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Ceca May Not Serve as an Adequate Predictive Sample for *Salmonella enterica* in Ground Turkey

ABSTRACT

Despite improvements in non-typhoidal *Salmonella enterica* prevalence in poultry under USDA-FSIS performance standards, human salmonellosis incidence has remained unchanged. Poultry, particularly ground turkey, has been linked to a significant portion of foodborne *Salmonella* outbreaks in the United States. Previous studies have identified ceca as a "gold standard" for *Salmonella* monitoring, but the predictive accuracy of this sample type in forecasting contamination in ground turkey remains unclear. The following two studies investigate the relationship between *Salmonella* prevalence in ceca and ground turkey by evaluating *Salmonella* test results between the two sample types. Results show differences in *Salmonella* detection and quantification, with higher contamination rates in ground turkey (28.0%) compared to ceca (2.9%). Additionally, the *Salmonella* serovars identified in ground turkey were more diverse than those found in ceca, and in some cases, ceca did not reflect the serovar composition of the final product. Statistical analysis further revealed that *Salmonella* prevalence in ceca was significantly lower than in ground turkey (p = 0.04). These findings suggest that ceca are not reliable predictors of *Salmonella* contamination in ground turkey, challenging their role in processing surveillance and highlighting the need for alternative sampling methods for effective risk assessment and control strategies in turkey processing.

INTRODUCTION

Despite reductions in the prevalence of non-typhoidal *Salmonella enterica* (henceforth referred to as *Salmonella*) in poultry products under the United States Department of Agriculture Food Safety and Inspection Services' (USDA-FSIS) performance standards, human salmonellosis incidence has remained unchanged for over a decade *(4,14)*. Poultry products have been attributed to over 24.9% of the total foodborne *Salmonella* cases in the United States (U.S.), with 5.2% being attributed to turkey *(11)*. In fact, according to a report from the Foodborne Disease Outbreak Surveillance System (FDOSS), between 1998 and 2012, poultry accounted for more foodborne disease outbreaks

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than any other single food category *(6)*. To further refine these estimates, between 2007–2021, 57 *Salmonella* outbreaks were linked to turkey products, particularly ground turkey. This includes the 2011 multistate outbreak of *Salmonella* Heidelberg *(3)*, the 2017–2019 multistate outbreak of *Salmonella* Reading *(10)*, and the 2021 multistate outbreak of *Salmonella* Hadar *(5)*. These public health events demonstrate the risk associated with *Salmonella* contamination in ground turkey and the diversity of the serovars associated with ground turkey outbreaks.

There are over 2,600 *Salmonella* serovars, many of which differ in their ability to cause human illness *(7)*. Due to these differences in pathogenicity and other attributes, it is important to evaluate *Salmonella* serovars alongside *Salmonella* detection and quantification. Considering the public health risk that *Salmonella* poses, there has been significant interest in identifying successful approaches for mitigating *Salmonella* contamination within poultry production. This is exemplified through the previously proposed USDA-FSIS Poultry Framework which was seeking to achieve "measurable reductions in human illnesses linked to *Salmonella* from poultry." Moreover, the poultry industry is actively seeking to determine if "upstream" sample testing can be used as a strategy for predicting the *Salmonella* prevalence, load, and serovars associated with final products. Taken together, both regulatory and industry momentum is driving towards the use of *Salmonella* testing strategies to guide control programs. Therefore, there is a need to identify productive sample types that can inform such programs.

Historically, ceca have been considered a "gold standard" sample for evaluating *Salmonella* status in poultry, as ceca often have presented the highest levels of *Salmonella* retrieval compared to other organs *(1, 16)*. For instance, Rostagno et al. found turkey ceca samples to show the highest prevalence of naturally occurring *Salmonella* compared to crop, cloaca, liver, large intestine, spleen, and gallbladder samples *(17)*. Similarly, a study by Wesley et al. found that on average ceca samples had higher recovery rates of naturally occurring *Salmonella* as compared to the spleen and crop in turkeys *(12)*.

