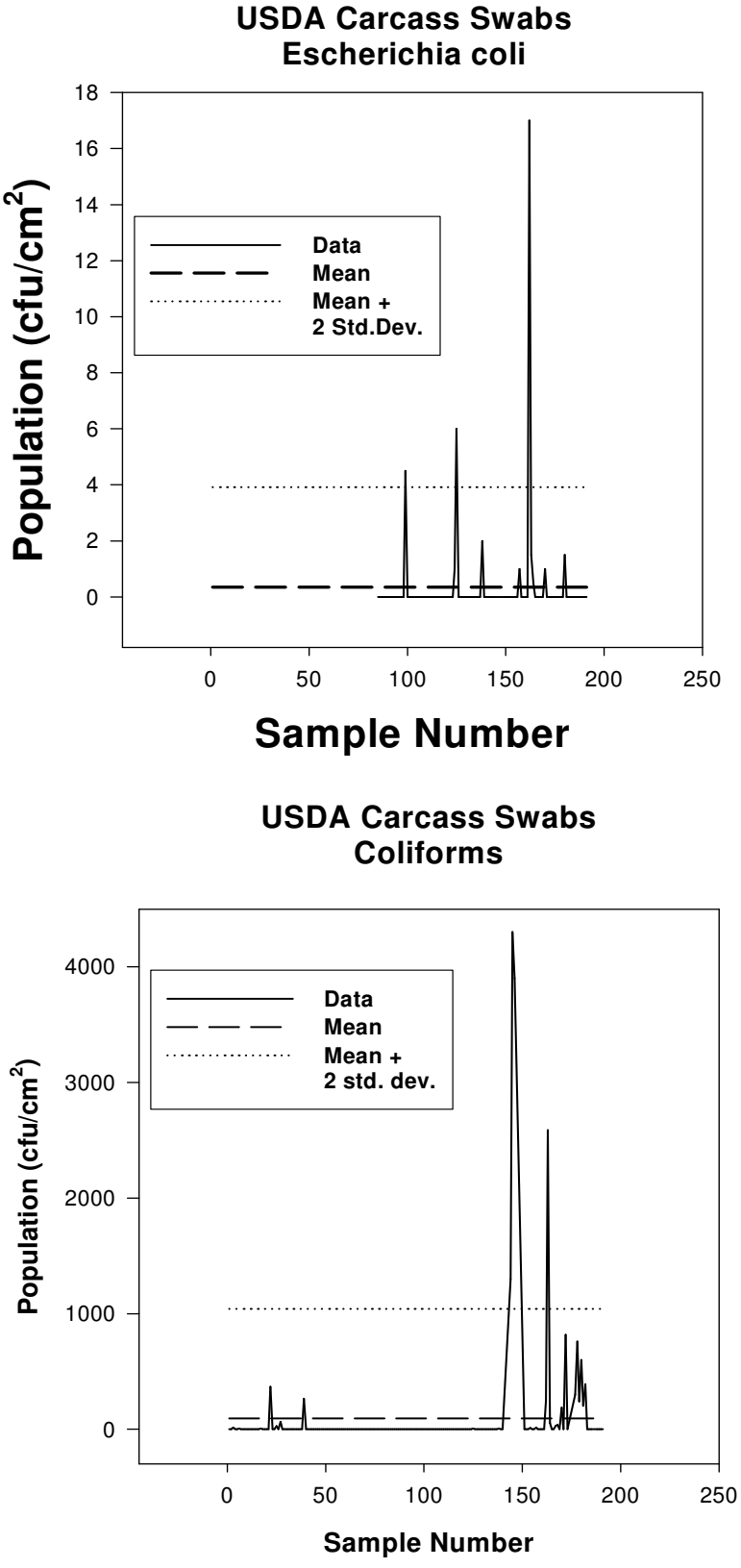


Figure 1. Populations of Coliforms and *Escherichia coli* Biotype I on carcasses.

