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High *Salmonella* load with serovar virchow dominance pose major public safety risk in postchill broiler carcasses

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ABSTRACT The objective of this study was to determine *Salmonella* contamination levels, presence and serovar distribution in broiler carcasses before and after chilling, as well as to evaluate the effectiveness of chilling process. A total of 96 pooled neck skin samples (**PNSS**) of 48 prechill (**PreC**) and 48 postchill (**PosC**) carcasses, representing 480 broilers collected in 6 mo' period were analyzed using ISO 6579-2:2012 Miniaturized Most Probable Number (**ISO-mMPN**) technique. Species confirmation and serovar identification was performed by *Salmonella*-specific real-time PCR (**Salm-PCR**) and conventional serotyping, respectively. Mean *Salmonella* count was 1.84 $\log_{10}$ MPN/g in PreC, and 1.48 $\log_{10}$ MPN/g in PosC samples, indicating a statistically significant reduction of 0.36 $\log_{10}$ MPN/g ($p < 0.05$) in the counts by plant's air chill system. *Salmonella* positivity reduced from 97.9% (47/48) in PreC to 85.42% (41/48) in PosC samples, confirmed by Salm-PCR with identified serovars as *S.* Virchow (89.77 %) followed by *S.* Schwarzengrund (9.09%) and *S.* Bredeney (1.14%). Persistence of high load and prevalence of *Salmonella* with serovar Virchow dominance (other than the ones mandated in current guidelines) in the final product contributes significant and up to date data to relevant literature, and provides unbiased epidemiological reference to legal authorities for future relevant revisions.

Key words: *Salmonella*, *serovar*, broiler, enumeration, real-time PCR, ISO

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INTRODUCTION

Salmonella spp. remain one of the leading causes of foodborne diseases worldwide. Poultry meat and products are recognized as the primary sources of *Salmonella* with broiler meat (4.4%) and turkey meat (3.6%) having the highest isolation rates among all fresh meat categories (EFSA, 2021). Additionally, the slaughterhouse hygiene criteria compliance test results still indicate positivity of *Salmonella* in 14% of broiler, 7.4% of turkey, 1.7% of pig and 1.2% of sheep samples examined (EFSA, 2022).

According to the EU One Health 2021 Zoonoses Report, salmonellosis continues to be the second most frequently reported foodborne gastrointestinal infection in the world, with an increase in incidence by 14.3% in 2021 compared to 2020, and 60,050 confirmed cases, 11,785 hospitalizations and 71 deaths in EU (EFSA, 2022). Also, annual 1.35 million infections, 26,500 hospitalizations and 420 deaths in the USA indicate the significance of the pathogen for public health (CDC, 2023).

Poultry meat has the highest production and consumption rate compared to other meats, where the poultry sector plays an important role to supply this meat to consumers, with significant economic contributions to both domestic and international market in Turkiye. Meanwhile, parallel to reports from other countries, this sector faces contamination problems with foodborne pathogens, such as non-typhoid salmonellae in the farm/production/end product, as threat to public health (Machado et al., 2020). Therefore, efforts are being made in each country by implementing various control programs, for example, the National *Salmonella* Control Program in Turkiye (in act since 2018); by improving upstream and downstream processes in poultry production and slaughtering, with support of scientific data, and enforcement of requirements in legal regulations for effective elimination of this pathogen.

Today, in risk of foodborne diseases assessment, almost all of the current legal regulations rely on detection, and on prevalence reduction of pathogens, here *Salmonella*, yet only a few aims to reduce the counts of *Salmonella* in positive samples to serve for estimating

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the possible effect of this pathogen load on public health (FSIS, 2015). Likewise, most of the current studies focus on determining the prevalence of *Salmonella* in poultry, while a few covers both quantitative (MPN technique) and qualitative detection of the pathogen, since microbiological risks to consumers can only be achieved by minimizing *Salmonella* counts in the final product (Berghaus et al., 2013; Yamatogi et al., 2016; Machado et al., 2017; Borges et al., 2019).

