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Comparison of selective enrichment and plating media for *Salmonella* isolation from broiler carcasses

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Abstract

Salmonella detection and isolation rely on different selective enrichment media, which can influence which serovars are detected. The objective of this study was to compare *Salmonella* recovery from broiler carcass rinses using three different selective enrichment protocols and three differential plating agars. Eight prechill broiler carcasses were collected at a commercial slaughter facility. Each carcass was subjected to whole carcass rinse procedure in buffered peptone water (BPW). An aliquot of the rinse and whole carcasses in the remaining rinse were incubated as a pre-enrichment before subculturing in selective enrichment broths (Rappaport Vassiliadis [RV], Tetrathionate Hajna [TT], and TT to RV in series [TT-to-RV]). Enriched samples were streaked on the three differential agars (Hektoen Enteric [HE], Brilliant Green Sulfa [BGS], and Xylose-Lysine-Tergitol-4 [XLT-4]). *Salmonella* was isolated from all eight carcasses. Considering all sample preparations as independent subsamples, *Salmonella* was detected in 88% (128/144) of subsamples with a 100% recovery from the TT-to-RV enrichment, and 92 and 71% from RV and TT broths, individually. A high concordance in recovery on BGS versus XLT-4 agar plates was observed compared to HE versus BGS and HE versus XLT-4 plates. These data suggest that choice of pre-enrichment method, selective enrichment medium, and differential agar can influence the recovery of *Salmonella* from poultry samples.

1 | INTRODUCTION

Salmonella is a leading foodborne bacterial pathogen in the United States, causing approximately 1.35 million illnesses each year with an estimated incidence of 17.1 cases/100,000 persons (CDC, 2021a; Tack et al., 2020). The gold standard for *Salmonella* recovery from contaminated foods currently relies on federally approved culture-based detection methods, which includes pre-enrichment to recover injured *Salmonella*, selective enrichment to inhibit other competing bacteria and allow *Salmonella* growth, and selective plating on agar media that helps with differentiating *Salmonella* from other bacteria (FDA, 2014; USDA, 2019). In addition to this method, *Salmonella* can also be detected using commercially available rapid screening methods such as PCR-based assays, although colony isolation still requires selective enrichment and subsequent plating.

Culture-based assessment of *Salmonella* on poultry carcasses by the United States Department of Agriculture-Food Safety and Inspection Service (USDA-FSIS) during poultry processing begins with rinsing broiler carcasses in buffered peptone water (BPW) or neutralizing BPW (nBPW) for 1 min and removing a 30-mL aliquot of the rinsate. This rinse aliquot is diluted twofold in BPW and pre-enriched for 24 hr. Neutralizing BPW was designed to eliminate the effect of antimicrobials used during processing so that they can no longer inhibit *Salmonella* during transport and pre-enrichment (USDA, 2019). Pre-enrichment is followed by 24 hr selective enrichment in Tetrathionate

Hajna (TT) and Rappaport Vassiliadis (RV) broths in parallel. These two media select for *Salmonella* by inhibiting the growth of other bacteria. For instance, TT broth contains tetrathionate, which is used as a terminal electron acceptor by *Salmonella*, and brilliant green, which inhibits the growth of gram-positive bacteria (Bernstein et al., 1999; D'Aoust, 1981; Daquigan, Grim, White, Hanes, & Jarvis, 2016; Winter et al., 2010). RV broth also selects for *Salmonella* by using low pH, high concentration of magnesium chloride to increase osmotic pressure, and malachite green to inhibit coliforms, *Proteus* spp., *Escherichia coli*, and other competing bacteria (Daquigan et al., 2016; Rappaport, Konforti, & Navon, 1956; Vassiliadis, 1983; Vassiliadis, Kalapothaki, Trichopoulos, Mavrommatti, & Serie, 1981). While these selective enrichments are usually performed in parallel, some protocols require that the broths are used in series where samples are selectively enriched in TT broth, and then subcultured into RV broth for a second enrichment (Rybolt, Wills, & Bailey, 2005; Volkova, Bailey, & Wills, 2009).