Additionally, studies have shown that *Salmonella* detection may be dependent on the infection route as well as the serovar present. For example, in a challenge study by Kallapura et al., broilers were orally and intratracheally challenged with serovar Typhimurium and Enteritidis *(13)*. Results demonstrated that *Salmonella* recovery from ceca, liver and spleen, and the trachea was lowest when Typhimurium was administered intratracheally *(13)*. This was further demonstrated by Jones-Ibarra et al. in a broiler challenge study that evaluated the route of infection for *Salmonella* utilizing six methods (i.e., oral, endotracheal, and four levels of transdermal scratch). In that study, *Salmonella* recovery in the ceca was dependent on the challenge method, with the highest numbers of *Salmonella* recovered in ceca from birds challenged through oral gavage *(12)*.

Finally, studies have shown that on-farm management practices such as feed withdrawal can also influence *Salmonella* recovery rates from organ samples. To illustrate this, a challenge study by Ramirez et al. found that *Salmonella* detection was higher in both crops and ceca samples following feed withdrawal *(15)*. Interestingly, in a second study that evaluated feed withdrawal in a commercial setting with naturally occurring *Salmonella*, crop samples followed the same trend observed during the challenge study, but ceca did not. During the commercial study, no significant difference was observed in *Salmonella* detection from ceca prior to feed withdrawal when compared to ceca post-feed withdrawal *(15)*. Similar findings were published by Corrier et al., which demonstrated that *Salmonella* recovered from ceca samples were not impacted by feed withdrawal *(8)*.

Collectively, these studies provide conflicting evidence regarding *Salmonella* harborage within ceca, demonstrating the need for further evaluation of the effectiveness of ceca as a predictor of *Salmonella* contamination, particularly for ground turkey. This research aims to evaluate the performance of ceca as an upstream processing predictive sample of *Salmonella* contamination in ground turkey. To achieve this objective, two independent studies evaluated naturally occurring *Salmonella* contamination between ceca and ground turkey samples from a commercial turkey processing establishment. The first study focused on the detection and enumeration of *Salmonella* between ceca and ground turkey. The second focused on characterizing *Salmonella* detection and serovar diversity between ceca and ground turkey samples.

MATERIALS AND METHODS

Study 1. Experimental design

A total of 660 ceca and 132 grind samples were analyzed, representing 66 individual turkey flocks, processed at a single turkey processing establishment. From each flock, 10 ceca sub-samples and two grind sub-samples were collected. Samples were collected during 13 distinct sampling time points from September 2022 to January 2023. A single cecum was collected from 10 individual turkey carcasses during evisceration, from each of the experimental flocks. A total of two 325 g grab samples were collected from two individual bins of ground product produced from each flock where the ceca had been sampled. Ground turkey samples were always collected from the first grind of the day, this ensured that all ground product was processed through a POSS (mechanical separation) system that had passed pre-operational sanitation. All ceca and grind samples were kept on ice, shipped to Kansas State University, and processed within 24 hours.

Sample enrichment

The BAX® System Real-Time PCR Assay (Hygiena, Camarillo, CA) was utilized for *Salmonella* detection

and quantification. Samples were processed according to the manufacturer's instructions. In full, ceca primary enrichments were made by adding one smashed cecum (including the cecal tonsil) to a solution consisting of 100 ml pre-warmed (42°C) BAX MP media (proprietary but is a rich media that consists of buffering agents and simple sugars) and 0.5 ml/liter BAX Quant Solution (novobiocin). Samples were then homogenized in a stomacher at 230 rpm for 60 s. Then, 30 ml of the ceca homogenate was transferred into a sterile bag containing 30 ml of pre-warmed (42°C) BAX MP media and 0.5 ml/liter BAX Quant Solution to make a 1:1 enrichment. The bag was then hand-massaged for approximately 15 s to homogenize the sample. Immediately after, the enrichments were incubated for 10 h at 42 ± 1°C for quantification lysates (see below) and an additional 14 h at 37 ± 1°C for detection lysates (total of 24 h; see below).

A similar process was followed for ground turkey. A 1:1 primary enrichment was made, adding 325 g of ground turkey to 325 ml of Buffered Peptone Water (BPW). The enrichment was homogenized, and a 1:1 ratio of 30 ml grind homogenate and 30 ml pre-warmed (42°C) BAX MP media containing 1 ml/liter BAX Quant solution was made and homogenized. The procedure for grind samples differed in the incubation timing, with lysates being made at 6 h for quantification and then incubated for an additional 18 h for detection lysates.