In Turkiye, *Salmonella* monitoring is similar to EU Commission Regulation (EC, 2003), and under the control of Turkish Food Codex (**TFC**) Regulation on Microbiological Criteria, which states only the detection of *Salmonella* Enteritidis (*S.* Enteritidis) and *Salmonella* Typhimurium (*S.* Typhimurium) serovars in post-chill broiler carcasses by ISO 6579 reference method (TFC, 2011). Despite this, current legislations have no criterion/limit regarding the enumeration of this pathogen in these samples. However, effectiveness of *Salmonella* control programs and risk analyses through legal regulations can only lead to better action policies with simultaneous analysis of qualitative and quantitative data (Mead et al., 2010).

Recent reports on *Salmonella* quantification in broiler carcasses during slaughtering process used various bacteriological methods as USDA-FSIS, FDA-BAM or their validated modifications (Yamatogi et al., 2016; Machado et al., 2017; Borges et al., 2019), and also as qPCR for rapid enumeration (Borges et al., 2019).

As in EU, the current reference method for *Salmonella* enumeration in foods in Turkiye is ISO 6579-2:2012 Microbiology of Food and Animal Feed-Horizontal Method for the Detection, Enumeration and Serotyping of *Salmonella*-Part 2: Enumeration by a Miniaturized Most Probable Number (**ISO-mMPN**) Technique standard (ISO, 2012). Up to our knowledge, only a few related studies reported the use of ISO-mMPN, to quantify *Salmonella* in broiler carcasses (Machado et al., 2020), broiler meat cuts (Perin et al., 2020), and burgers and sausages (Roccato et al., 2015).

This study reports the first time use of ISO-mMPN in its current version to determine *Salmonella* levels in addition to presence and serovar distribution in pre-chill (**PreC**) and post-chill (**PosC**) broiler carcasses in Turkiye. Also, effectiveness of the carcass chilling stages in the slaughter process was evaluated based on *Salmonella* contamination levels.

MATERIALS AND METHODS

Samples

From a poultry slaughterhouse in Turkiye, with average 200,000 broiler/d slaughter capacity, which was visited between August 2021- January 2022 (Table 1), 96 (48 PreC and 48 PosC) pooled neck skin samples (**PNSS**) representing 480 broiler (Ross 308) carcasses were collected.

Standard Strains

S. Enteritidis 64K (M. Y. Popoff, Institut Pasteur, Paris Cedex 15, France) and *S.* Typhimurium NCTC 12416 (Refik Saydam, Turkish Public Health Agency, Ankara) as positive controls.

Sampling

ISO 17604:2015 Section 8.2.3.1. (ISO, 2015) requirements were followed to obtain 1 unit PNSS, where10 to 12 g neck skin of 5 broiler carcasses (total 50−60 g) were aseptically excised into 500 mL stomacher bags, and transferred to the laboratory in coolers in 1 h for analysis.

Enumeration and Detection of Salmonella by ISO-mMPN Technique

After manually massaging PNSS in stomacher bag from outside for 1 min, 25 g aliquot was aseptically transferred into a new sterile 500 mL stomacher bag with 225 mL Buffered Peptone Water (BPW, OXOID, CM1049), and homogenized in stomacher at 230 rpm for 1 min as 10^{-1} dilution (initial suspension - **IS**) of the sample. Then, for dilution and non-selective pre-enrichment, 2 mL BPW was aliquoted to all of the 2nd, 3rd and 4th row wells of a sterile 12-well plate, leaving the first-row wells empty. Then, 2.5 mL of IS was transferred to each 3 well in the first row. For the first 5^{-1} dilution, 0.5 mL of thoroughly mixed aliquot from the wells of IS in the first row were pipetted into 3 wells with 2 mL BPW in the 2nd row. Similar procedure was applied in consecutive columns to obtain the 2nd 5^{-1} (5^{-2}) and the 3rd 5^{-1} (5^{-3}) dilutions, and the plates were incubated at 37 °C for 18 h. Additionally, IS of all collected samples were incubated at 37 °C for 18 h to determine presence of *Salmonella* (ISO, 2012).