For differential plating, xylose-lysine-tergitol-4 (XLT-4) is a common differential agar used for *Salmonella* isolation; presumptive *Salmonella* form distinctive black colonies on this agar due to H_2S production. The addition of Tergitol-4 improves recovery of *Salmonella* while inhibiting other competing bacteria (Miller, Tate, Mallinson, & Scherrer, 1991, 1992). However, XLT-4 is limited because sometimes atypical *Salmonella* (H_2S negative) are present and cannot be easily detected; therefore, a second differential agar is often used (FDA, 2014; Lin, Yan, Lin, & Chen, 2014; Mourão et al., 2020). Brilliant green sulfa (BGS) agar differentiates *Salmonella* from other bacteria by colonies that are pinkish red or opaque in appearance and surrounded by red halo in the medium while inhibiting *E. coli* and *Proteus* spp. (USDA, 2019). Hektoen Enteric (HE) agar inhibits gram-positive bacteria and differentiates *Salmonella* using bile salts, bromothymol blue, and acid fuchsin dyes to produce blue to blue-green colonies with a black center (Chang et al., 1999; Goo, Ching, & Gooch, 1973; King et al., 2005; Kristensen, Lester, & Jürgens, 1925).

Studies have demonstrated that the type of sample preparation and media choice can influence the quantity and identity of *Salmonella* that are recovered. For instance, it has been shown that the 1-min carcass rinse is not sufficient to release all *Salmonella* on the carcass into the pre-enrichment solution, whereas an overnight whole carcass pre-enrichment typically identifies additional *Salmonella* (Cox et al., 2019; Cox & Blankenship, 1975; Lillard, 1988; Simmons, Fletcher, Berrang, & Cason, 2003). Previous studies have also suggested that different *Salmonella* serovars can grow better in different enrichment media; thus, the choice of selective enrichment can influence which *Salmonella* are detected (Cox et al., 2019, 2020; Gorski, 2012; Singer, Mayer, Hanson, & Isaacson, 2009; Temelli, Eyigor, & Carli, 2010). The purpose of this study was to compare *Salmonella* recovery from pre-enriching an aliquot of carcass rinsate or the whole carcass itself. Three different selective enrichment protocols (RV, TT, and TT-to-RV) and three differential plating agars (HE, BGS, and XLT-4) were tested.

2 | MATERIALS AND METHODS

2.1 | Sample collection and *Salmonella* isolation

Eight poultry carcasses, representative of two flocks (four from each flock, collected on different days), were collected from the evisceration line of a commercial poultry processing plant prior to chilling. *Salmonella* was isolated from the carcasses following the modified USDA-MLG protocol (USDA, 2019). The carcasses were rinsed in 400 mL of BPW (VWR, Radnor, PA) for 1 min before a 30-mL aliquot referred to as rinse aliquot (RA) pre-enrichment was removed and diluted twofold in a fresh BPW and then incubated at 37°C for 20–24 hr. An alternative pre-enrichment in BPW was also obtained by incubating the whole carcass in the remaining 370 mL BPW referred to as whole carcass pre-enrichment (WCE) at 37°C for 20–24 hr. After incubation, both pre-enrichment broths were added to 10 mL each of TT and RV broths (VWR) by transferring 0.5 and 0.1 mL, respectively, and incubated at 42°C for 24 hr. A third enrichment step was also included by transferring 0.1 mL of the TT enriched cultures after incubation into 10 mL RV broth and incubated at 42°C for 24 hr. A 10-μL loopful of the overnight enriched samples (TT, RV, and TT-to-RV) were plated onto selective agars HE, BGS, and XLT-4 (VWR) and incubated at 37°C for 24 hr. After incubation, up to two presumptive *Salmonella* colonies were picked from each plate and serotyped using either *Salmonella* multiplex assay for rapid typing (Leader, Frye, Hu, Fedorka-Cray, & Boyle, 2009) or sent to National Veterinary Services Laboratories in Ames, IA for serotyping. A diagram of the sampling scheme is shown in Figure 1.

2.2 | Statistical analyses

Salmonella recovery from the pre-enrichment and selective enrichment media was compared using the Mann–Whitney test and the level of significance was .05. The 2-tailed *p*-value was reported.