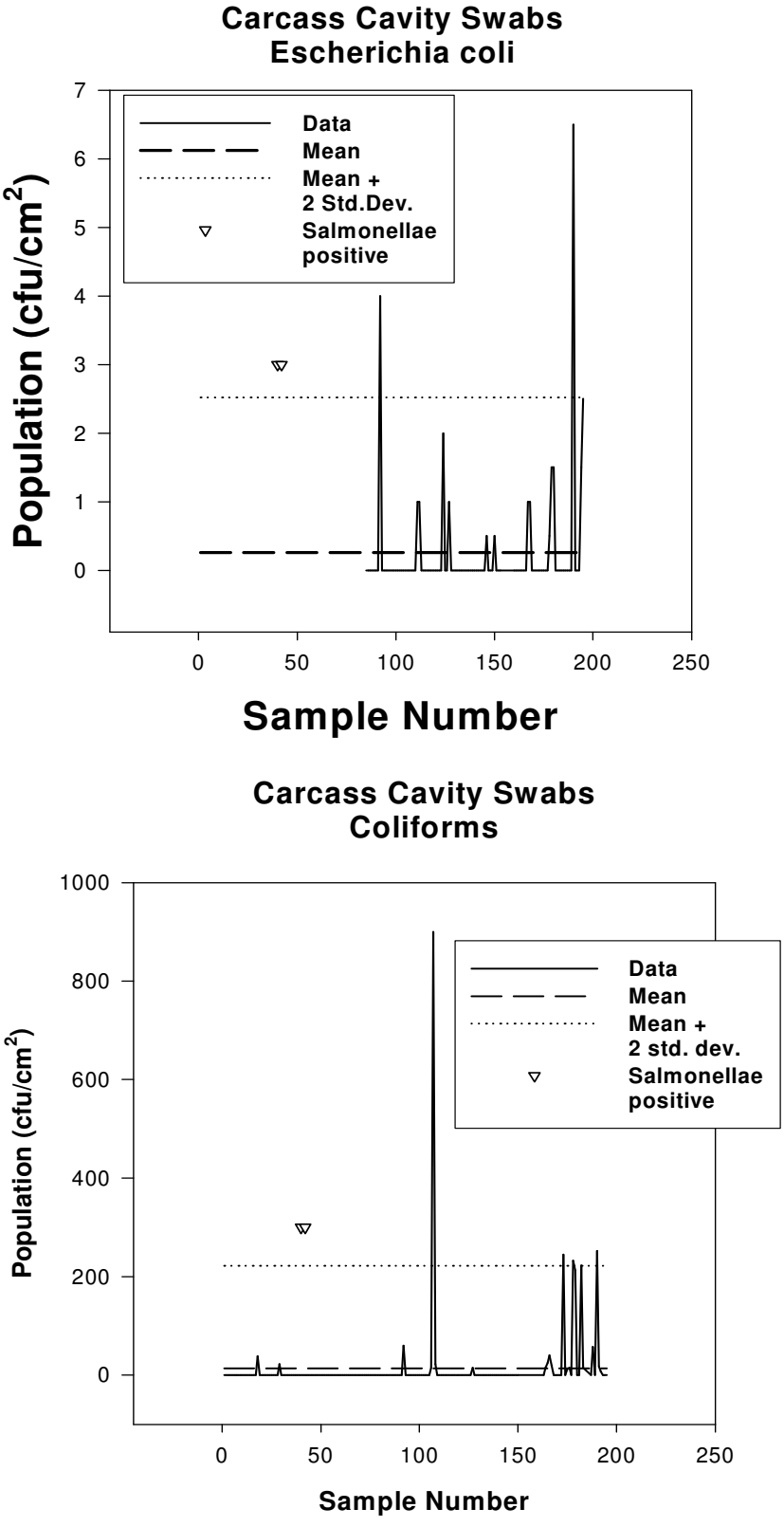


Figure 2. Populations of Coliforms and *Escherichia coli* Biotype I, and presence of salmonellae on carcass cavities.