Table 1. Flock information and number of PreC and PosC PNSS of slaughtered broilers.

Sampling No	Flock size	Number of house/flock	Flock age (d)	Average live weight (g)	Number of PNSS (PreC, PosC)
1	41,650	3	40	2.395	10 (5, 5)
2	17,000	1	40	2.300	20 (10, 10)
3	19,500	1	42	2.725	6 (3, 3)
4	4,400	1	44	2.825	30 (15, 15)
5	18,000	1	44	2.900	30 (15, 15)
Total			42*	2.629*	96 (48, 48)

*Mean value.

After incubation, 20 μL of each dilution from the pre-enrichment plate was inoculated onto the surface edge of a prepared 12-well plate with 2 mL of Modified Semi-Solid Rappaport-Vassiliadis Agar (MSSRVA, OXOID, CM0669) with Novobiocin Supplement (OXOID, SR0181), and incubated at 41.5°C for 24 h. Additionally, 100 μL from each preincubated IS was inoculated to MSSRVA in 90 mm petri dishes and incubated at 41.5 ° C for 24 h. Following incubation, white/gray-white, turbid zone radiating from inoculation point was considered as typical/suspect, while plates with negative results were reincubated for 24 h (ISO, 2012).

Selection from the MSSRVA *Salmonella* suspect growth was determined by starting from the highest dilution wells to further dilutions in the order of 3-2-1, and 1 μL from the inner part of the turbid zone was streaked onto Xylose Lysine Deoxycholate Agar (XLDA, OXOID, CM0469) and Brilliance Salmonella Agar (BSA, OXOID, CM1092) with Salmonella Selective Supplement (OXOID, SR0194), and incubated at 37°C for 24 h, followed by a further incubation for 24 h in case of no visible suspect colonies after first incubation. Red colonies with black centers with light reddish transparent zones on XLDA, and purple, shiny, smooth round-shaped colonies on BSA were considered as typical/suspect (ISO, 2012). At least 1 isolated, typical colony from XLDA and BSA was streaked onto MacConkey Agar (OXOID, CM0115), and then to Nutrient Agar (NA, OXOID, CM0003), and incubated at 37°C for 24 h for biochemical identification by API 20E (Biomerieux, 20100). In case of a negative result, same procedure was performed on 4 more typical colonies found on XLDA and BSA. Pure isolates grown in Brain Heart Infusion Broth (BHIB, OXOID, CM1135) was mixed with 50 % sterile glycerol, and stored in -80°C (ISO, 2012) for conventional serotyping. In addition, for template preparation in *Salmonella*-specific real-time PCR (**Salm-PCR**) analysis, a loopful of NA pure culture was homogenized in 500 μL sterile PCR-grade water, and stored in -20°C.

Number of wells with positive and confirmed results for each dilution was counted and *Salmonella* spp. load was calculated using ISO 7218:2007/Amd.1:2013 Microbiology of Food and Animal Feeding Stuffs-General Requirements and Guidance for Microbiological Examinations standard, and mMPN calculation program, version 6 (Jarvis et al., 2010; International Organization for Standardization ISO, 2013).

Confirmation by Salm-PCR Analysis

Template DNA from each biochemically verified *Salmonella* spp. was isolated following the procedure mentioned in part 2.3.1 of Foodproof StarPrep One Kit (Biotecon, S400 07, Germany) manual. Briefly, preparations stored in -20°C were thawed, homogenized by vortexing (Stuart, SA8), and centrifuged at 8,000 × g for 5 min (Thermo Scientific, MicroCL 17). After the supernatant was removed, 200 μL lysis buffer was added to the pellet, vortexed, incubated at 97.5°C in a block heater (Techne, DB-2D-FDB02DD) for 10 min, followed by a final vortexing and centrifugation at 13,000 × g for 2 min.