3 | RESULTS

Eight carcasses were each pre-enriched using two different preparations RA and WCE. The pre-enriched samples were enriched under three different selective enrichment conditions (TT, RV, and TT-to-RV) before plating onto three differential agars (HE, BGS, and XLT-4). Considering all combinations as independent subsamples, a total of 144 subsamples were processed. *Salmonella* was identified in 88% (128/144) of subsamples, with more *Salmonella* positive subsamples following RV broth (96%; 46/48) enrichment than TT broth (71%; 34/48) enrichment. *Salmonella* was recovered from all TT-to-RV broth enrichment subsamples (100%; 48/48) (Table 1).

Five *Salmonella* serovars were identified in this study with *Salmonella* serovars Typhimurium and Schwarzengrund being the most prevalent (recovered from each of seven carcasses), followed

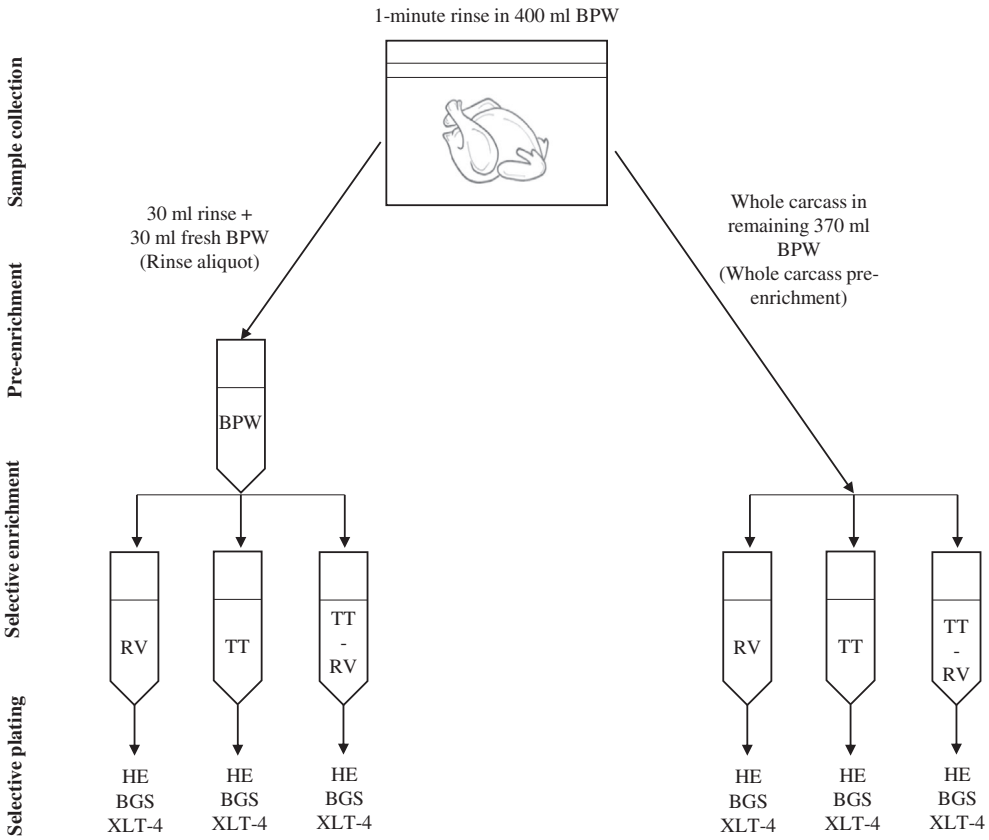

FIGURE 1 Schematic of sample collection and culture conditions. Figure shows workflow of *Salmonella* isolation by conventional and experimental culture conditions. BGS, brilliant green sulfa agar; BPW, buffered peptone water; HE, Hektoen Enteric agar; RV, Rappaport Vassiliadis broth; TT, tetrathionate broth; XLT-4, xylose-lysine-tergitol-4 agar

TABLE 1 Serovars of *Salmonella* recovered from chicken carcasses sampled by rinse or whole carcass pre-enrichment according to selective enrichment and plating media