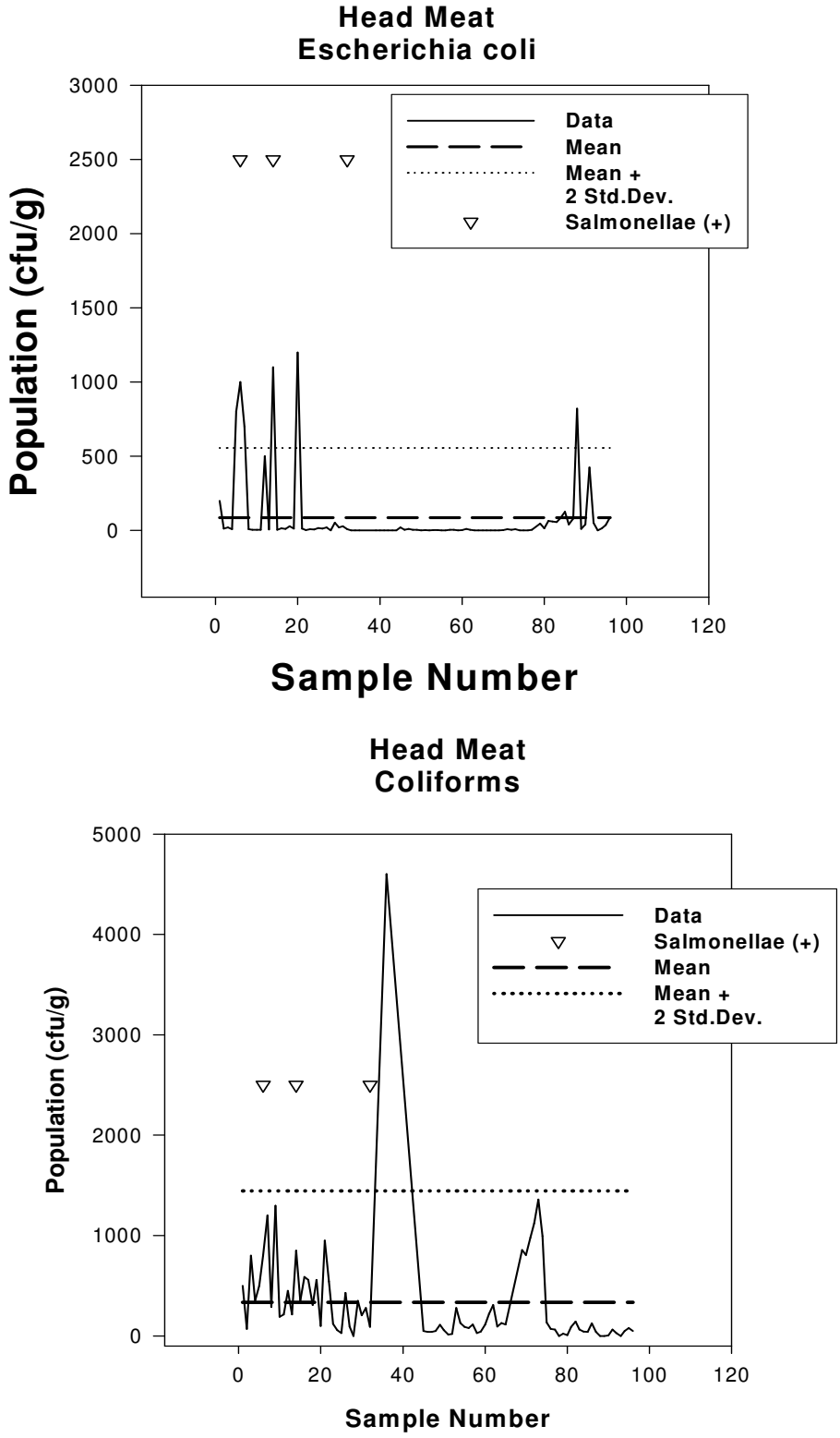


Figure 3. Populations of Coliforms and *Escherichia coli* Biotype I, and presence of salmonellae in head meat.