Each template DNA with a concentration of 100 ng/μL, and absorbance values between 1.6 and 2.0 (Nanodrop Spectrophotometer, Thermo Scientific, ND-1000, USA) was used as template for Salm-PCR analysis (LightCycler 2.0 Instrument, Roche, 03531414201, Germany), which was performed by using a Foodproof Salmonella Detection Kit (Biotecon, R310 27, Germany). The total PCR reaction volume was 20 μL comprised of 5 μL of template DNA added into 15 μL PCR mix (13 μL of Foodproof Salmonella Master Mix [ready-to-use primer and hybridization probe mix], 1 μL of Foodproof Salmonella Enzyme Solution [FastStart Taq DNA Polymerase and Uracil-DNA Glycosylase, heat labile, for prevention of carry-over contamination], 1 μL of Foodproof Salmonella Internal Control. The Foodproof Salmonella Control template DNA and PCR-grade water were used as PCR positive and negative controls, respectively. The amplification protocol (preincubation: 2 min at 40°C and 10 min at 95°C; amplification: 45 cycles of 0 s denaturation at 95°C, binding and fluorescence signal readout at the end for 30 s at 59°C, and 5 s elongation at 72°C; and cooling for 30 s at 40°C) and data analysis was performed as indicated in the kit insert, and by the LightCycler software version 4.1, respectively.

Conventional Serotyping

Serological identification of *Salmonella* spp. isolates was performed by conventional serotyping according to the White-Kauffmann-Le Minor Scheme (Grimont and Weill, 2007), to Guibourdenche et al. (2010), and to Issenhuth-Jeanjean et al. (2014) by using commercial O- and H- antisera (Becton-Dickinson). Slide agglutination and tube agglutination tests were applied for the analyses of somatic and flagellar phase antigens, respectively. Also, for confirmatory purposes, selected *Salmonella* spp. isolates were serotyped by the National Enteric Pathogens Reference Laboratory (Turkish Ministry of Health, General Directorate of Public Health, Department of Microbiology Reference Laboratories and Biological Products).

Statistical Analyses

Salmonella load in positive PreC and PosC samples were analyzed by SPSS version 24. Data normality and homogeneity values were measured by Kolmogorov-Smirnov and Levene tests, respectively. PreC and PosC samples of normality and homogeneity were compared by Independent-Samples T Test analysis, and significant differences between groups were determined at $p < 0.05$ (Stehlik-Barry and Babinec, 2017).

RESULTS

In this study, mean PreC *Salmonella* count of 1.84 $\log_{10}$ MPN/g declined to 1.48 $\log_{10}$ MPN/g in PosC

Table 2. Salmonella spp. counts in PreC and PosC PNSS of slaughtered broilers.

				Number of *Salmonella* spp. log10 (MPN/g)				
				PreC		PosC		
Sampling no	n	Sample type	No of positives/total PNSS	Mean	SD	Mean	SD	*P* value
1	10	PreC	4/5	2.03	0.40	1.10	0.45	0.02*
		PosC	4/5					
2	20	PreC	10/10	2.52	0.42	2.13	0.17	0.03*
		PosC	8/10					
3	6	PreC	3/3	1.33	0.12	1.20	-	0.42
		PosC	1/3					
4	30	PreC	12/15	1,45	0.65	1.06	0.61	0.16
		PosC	10/15					
5	30	PreC	13/15	1.72	0.63	1.53	0.63	0.43
		PosC	14/15					
Total	96	PreC	42/48	1.84	0.68	1.48	0.65	0.02*
		PosC	37/48					

*: Significant at $p < 0.05$ level.

carcass samples after air chilling, with a statistically significant difference of 0.36 $\log_{10}$ MPN/g ($p < 0.05$) (Table 2).