		RV			TT			TT-RV dual		
Carcass	Sample	HE	BGS	XLT4	HE	BGS	XLT4	HE	BGS	XLT4
1	RA	Kent	Kent	Kent, Typm	–	Kent	Kent	Kent	Kent	Kent
	WCE	–	Schw, Typm	Kent	–	Kent, Schw	Kent	Kent, Typm	Kent, Typm	Kent, Typm
2	RA	Kent, Typm	Kent, Typm	Kent	–	Kent, Typm	Typm	Kent	Kent, Typm	Kent, Typm
	WCE	Kent	Kent	Kent	–	Kent, Typm	Kent	Kent, Typm	Kent, Typm	Kent
3	RA	Kent	Kent	Kent	–	Kent	Kent	Kent	Kent	Kent
	WCE	Schw	Schw	Schw	–	Kent, Schw	Kent, Typm	Schw, Typm	Schw, Typm	Typm
4	RA	Hada	Hada	Hada	Hada	Hada	Hada	Hada	Hada	Hada
	WCE	Kent	Kent, Schw	Hada, Kent	Hada	Hada	Hada	Hada	Hada, Kent	Hada, Kent
5	RA	Schw	Schw	Schw	–	Entr	Entr	Typm	Typm	Typm
	WCE	–	Schw	Schw	–	Kent	Kent	Kent	Kent	Kent
6	RA	Schw	Schw	Typm	–	Schw	Entr, Schw	Kent, Typm	Entr, Typm	Entr, Typm
	WCE	Schw	Schw	Typm	–	Schw	Typm	Kent, Typm	Entr, Typm	Entr, Typm
7	RA	Entr	Entr	Entr	–	Entr	Entr	Entr	Entr	Entr
	WCE	Schw	Schw	Schw	–	Entr	Entr, Schw	Typm	Typm	Typm
8	RA	Typm	Typm	Typm	–	Entr	Entr, Typm	Typm	Typm	Typm
	WCE	Schw	Schw	Schw	–	Entr, Typm	Schw	Typm	Entr, Schw	Schw
Total		14/16	16/16	16/16	2/16	16/16	16/16	16/16	16/16	16/16

Abbreviations: Entr, Enteritidis; Hada, Hadar; Kent, Kentucky; RA, rinse aliquot; Schw, Schwarzengrund; Typm, Typhimurium; WCE, whole caracss pre-enrichment.

	Rinse aliquot				Whole carcass			
Salmonella serovars	RV	TT	TT-RV dual	Total	RV	TT	TT-RV dual	Total
Enteritidis	1	4	2	7	0	2	2	4
Hadar	1	1	1	3	1	1	1	3
Kentucky	3	3	4	10	3	4	5	12
Schwarzengrund	2	1	0	3	7	5	2	14
Typhimurium	4	2	4	10	2	4	6	12

TABLE 2 Number of *Salmonella* serovars recovered from eight carcasses according to sample method and enrichment media

Note: *p*-value (RA): RV versus TT = .92; RV versus TT-RV = .92; TT versus TT-RV = .92. *p*-value (WCE): RV versus TT = .53; RV versus TT-RV = .76; TT versus TT-RV = 1.

by serovars Kentucky and Enteritidis recovered from six and four carcasses, respectively, while serovar Hadar was the least prevalent (found on one carcass) (Table 1). Multiple serovars were recovered from all carcasses: four serovars were recovered from Carcasses 5 and 6, three serovars were detected from each of four carcasses, and two serovars were recovered from each of two carcasses. Overall, serovars Kentucky, Schwarzengrund, and Typhimurium were detected more in WCE subsamples (total $n = 12$, 14, and 12, respectively) than RA subsamples ($n = 10$, 3, and 10), while there were more serovar Enteritidis detected in RA subsamples ($n = 7$) than WCE subsamples ($n = 4$). However, there were no differences in the detection of serovar Hadar from both pre-enrichment conditions (Table 2). We sought to evaluate the influence of the selective enrichment media relative to each pre-enrichment condition on serovars detected in subsamples. We found that the differences were not significant for RV versus TT, RV versus TT-to-RV, and TT versus TT-to-RV enrichments (all Mann–Whitney *p*-values were >.05; Table 2). However, there were instances where a serovar was detected more often in one enrichment media than others. For example, in Carcasses 5, 6, and 8, serovar Enteritidis was only detected following selective enrichment in TT broth but not after RV broth enrichment, for both the RA and WCE samples. Furthermore, we observed better enrichment of serovar Schwarzengrund following RV broth enrichment than in TT or TT-RV broth enrichment; for Carcass 5, serovar Schwarzengrund was recovered from all five preparations following RV broth enrichment but not from any of the other media conditions.