Lysates preparation

Once samples had been incubated for 10 and 6 h (for ceca and grind, respectively), lysates were created following manufacturer's instructions from each positive sample for quantification purposes. In brief, lysates were made by pipetting 5 µl of homogenate into cluster tubes with 200 µl of lysis reagent containing protease and lysis buffer. Tubes were then heated at 37°C for 20 minutes, followed by 95°C for 10 minutes, and cooled for 5 minutes at 4°C. The process for making lysates for detection follows the same procedure as previously described.

***Salmonella* detection and quantification assay**

Quantitative PCR (qPCR) was performed first in the detection lysates. Detection lysates (30 µl) were transferred into tubes containing PCR tablets; tablets were kept in a cooling block for 10 min, allowing pellets to dissolve. After the detection assay, samples yielding a negative result were recorded as negative and discarded. Samples that produced a positive outcome for detection were recorded as positive, and subsequent qPCR was conducted for quantification. Using the quantification lysates, samples were identified as positive or negative for the BAX System SalQuant® assay (Package 5.0.1). Samples negative for quantification assay were considered positive but below the quantifiable threshold. *Salmonella* levels were estimated for quantification assay positive samples by comparing CT values to a fitted *Salmonella* concentration curve provided by the manufacturer.

Study 2. Sample collection, *Salmonella* prevalence testing, and serotyping

Ceca were collected at a single processing establishment (same as from Study 1) from 22 different turkey flocks (labeled A–V). Samples were collected from the first processed flock of each collection day to ensure no cross-contamination from other flocks. At each plant visit, ceca were collected at evisceration for each flock as six composite sub-samples containing 10 whole individual cecum, for a total of 60 ceca representing each flock. For ground turkey, raw materials from each flock were tracked and a single composite sample was collected from each of six bins of ground turkey (6 composite sub-samples per flock). In the laboratory, 30 ml of BPW was added to each ceca composite sample and 1625 ml of BPW was added to each ground turkey composite. Samples were then stomached at 230 rpm for 2 min to homogenize. Following this, 30 ml of each sample was added to 30 ml of BPW for pre-enrichment, and incubated for 20-24 hours at 37°C. The BAX® System Real-Time PCR Assay (Hygiena, Camarillo, CA) was used to screen each sample for *Salmonella* presence following the manufacturer's instructions. For qPCR-positive samples, 1 ml of the BPW culture was transferred to tetrathionate broth and incubated at 42°C for 20–24 hours. Samples were then streaked onto XLT-4 plates and incubated for 24 hours at 37°C. Typical and atypical colonies were then isolated from the XLT-4 plates and serotyped by serum agglutination (Avantor Sciences, Radnor, PA). Vaccine strains were identified following the same methodology, however, serotype results for the vaccine strain are reported as O group B: Untypeable. Briefly, phenotypic and biochemical properties were used to identify and confirm the vaccine strains. Colonies are examined on XLT-4 agar, confirming that the vaccine strain is H2S negative. The probable vaccine colony is then struck on MacConkey agar with maltose as it is negative for maltose fermentation compared to the wild type. Finally, the biochemical ID was confirmed using an API 20E strip and screening the colony for agglutination with *Salmonella* O Group B antiserum. Vaccine strain data is included in the serotype data for Study 2.

Statistical analysis

For Study 1, a generalized linear mixed model was fitted to a binary response indicative of *Salmonella* detection for each of the sample types. The logit link was used to connect the Bernoulli probability of detection with a linear predictor that included fixed effects of sample type (ceca vs ground turkey) on a flock and sub-sample level. All statistical models were fitted using the GLIMMIX procedure of SAS (version 9.4, SAS Institute, Cary, NC). Estimated least square means and corresponding 95% confidence intervals (CI) are