Salmonella prevalence was determined as 47 (97.92%) and 41 (85.42%) in 48 PreC and 48 PosC samples, respectively. Results from conventional serotyping indicated the most prevalent serovar as *S.* Virchow (6,7,14:r:1,2) (79/88, 89.77%) followed by *S.* Schwarzengrund (1,4,12,27:d:1,7) (8/88, 9.09%) and *S.* Bredeney (1,4,12,27:l,v:1,7) (1/88, 1.14%) (Table 3).

DISCUSSION

The most significant finding in our study was a decline of 0.36 $\log_{10}$ MPN/g in the mean 1.84 $\log_{10}$ MPN/g PreC *Salmonella* count to 1.48 $\log_{10}$ MPN/g in PosC carcass samples ($p < 0.05$) (Table 2). Among the studies particularly investigating number of this pathogen in broiler carcasses, sampled from different stages of the slaughter process, Berghaus et al. (2013) and Borges et al. (2019) reported that their PreC whole carcass rinse *Salmonella* counts of 2.57 $\log_{10}$ MPN and 1.74 $\log_{10}$ MPN reduced to 2.32 $\log_{10}$ MPN and 1.48 $\log_{10}$ MPN in PosC samples, respectively, after immersion chilling. The significance in reduction of *Salmonella* counts in the studies as 0.25 $\log_{10}$ MPN (Berghaus et al., 2013) and 0.26 $\log_{10}$ MPN (Borges et al., 2019) were both attributed to the efficiency of the chilling systems used in the plants. Similarly, effective chilling of the carcasses in our study, was the major contributor to the significant reduction of the pathogen. Our findings are in accordance with the results of Berghaus et al. (2013) and Borges et al. (2019), as well as Machado et al., 2020, who also reported a statistically significant difference between their PreC and PosC skin-on meat samples' *Salmonella* counts ($p \leq 0.0001$). A 0.03 MPN/g (below detectable limit) counts from carcass rinse water, reported by Yamatogi et al. (2016), was linked to 5 ppm chlorine addition to chill-water tank to inactivate the pathogen, is in contrast to similar studies' and our results. Despite proven effectiveness of the air or immersion chilling steps in slaughter processes, the relatively high *Salmonella* counts in the final product in our study and the studies mentioned above except Yamatogi et al. (2016), can mainly be related to inefficient inside/outside bird washing after evisceration, when solely the "within slaughter"-related factors are considered. Thereupon, detailed discussions with authorized personnel, plant management decided to include a second washing system prior chilling tunnel to the slaughter line to obtain a safer end product. Nevertheless, possibility of high initial *Salmonella* load in live broilers entering slaughter,

Table 3. Occurrence and serovar distribution of *Salmonella* spp. in PreC and PosC PNSS of slaughtered broilers.

			Serovar (%)		
Sampling no	Sample type (n)	No of positive samples (%)	Virchow (6,7,14:r:1,2)	Schwarzengrund (1,4,12,27:d:1,7)	Bredeney (1,4,12,27:l,v:1,7)
1	PreC (5)	4 (80.00)	3	1	-
	PosC (5)	4 (80.00)	2	2	-
2	PreC (10)	10 (100.00)	9	1	-
	PosC (10)	8 (80.00)	5	3	-
3	PreC (3)	3 (100.00)	3	-	-
	PosC (3)	1 (33.33)	-	1	-
4	PreC (15)	15 (100.00)	15	-	-
	PosC (15)	13 (86.67)	13	-	-
5	PreC (15)	15 (100.00)	15	-	-
	PosC (15)	15 (100.00)	14	-	1
	PreC (48)	47 (97.92)	45 (95.75)	2 (4.25)	-
Total	PosC (48)	41 (85.42)	34 (82.93)	6 (14.63)	1 (2.44)
	Overall (96)	88 (91.67)	79 (89.77)	8 (9.09)	1 (1.14)

density of carcasses giving rise to both contaminated water droplet suspension in air chiller, and cross-contamination among carcasses in immersion chiller could be other contributors for the pathogen's persistence in non-negligible numbers in the final product.