There was a higher concordance in *Salmonella* recovery from all enrichment media (TT, RV, and TT-to-RV) when plated on either BGS or XLT-4 agars compared to HE agar with the highest agreement from the TT-to-RV enrichment broth (Table 1). This concordance was also observed between HE agar and both BGS and XLT-4 agars for samples enriched in RV and TT-to-RV broths than TT broth (Table 1). This appeared to be driven by a much lower *Salmonella* recovery on HE agar after selective enrichment in TT broth. For each plate where there were multiple colonies, we picked two colonies and in 38 out of 144 subsamples, two different serovars were identified. This was more pronounced in samples enriched in TT and TT-to-RV enrichment broths compared to RV broth (Table 3). Across all enrichment media, there were more instances where *Salmonella* serovars Kentucky and Typhimurium identified together ($n = 10$) than other serovars. There was also a higher occurrence of serovars Enteritidis and Typhimurium together ($n = 4$) in the enrichment media compared to other serovar combinations (Table 3).

TABLE 3 Occurrence of two serovars detected on chicken carcasses by enrichment media

Two serovars	RV	TT	TT-RV dual	Total
Enteritidis–Typhimurium	–	2	2	4
Enteritidis–Schwarzengrund	–	2	1	3
Hadar–Kentucky	1	–	1	2
Kentucky–Typhimurium	2	3	5	10
Kentucky–Schwarzengrund	1	2	–	3
Schwarzengrund–Typhimurium	1	–	1	2
Total	5	9	10	–

4 | DISCUSSION

Salmonella outbreaks are commonly attributed to poultry and poultry products, hence, the USDA-FSIS requires monitoring of *Salmonella* during poultry processing to reduce contamination and ensure food safety (CDC, 2021b; USDA-FSIS, 2015). Culture-based *Salmonella* isolation procedures rely on the use of a variety of selective and differential media, which can influence *Salmonella* recovery (Cox et al., 2019, 2020; Gorski, 2012; Singer et al., 2009). All carcasses examined in this study were contaminated with *Salmonella*; however, *Salmonella* was not recovered under all culture conditions. The pre-enrichment step of the *Salmonella* detection protocol is important, as it allows the repair and resuscitation of cells that are damaged due to antimicrobial used during processing (Hoorfar & Baggesen, 1998). Whole carcass pre-enrichment was more sensitive than the RA pre-enrichment, as demonstrated by the diversity in serovars recovered. The FSIS *Salmonella* isolation protocol utilizes a rinse aliquot of 30 mL that is incubated overnight (USDA, 2019), but this may not be sufficient to resuscitate some serovars. For example, from Carcass 3, serovar Schwarzengrund was detected from the WCE samples and not from RA samples across all culture conditions. *Salmonella* serovar Schwarzengrund has been reported to form strong attachment to surfaces (Obe & Shariat, 2021) meaning this serovar might also

be attaching strongly to broiler skin surface and a 1-min carcass rinse may not be sufficient to detach it into the medium during sample collection (Borges et al., 2018; Cox et al., 2019; Obe & Shariat, 2021).