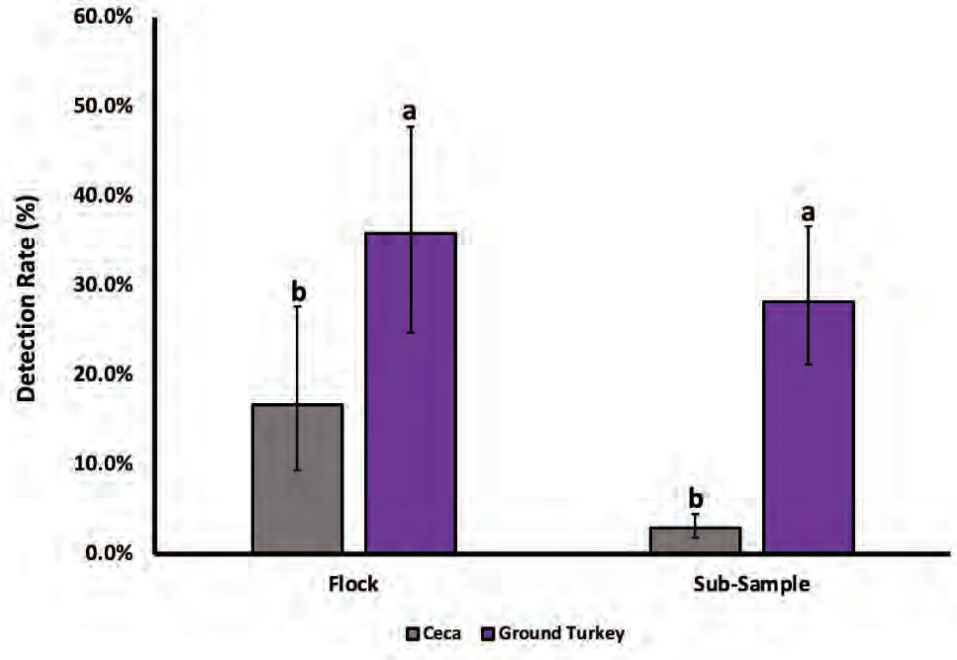

Figure 1. Estimated *Salmonella* detection rates (%) in ceca and ground turkey at the flock (n = 66) and sub-sample levels (ceca n = 660; ground turkey n = 131) from Study 1. Whiskers represent 95% confidence intervals. Different superscripts indicate statistically significant differences between groups (α = 0.05).

Flock ID	Ceca (10 sub-samples)		Ground turkey (2 sub-samples)	
	Detection	Quant	Detection	Quant
3	2	1	2	2
6			1	1
10	1	0		
11			1	0
12	1	0		
13			1	1
15			2	2
17	1	1		
20			2	0
22			2	0
24			2	0
25	1	0		
26	2	1		
28			2	2
29	5	1	2	2
31			2	2
32			1	1
33	1			
35			2	1
38			2	2
43			1	1
44	2	1	2	2
47	2	0		
49			1	1
52			1	1
55			2	1
59			2	1
61			1	1
63			2	0
65	1	0		
66			1	0

Salmonella Quantification (CFU/g or ml)
>100
10-100
1-9.9
<1
non-quantifiable

Figure 2. *Salmonella* quantification in positive ceca and ground turkey samples in Study 1. For each flock, 10 ceca samples and 2 ground turkey samples were collected. Values indicate the number of subsamples that tested positive (detection column) and the number of those that were quantifiable (Quant column) for each sample type. Colors represent estimated *Salmonella* levels as indicated, expressed in CFU/g or CFU/mL.