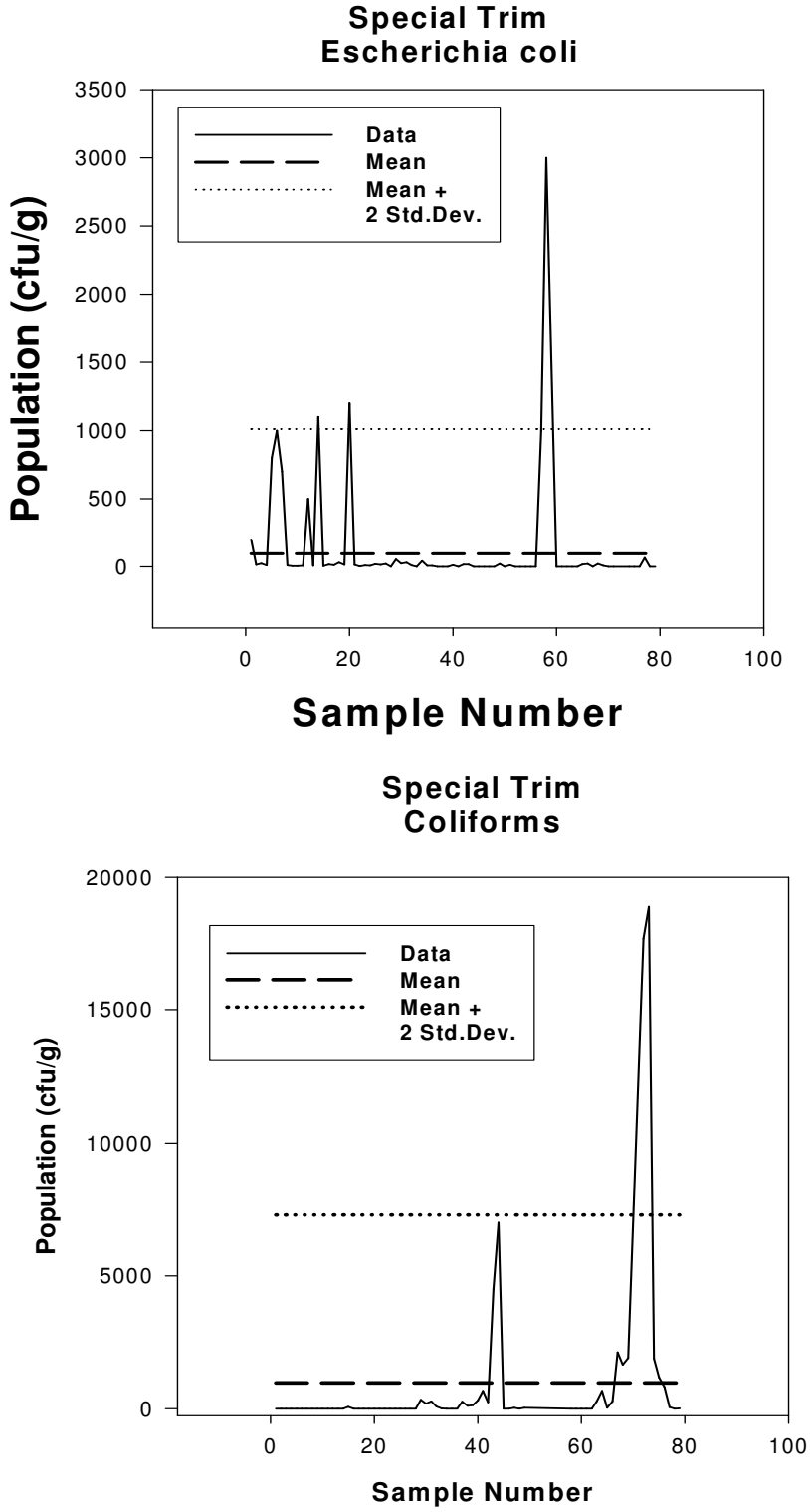


Figure 4. Populations of Coliforms and *Escherichia coli* Biotype I, and presence of salmonellae in special trim.