There were no significant differences in *Salmonella* recovery between the selective enrichment preparations tested and this is likely due to the variability of *Salmonella* presence across the different carcasses. Nevertheless, the data presented here suggest that serovars identified can differ depending on the selective enrichment medium and differential agar utilized. This was most striking with preferential selection of serovar Schwarzengrund following enrichment in RV broth and, albeit not as striking, with serovar Enteritidis selection in TT broth. We previously analyzed these same samples following enrichment using a high-throughput sequencing approach that identifies all *Salmonella* serovars in an individual sample and saw similar trends for serovars Schwarzengrund and Enteritidis, without the complexity of potential plating biases (Cox et al., 2019). Improved selection for serovar Schwarzengrund in RV broth is also supported by another recent study showing it was present at a higher relative frequency in samples pre-enriched in BPW supplemented with malachite green, which is a selective component of RV broth (Rasamsetti, Berrang, Cox, & Shariat, 2021). These findings are important as some *Salmonella* monitoring programs of live poultry go directly into TT broth and thus may exclude serovar Schwarzengrund during the enrichment (NPIP, 2014). Given recent outbreaks caused by this serovar, our findings here stress the importance of parallel enrichments (CDC, 2019). The TT-to-RV protocol appears to be sensitive for detecting serovars Kentucky and Typhimurium, which could be because both serovars were preferentially enriched in TT broth compared to RV broth. We did not find HE agar to be a particularly effective agar in this study as following TT broth enrichment, it only isolated serovar Hadar, which was also found on XLT-4 and BGS agar plates. We included HE agar in this study as it is used alongside XLT-4 agar in some protocols (FDA, 2014), although we conclude that in the current samples, enriched under tested conditions, HE agar was not as effective as either XLT-4 or BGS agar.

Controlled studies in the future with known starting amounts of different serovars could be used to establish the sensitivity of different culture conditions for *Salmonella* recovery and how competition between *Salmonella* serovars can impact recovery on different agars. Results from the current study suggest that whole carcass pre-enrichment might be necessary to release and to resuscitate some *Salmonella* serovars and using multiple selective protocols is important for recovering different serovars from poultry samples.

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CONFLICT OF INTEREST

The authors declare no potential conflict of interest.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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REFERENCES

Bernstein, H., Payne, C. M., Bernstein, C., Schneider, J., Beard, S. E., & Crowley, C. L. (1999). Activation of the promoters of genes associated with DNA damage, oxidative stress, ER stress and protein malfolding by the bile salt, deoxycholate. *Toxicology Letters*, *108*(1), 37–46. https://doi.org/10.1016/s0378-4274(99)00113-7

Borges, K. A., Furian, T. Q., Souza, S. N., Menezes, R., Tondo, E. C., Salle, C. T. P., … Nascimento, V. P. (2018). Biofilm formation capacity of *Salmonella* serotypes at different temperature conditions. *Pesquisa Veterinária Brasileira*, *38*, 71–76. https://doi.org/10.1590/1678-5150-PVB-4928

CDC. (2019). *Outbreak of Salmonella infection*. Retrieved from https://www.cdc.gov/salmonella/schwarzengrund-03-19/index.html

CDC. (2021a). *Salmonella*. Retrieved from https://www.cdc.gov/salmonella/index.html

CDC. (2021b). *Reports of selected Salmonella outbreak investigations*. Retrieved from https://www.cdc.gov/salmonella/outbreaks.html

Chang, C.-T., Yuo, C.-Y., Shen, H.-C., Li, A.-M., Chen, C.-Y., Chou, J. I., & Huang, S. P. (1999). Recovery of *Salmonella* by using selenite brilliant green sulfa enrichment broth. *Journal of Clinical Microbiology*, *37*(12), 4120–4123. https://doi.org/10.1128/JCM.37.12.4120-4123.1999

Cox, N. A., Berrang, M. E., House, S. L., Hinton, A., Eric Line, J., & Wiggins, L. T. (2020). Detection of multiple naturally occurring *Salmonella* serotypes from commercial broiler carcasses with conventional methods. *Journal of Food Safety*, *40*(2), 1–5. https://doi.org/10.1111/jfs.12761

Cox, N. A., Berrang, M. E., House, S. L., Medina, D., Cook, K. L., & Shariat, N. W. (2019). Population analyses reveal preenrichment method and selective enrichment media affect *Salmonella* serovars detected on broiler carcasses. *Journal of Food Protection*, *82*(10), 1688–1696. https://doi.org/10.4315/0362-028X.JFP-19-166

Cox, N. A., & Blankenship, L. C. (1975). Comparison of rinse sampling methods for detection of salmonellae on eviscerated broiler carcasses. *Journal of Food Science*, *40*(6), 1333–1334. https://doi.org/10.1111/j.1365-2621.1975.tb01086.x

D'Aoust, J.-Y. (1981). Update on preenrichment and selective enrichment conditions for detection of *Salmonella* in foods. *Journal of Food Protection*, *44*(5), 369–374. https://doi.org/10.4315/0362-028X-44.5.369

Daquigan, N., Grim, C. J., White, J. R., Hanes, D. E., & Jarvis, K. G. (2016). Early recovery of *Salmonella* from food using a 6-hour non-selective pre-enrichment and reformulation of tetrathionate broth. *Frontiers in Microbiology*, *7*, 2103.