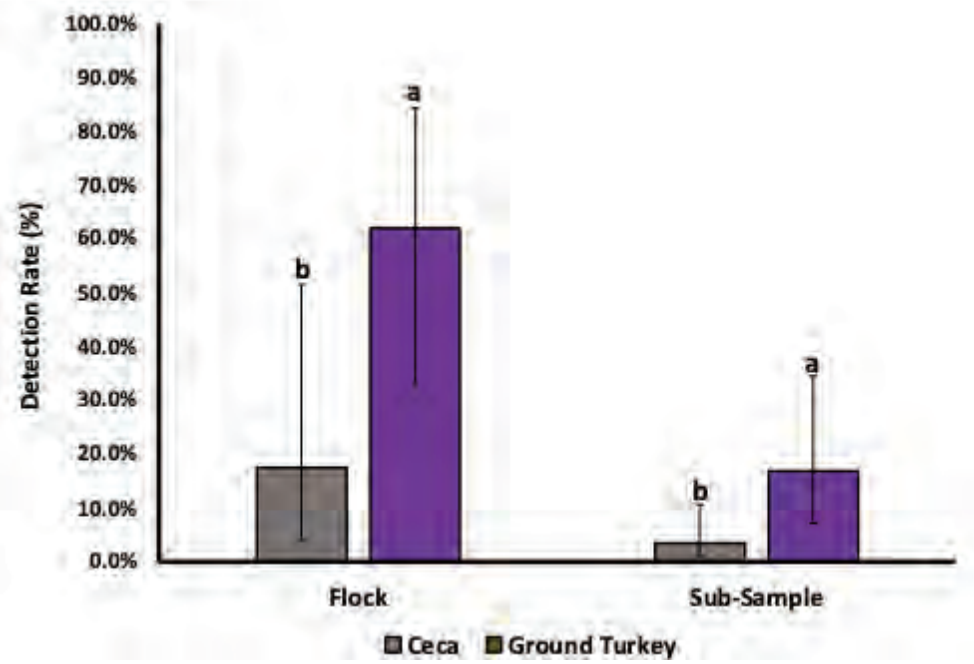

Figure 3. *Salmonella* detection (%) in ceca and ground turkey at the flock (n = 22) and sub-sample levels (ceca n = 132; ground turkey n = 132) from Study 2. Whiskers represent 95% confidence intervals. Different superscripts indicate statistically significant differences between groups (α = 0.05).

presented. Overdispersion was evaluated using the maximum likelihood fit statistic of Pearson chi-square/df. No evidence for overdispersion was apparent in the final model used for inference, which was fitted using a maximum likelihood estimation technique.

For Study 2, a two-sample *t*-test was used to compare *Salmonella* prevalence across ceca and ground turkey sample types using the JMP Pro 17 software.

RESULTS

Study 1 Results. At the flock level, a higher percentage of *Salmonella*-positive flocks were detected in ground turkey samples compared to ceca samples ($p = 0.0179$; *Fig. 1*). Specifically, 11 out of 66 flocks (16.7%, 95% C.I. (9.4%, 27.7%)) tested positive for *Salmonella* in ceca samples, whereas 23 out of 66 flocks (35.8% (24.7%, 47.8%)) tested positive in ground turkey samples. Notably, only three flocks (Flocks 3, 29, and 44) tested positive in both sample types *(Fig. 2)*. There was no correlation between number of positive ceca subsamples nor their *Salmonella* load and the *Salmonella* incidence or load in ground turkey. Higher *Salmonella* detection rates were also observed at the sub-sample level ($p \leq 0.01$; *Fig. 3*), with 19 out of the total 660 sub-samples (2.9% (1.8%, 4.5%)) testing positive. Of the 19 positive samples, only 6 (31.6%) were quantifiable. In contrast, 37 out of 131 ground turkey sub-samples (28.2% (21.2%, 36.6%)) tested positive, of which 25 (67.6%) were quantifiable.

Among the 19 positive ceca sub-samples, 11 flocks were represented, with only five flocks (Flocks 3, 17, 26, 29, and 46) having quantifiable *Salmonella* levels, thus statistical analysis was not possible. However, quantification data for these samples ranged from 0.45 to 1.87 log CFU/ml. In the case of the 37 positive ground turkey sub-samples, 23 flocks were represented, and 18 flocks had quantifiable levels of *Salmonella*. The concentration range in ground turkey samples was broader, with the lowest average *Salmonella* concentration being -0.30 log CFU/g and the highest being 2.54 log CFU/g.

Study 2 Results. For flock-level detection results, *Salmonella* was found in the ceca in five out of 22 flocks (22.7%; *Fig. 4*). In contrast, 13 out of 22 flocks (59.1%) tested positive for *Salmonella* in ground turkey samples. Of the five flocks with *Salmonella*-positive ceca samples, only four also tested positive in ground turkey. Notably, *Salmonella* was detected in ground turkey samples from an additional nine flocks where ceca samples were negative for *Salmonella*. As observed in Experiment 1, *Salmonella* prevalence in turkey ceca was significantly lower compared to ground turkey ($p = 0.04$). On a subsample basis, 12 out of 132 ceca samples (9.1%) tested positive for *Salmonella*, while 34 out of 132 ground turkey samples (25.8%) were positive.