As another result of this study, 47 (97.92%) and 41 (85.42%) of 48 PreC and 48 PosC samples found to harbor *Salmonella*, respectively, with the most prevalent serovar as *S.* Virchow (79/88, 89.77%) followed by *S.* Schwarzengrund (8/88, 9.09%) and *S.* Bredeney (1/88, 1.14%) (Table 3). When recent studies focusing on *Salmonella* enumeration by MPN technique, and also reporting prevalence and serovar information of this pathogen, Berghaus et al. (2013) found *Salmonella* in 18.2% and 2.4% of their pre-chilling and post-chilling carcass rinses in USA, and identified *S.* Kentucky (61%), *S.* Enteritidis (16.9%) and *S.* Schwarzengrund (6%) as the 3 most prevalent serovars, where the detection rate of serovar Schwarzengrund showed similarity to our study findings. Rasamsetti et al. (2022) reported that *Salmonella* prevalence varied greatly between 3 different plants in USA, and reported 66.7, 8.3, and 100% for pre-chill, and 8.3, 0.0, and 16.67% rates for post-chill carcass drip waters, respectively. Presence of *S.* Schwarzengrund within the 4 most prevalent serovars (*S.* Infantis, *S.* Kentucky, *S.* Typhimurium) in the study appears to have accordance to our data. In Brazil, Yamatogi et al. (2016) detected *Salmonella* in 58% of post-chilling samples, and reported presence of *S.* Schwarzengrund (1.13%), and *S.* Bredeney (0.56%) after 3 major serovars as Mbandaka (21.47%), Seftenberg (17.51%), and Enteritidis (14.12%). The study's serovar profile harboring both Schwarzengrund and Bredeney shows similarity to our data. From the same country, Machado et al., 2020 indicated 26.4% of pre-chill and 16.2% of postchill carcasses carried the pathogen, with the most frequent serovar as Minnesota (88.09%). Boubendir et al. (2021) found a 2 h chlorine contact time caused a statistically significant ($p < 0.01$) pathogen elimination on carcasses by comparing different cooling systems from 2 poultry processing plants, where *Salmonella* prevalence in plants 1 and 2 before cooling (37.5% and 38.5%), after water cooling (45% and 5%) reduced to 2.5% in plant 1after air cooling, and to 0% by cooling with cetylpyridinium chloride included air in plant 2. Similar to ours, *S.* Schwarzengrund was one of the 3 most commonly identified serovars reported in the study. *Salmonella* prevalence rates in the studies mentioned above were in the range of 8.3% to 100% in pre-chilling and 0 to 58% in postchilling carcasses. Prevalence of *Salmonella* in our PreC was similar to Rasamsetti et al. (2022) and higher than the rates reported by Machado et al., 2020 and Berghaus et al. (2013). Our PosC *Salmonella* detection rate was higher than the findings of all other indicated studies (Berghaus et al., 2013; Yamatogi et al., 2016; Machado et al., 2020; Boubendir et al., 2021; Rasamsetti et al., 2022). In brief, variations in *Salmonella* prevalence rates in the studies and ours could mainly originate from management and slaughter/cooling systems used in the plant, as well as the study design. Additionally, sampling year/interval, geographical region/circulating serovars, and detection/serotyping method could be the most important factors affecting prevalence and serovar distribution.