FDA. (2014). *BAM: Salmonella*. Retrieved from https://www.fda.gov/food/laboratory-methods-food/bam-chapter-5-salmonella#Isol

Goo, V. Y. L., Ching, G. Q. L., & Gooch, J. M. (1973). Comparison of brilliant green agar and hektoen enteric agar media in the isolation of salmonellae from food products. *Applied Microbiology*, *26*(3), 288–292.

Gorski, L. (2012). Selective enrichment media bias the types of *Salmonella enterica* strains isolated from mixed strain cultures and complex enrichment broths. *PLoS One*, *7*(4), e34722. https://doi.org/10.1371/journal.pone.0034722

Hoorfar, J., & Baggesen, D. L. (1998). Importance of pre-enrichment media for isolation of *Salmonella* spp. from swine and poultry. *FEMS Microbiology Letters*, *169*(1), 125–130. https://doi.org/10.1111/j.1574-6968.1998.tb13308.x

King, D. A., Lucia, L. M., Castillo, A., Acuff, G. R., Harris, K. B., & Savell, J. W. (2005). Evaluation of peroxyacetic acid as a post-chilling intervention for control of *Escherichia coli* O157:H7 and *Salmonella Typhimurium* on beef carcass surfaces. *Meat Science*, *69*(3), 401–407. https://doi.org/10.1016/j.meatsci.2004.08.010

Kristensen, M., Lester, V., & Jürgens, A. (1925). On the Use of trypsinized casein, brom-thymol-blue, brom-cresol-purple, phenol-red and brilliant-green for bacteriological nutrient media. *British Journal of Experimental Pathology*, *6*(6), 291–299.

Leader, B. T., Frye, J. G., Hu, J., Fedorka-Cray, P. J., & Boyle, D. S. (2009). High-throughput molecular determination of *Salmonella enterica* serovars by use of multiplex PCR and capillary electrophoresis analysis. *Journal of Clinical Microbiology*, *47*(5), 1290–1299. https://doi.org/10.1128/JCM.02095-08

Lillard, H. S. (1988). Comparison of sampling methods and implications for bacterial decontamination of poultry carcasses by rinsing. *Journal of Food Protection*, *51*(5), 405–408. https://doi.org/10.4315/0362-028X-51.5.405

Lin, D., Yan, M., Lin, S., & Chen, S. (2014). Increasing prevalence of hydrogen sulfide negative *Salmonella* in retail meats. *Food Microbiology*, *43*, 1–4. https://doi.org/10.1016/j.fm.2014.04.010

Miller, R. G., Tate, C. R., Mallinson, E. T., & Scherrer, J. A. (1991). Xylose-lysine-tergitol 4: An improved selective agar medium for the isolation of *Salmonella*. *Poultry Science*, *70*(12), 2429–2432. https://doi.org/10.3382/ps.0702429

Miller, R. G., Tate, C. R., Mallinson, E. T., & Scherrer, J. A. (1992). Erratum: Xylose-lysine-tergitol 4: An improved selective agar medium for the isolation of *Salmonella*. *Poultry Science*, *71*(2), 398. https://doi.org/10.3382/ps.0710398

Mourão, J., Rebelo, A., Ribeiro, S., Peixe, L., Novais, C., & Antunes, P. (2020). Atypical non-H_2S-producing monophasic *Salmonella Typhimurium* ST3478 strains from chicken meat at processing stage are adapted to diverse stresses. *Pathogens*, *9*(9), 701. https://doi.org/10.3390/pathogens9090701

NPIP. (2014). *National poultry improvement plan program standards*. Retrieved from http://www.poultryimprovement.org/documents/NPIPProgramStandards.pdf

Obe, T. O. & Shariat, N. W. S. (2021). Differences in biofilm formation of *Salmonella* serovars on two surfaces under two temperature conditions (under review).