Unlike Study 1, Study 2 included serovar analysis, identifying three serovars from *Salmonella*-positive ceca samples: Hadar (two flocks, D and O), Cubana (one flock, I), and Uganda (two flocks, J and L; *Fig. 4*). These same serovars

TABLE 1. Serovars identified in Study 2

Flock identifier	Ceca serovar	Ground turkey serovar(s)[a]
D	Hadar	Hadar
I	Cubana	ST-vax, Cubana
J	Uganda	Uganda
L	Uganda	Uganda
O	Hadar	
C		ST-vax
H		ST-vax
M		Typhimurium
N		Senftenberg
P		ST-vax
Q		ST-vax
R		Hadar, Teddington
S		Reading
T		ST-vax

[a]ST-vax indicates live-attenuated serovar Typhimurium

were also found in ground turkey from the corresponding flocks, except for Flock O where the ground turkey samples were negative for *Salmonella*. Additional serovars were detected in the ground turkey samples, including Typhimurium (seven flocks, C, H, I, M, P, Q, T), Senftenberg (one flock, N), Teddington (one flock, R), Reading (one flock, S). Of the seven serovar Typhimurium positive samples, six were the vaccine strain. In two flocks, flocks I and R, two serovars were isolated. For the four flocks that were positive for *Salmonella* in both ceca and ground turkey samples, the serotyping results were consistent between the two sample types, including the three ceca samples with multiple subsamples that tested positive. However, in Flock O, serovar Hadar was detected in ceca samples, but all ground turkey samples were negative.

Serovar Typhimurium was the most frequently isolated serovar in ground turkey, found seven of 13 (54.0%) of positive samples. Six of the seven (86.0%) serovar Typhimurium isolates were typed as the vaccine strain. This vaccine, commonly used in turkey production to reduce *Salmonella* colonization, was notably absent from *Salmonella*-positive ceca samples, which may be due to the lower prevalence of *Salmonella* in this sample type.

DISCUSSION

The results of Study 1 and Study 2 provide valuable insights into the efficacy of ceca sampling for predicting *Salmonella* contamination in ground turkey. Across both studies, ceca samples consistently demonstrated lower detection rates than ground turkey at both the flock and subsample levels. Specifically, ceca samples exhibited significantly lower detection rates, fewer positive results overall, and a narrower range of serotypes compared to ground turkey samples. These findings underscore the reduced sensitivity of ceca sampling as a tool for *Salmonella* detection during turkey processing. The discrepancy between these two sample types calls into question the appropriateness of ceca sampling for broader *Salmonella* surveillance in ground turkey processing.

In Study 1, *Salmonella* prevalence in ceca samples was substantially lower than in ground turkey samples. Specifically, 16.6% of flocks tested positive for *Salmonella* in ceca, compared to 34.8% in ground turkey. Furthermore, only 2.9% of ceca sub-samples were positive, with merely 31.6% of these positive ceca samples being quantifiable. In contrast, ground turkey samples exhibited a higher *Salmonella* prevalence, with 28.0% of subsamples testing positive and 67.6% of those being quantifiable. This contrast between the detection rates in ceca and ground turkey samples suggests that ceca may not reliably reflect *Salmonella* contamination in the final product.

Quantification data further emphasizes this point. While *Salmonella* quantification in ceca samples was generally low, with only a few flocks showing quantifiable levels, ground turkey samples exhibited a broader range of *Salmonella* concentrations. Notably, the highest concentration in

ground turkey was substantially higher than in ceca samples, potentially reflecting differences in environmental conditions or microbial dynamics between these two sample types. The observed disparity in *Salmonella* level between ceca and ground turkey samples may suggest multiple contributing factors, including the possibility that ceca samples fail to capture the full extent of contamination present in ground turkey or that ground turkey samples represent multiple birds while ceca samples typically reflect only one bird. This raises important questions about the appropriate experimental unit for such studies—whether it should be the individual bird, the subsample, or the entire flock.

Study 2 corroborated these findings, with *Salmonella* prevalence in ceca samples collected at evisceration (22.7%) being significantly lower than that observed in ground turkey (59.1%). Additionally, 25.8% of ground turkey sub-samples tested positive for *Salmonella*, compared to only 9.1% of ceca sub-samples. These results were statistically significant (p = 0.04), further supporting the notion that ceca samples are less sensitive for *Salmonella* detection than ground turkey samples. Furthermore, Study 2 highlighted the detection of *Salmonella* in ground turkey from nine flocks that were negative for *Salmonella* in ceca samples, further illustrating the lack of concordance between the two sample types.