In our work, we observed a dominancy of *S.* Virchow followed by *S.* Schwarzengrund, while there was no *S.* Enteritidis or *S.* Typhimurium in any of the samples examined. This finding is noteworthy in terms of public health and industrial practices. In terms of public health, presence of serovar Virchow in Turkiye had only been reported in 2 discrete extraintestinal infections without indication of the source for the pathogen. Thus, up to our knowledge, there is no published data indicating a foodborne gastrointestinal infection or outbreak related to serovar Virchow in our country (Bahar et al., 2006; Gulcan et al., 2012). In contrast, there are a number of recent reports for Virchow's persistence in broiler meat/environment-related cross-border outbreaks since 2017 in 5 European Union/European Economic Area (**EU/EEA**) countries, the United Kingdom, and the USA. The number of confirmed cases in this report was indicated to represent only a small proportion of all infections in the EU/EEA, partly due to the varying sequencing capacities of countries (ECDC-EFSA, 2023). In the same report, possibility of infections affecting any age group, and implementation of further investigations to identify the contamination source(s)/point(s) along the chicken meat production chain, including the primary production upstream lines to allow appropriate control measures was emphasized. Also, in 2022, another Virchow outbreak was reported from Australia updating the serovar's persisting emergence worldwide (Padrotta et al., 2022). In terms of poultry industry practices, Virchow has a proven persistence of under environmental stress by biofilm formation (Ariafar et al., 2019), which could be one of the main reasons of its predominance in our study. This is of major concern in broiler slaughter processing, where the bacterium can easily find niches to escape from the cleaning and disinfection practices, and survive on the final product as threat to public health. Additionally, prevalence of (live) broiler (meat) related serovar Virchow isolates' high antimicrobial resistance (Avsaroglu et al., 2007; Jeon et al., 2019; Fowler et al., 2021) is a major problem both in disseminating resistance genes in poultry environments, and during treatment of human Virchow infections. Thus, all this data has unbiased value in updating the existing guidelines/recommendations to monitor/screen salmonellae in control programs. Additionally, current data indicated an incline in serovar Schwarzengrund's prevalence from poultry samples in the Americas (Diaz et al., 2021), and this pathogen's invasive, multidrug resistant traits causing sporadic illnesses, chronic complications, as well as outbreaks over many countries from USA, Europe and Asia (Li et al., 2021). Finally, our serovar distribution rates indicate that Virchow and Schwarzengrund require emphasis in relation to investigation-based updates in circulating serovars in poultry industry in Turkiye.

CONCLUSIONS

This study determined the contamination level and prevalence of *Salmonella* in broiler carcass samples for the first time by ISO-mMPN technique in Turkiye, highlighting the equal importance of both detection and serovar identification in estimating the risk of this pathogen for public health. Detection of *Salmonella* in majority of the PosC carcass samples (85.42%) suggested that the actions of the ongoing control program in our country have not reached the intended reduction levels yet, at least for the poultry farms providing live broilers to this slaughterhouse. Although there was a significant reduction in *Salmonella* levels between PreC and PosC stages of the slaughter process (0.36 $\log_{10}$ MPN/g), mean count of 1.48 $\log_{10}$ MPN/g in the final product indicated insufficient pre-chill processes.

The dominant serovar was *S.* Virchow (%89.77) followed by *S.* Schwarzengrund (%9.09). To the best of our knowledge, there is no study in our country, in which these 2 serovars were determined with similar prevalence rates in broilers. Therefore, besides contributing original data to current literature, results reveal broilers as asymptomatic carriers of highly pathogenic and invasive *Salmonella* serovars other than *S.* Enteritidis and *S.* Typhimurium. Circulation of 2 worldwide important pathogenic serovars in broilers in Turkiye in considerably high numbers and rates has potential to serve as unbiased data to regulatory authorities in updating the current mandatory requirements of only *S.* Enteritidis and *S.* Typhimurium absence in broiler meats.

Additionally, this study provided factual data to the plant management in evaluating and revising their critical stages for pathogen reduction. Study results have the potential to be employed in shaping future guidelines and practices as relevant updates both in the National *Salmonella* Control Program, and in the TFC Regulations on Microbiological Criteria as unbiased reference information.

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DISCLOSURES

The authors declare that they have no conflict of interest.

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