Rappaport, F., Konforti, N., & Navon, B. (1956). A new enrichment medium for certain salmonellae. *Journal of Clinical Pathology*, *9*(3), 261–266. https://doi.org/10.1136/jcp.9.3.261

Rasamsetti, S., Berrang, M., Cox, N. A., & Shariat, N. W. (2021). Selective pre-enrichment method to lessen time needed to recover *Salmonella* from commercial poultry processing samples. *Food Microbiology*, *99*, 103818. https://doi.org/10.1016/j.fm.2021.103818

Rybolt, M. L., Wills, R. W., & Bailey, R. H. (2005). Use of secondary enrichment for isolation of *Salmonella* from naturally contaminated environmental samples. *Poultry Science*, *84*(7), 992–997. https://doi.org/10.1093/ps/84.7.992

Simmons, M., Fletcher, D. L., Berrang, M. E., & Cason, J. A. (2003). Comparison of sampling methods for the detection of *Salmonella* on whole broiler carcasses purchased from retail outlets. *Journal of Food Protection*, *66*(10), 1768–1770. https://doi.org/10.4315/0362-028x-66.10.1768

Singer, R. S., Mayer, A. E., Hanson, T. E., & Isaacson, R. E. (2009). Do Microbial interactions and cultivation media decrease the accuracy of *Salmonella* surveillance systems and outbreak investigations? *Journal of Food Protection*, *72*(4), 707–713. https://doi.org/10.4315/0362-028X-72.4.707

Tack, D. M., Marder, E. P., Griffin, P. M., Cieslak, P. R., Dunn, J., Hurd, S., … Geissler, A. L. (2020). Preliminary incidence and trends of infections with pathogens transmitted commonly through food—Foodborne Diseases Active Surveillance Network, 10 U.S. sites, 2016–2019. *American Journal of Transplantation*, *69*(17), 509–514. https://doi.org/10.1111/ajt.15412

Temelli, S., Eyigor, A., & Carli, K. T. (2010). *Salmonella* serogroup detection in poultry meat samples by examining multiple colonies from selective plates of two standard culture methods. *Foodborne Pathogens and Disease*, *7*(10), 1229–1234. https://doi.org/10.1089/fpd.2010.0570

USDA. (2019). *Microbiology laboratory guidebook—Isolation and identification of Salmonella from meat, poultry, pasteurized egg, and catfish products and carcass and environmental sponges*. Retrieved from https://www.fsis.usda.gov/sites/default/files/media_file/2021-03/mlg-4.pdf

USDA-FSIS. (2015). *FSIS compliance guideline: Modernization of poultry slaughter inspection microbiological sampling of raw poultry*. Retrieved from https://www.fsis.usda.gov/sites/default/files/import/Microbiological-Testing-Raw-Poultry.pdf

Vassiliadis, P. (1983). The Rappaport-Vassiliadis (RV) enrichment medium for the isolation of salmonellas: An overview. *Journal of Applied Bacteriology*, *54*(1), 69–76. https://doi.org/10.1111/j.1365-2672.1983.tb01302.x

Vassiliadis, P., Kalapothaki, V., Trichopoulos, D., Mavrommatti, C., & Serie, C. (1981). Improved isolation of salmonellae from naturally contaminated meat products by using Rappaport-Vassiliadis enrichment broth. *Applied and Environmental Microbiology*, *42*(4), 615–618. https://doi.org/10.1128/AEM.42.4.615-618.1981

Volkova, V. V., Bailey, R. H., & Wills, R. W. (2009). *Salmonella* in broiler litter and properties of soil at farm location. *PLoS One*, *4*(7), e6403. https://doi.org/10.1371/journal.pone.0006403

Winter, S. E., Thiennimitr, P., Winter, M. G., Butler, B. P., Huseby, D. L., Crawford, R. W., … Bäumler, A. J. (2010). Gut inflammation provides a respiratory electron acceptor for *Salmonella*. *Nature*, *467*(7314), 426–429. https://doi.org/10.1038/nature09415

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