Serovar analysis conducted in Study 2 also provides critical context for these findings. The same serovars identified in ceca samples were found in ground turkey samples from the same flocks, with the exception of Flock O. This suggests that, in general, when ceca samples are positive, there is good concordance with serovars found in ground turkey. However, several other serovars, including Typhimurium and Senftenberg, were identified exclusively in ground turkey samples, which emphasizes the discrepancy between ceca and ground turkey sampling for *Salmonella*. The discordance in the serovar Typhimurium vaccine strain presence in paired ceca and ground turkey samples raises important concerns regarding pre-harvest vaccine studies as ceca testing is often used, alongside other organs, to determine vaccine efficacy. This further calls into question the dependence on ceca as a gold standard even for pre-harvest surveillance and mitigation strategies.

These results align with previous research that suggests ceca samples are not reliable predictors of *Salmonella* contamination in turkey carcasses or ground turkey products. For instance, Wesley et al. reported a wide variation in *Salmonella* prevalence in ceca samples, with an average prevalence of 29.7%, while 71.4% of carcasses sampled pre-chill tested positive for *Salmonella (21)*. Similarly, Kallapura et al. found that *Salmonella* prevalence was significantly higher in trachea samples compared to ceca samples, further questioning the utility of ceca as a reliable indicator of contamination in final products *(13)*.

The observed discrepancies between ceca and ground turkey samples suggest the possibility of two distinct *Salmonella* populations within the turkey production system *(19, 20)*. This finding is supported by data collected from retail turkey meat and ceca by the National Antimicrobial Resistance Monitoring System (NARMS). From 2021, NARMS reported *Salmonella* recovery from 12.2% of retail ground turkey products tested but only 9.5% of ceca samples *(19, 20)*. Further, NARMS found a greater diversity of serovars in ground turkey product (26 serovars) than in turkey ceca (14 serovars) collected in the same year *(19, 20)*. While NARMS multidrug resistance data for *Salmonella* indicated a slightly higher level of antimicrobial resistance in ceca than in ground turkey, this difference was not significant and there was additionally no difference in multidrug resistance between ceca (28.9%) and ground turkey (25.6%) *(19, 20)*. Ceca-associated *Salmonella* populations appear to be associated with the gut microbiota and are indicative of intestinal and fecal contamination. In contrast, *Salmonella* detected in ground turkey could arise from multiple sources, including cross-contamination between turkey carcasses during processing, combination of the various product components, and internalization of *Salmonella* within the bird's bones, tissues, etc. *(9, 16, 18)*. The significantly higher prevalence and diversity of serovars in ground turkey samples further support this hypothesis.

The presence of certain serovars exclusively in ground turkey samples, particularly vaccine strains, raises additional questions about how processing environments and handling practices influence *Salmonella* populations. If vaccine strains are absent from ceca but present in ground turkey, this may further suggest the likelihood of *Salmonella* internalization within birds. In a paired study with Experiment 2, the vaccine strain was found only in mechanically separated turkey and ground turkey, with the exception of a single farm sample. Importantly, it was not detected in any plant samples (pre-scald, pre-chill; *(2)*). Such findings underscore the need for a more comprehensive surveillance strategy that accounts for both external and internal sources of *Salmonella* contamination. By considering the potential existence of two distinct *Salmonella* populations, future research can focus on identifying critical points in the production process where contamination risk is highest. This approach could help refine sampling methodologies and intervention strategies, ultimately improving *Salmonella* control measures and enhancing food safety in ground turkey production.

The findings from both studies highlight the limited effectiveness of ceca sampling for predicting *Salmonella* contamination in ground turkey. Given the low prevalence and quantifiable *Salmonella* load in ceca samples, combined with the higher prevalence, broader range of quantifiable *Salmonella*, and increased serovar diversity in ground turkey samples, it is evident that post-harvest ceca sampling is an inadequate tool for assessing *Salmonella* risk in ground turkey. These findings carry significant implications for poultry producers and regulatory bodies, as reliance on

ceca sampling for *Salmonella* surveillance may result in underestimations of contamination risks in ground turkey products.

Future studies should explore alternative sample types that may provide more accurate and consistent data on *Salmonella* prevalence and quantification. Additionally, studies should focus on developing improved *Salmonella* monitoring strategies that incorporate both pre-harvest and post-harvest sampling to more comprehensively capture contamination risks throughout the entire production process. By enhancing the accuracy of *Salmonella* upstream detection, producers can implement more targeted interventions to reduce contamination risks in ground turkey and other poultry products, ultimately improving food safety outcomes for consumers.

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