Original article

Salmonella in Food Environments in Canteens: A Focus on Antibiotic and Disinfectant Resistance Patterns

Şebnem Pamuk[1], Metin Erdoğan[2], Yeliz Yildirim[3], Nurhan Ertas Onmaz[3]

[1]Afyon Kocatepe University, Faculty of Veterinary Medicine, Department of Food Hygiene and Technology, Afyonkarahisar, Turkey; [2]Afyon Kocatepe University, Faculty of Veterinary Medicine, Department of Medical Biology and Genetics Afyonkarahisar, Turkey; [3]Erciyes University, Faculty of Veterinary Medicine, Department of Veterinary Public Health Kayseri, Turkey

Abstract. The objective of this study was to determine the molecular characterization and antibiotic and disinfectant resistance potential of *Salmonella* isolates from food related areas in canteens. This study was performed in food related areas as well as food handlers in student canteens in University campus to trace source of *Salmonella* contamination with a special focus on antibiotic and disinfectant resistance of the isolates. *Salmonella* isolates were identified by conventional and molecular techniques. Genetic similarity, antibiotic and disinfectant resistance patterns of the isolates were performed by sequence analyzing, disc diffusion and PCR, respectively. *Salmonella* contamination was determined from hand (Newport and Infantis), knife handle (Newport) and grilled chicken (Koessen) samples. The identity of the 16S rRNA sequence of two Newport isolates (knife handle and hand) from Canteen 4 and Canteen 6 were found 100% identic. Multidrug resistance (MDR) was observed among all *Salmonella* isolates with resistance to at least five or more antibiotics. *sugE* and *qacEΔ1* disinfectant genes were determined in 2 and 1 isolate respectively while cross-resistance to antibiotics and disinfectants in three isolates were detected. The results of this study indicate that the food-handlers and food preparation equipments may serve as reservoirs for cross-resistant *Salmonella*, a potential public health concern. Therefore, periodic training programmes should effectively be implemented for food handlers. Owing to the growing concern that antibiotic resistant mutants could be induced by improper disinfectant use, unnecessary and misuse of disinfectants should be avoided, especially on food contact surfaces.

Key words: antibiotic resistance, disinfectant resistance, food environments, public health, S*almonella*

Introduction

Every year, approximately 3 million children die of diarrhea, and hundreds of millions of people suffer from diarrhea attacks and complications mainly caused by food-borne pathogens, among which *Salmonella* is one of the most commonly isolated (1, 2). At the present, over 2500 *Salmonella s*erotypes have been identified; more than 50% of these serotypes belong to *Salmonella* Enterica Subsp. Enterica and many of these serovars are able to cause illness such as enteric fever, bacteremia, gastroenteritis in both humans and animals (3, 4) *S. Enterica Subsp. Enterica Serovar* Enteritidis (*S.* Enteritidis) and *S. Enterica Subsp. Enterica Serovar* Typhimurium (*S.* Typhimurium) are the most common causative agents of food-borne gastroenteritis (5).

Due to surveillance, prevention and treatment costs, antibiotic resistant *Salmonella* infections are considered among the major public health concerns worldwide. It has been reported that human antibiotic resistant *Salmonella* infections are often caused by contaminated food (6). It is suggested that *Salmonella* could survive on surfaces and equipment used for preparing food after conventional cleaning and sanitation

practices (7, 8, 9). Ability of *Salmonella* in food environment could to adhere and form biofilm on different food contact surfaces, allowing resistance to different conditions including disinfectants (10). Disinfectants, especially quaternary ammonium compounds (QACs), are commonly used for food contact surfaces and other equipment in the food industry to prevent contamination of raw materials and products with pathogens and spoilage microorganisms (11, 12). In recent years, concerns about disinfectant tolerance have gradually increased mainly based on the fact that disinfectant use may induce evolution of cross-resistance to antibiotics (13) which in turn may lead to a great challenge in the control of pathogens. The aim of this study was to determine evaluate antimicrobial susceptibility and disinfectant resistance of *Salmonella* isolates obtained from food environments at canteens as well as their genetic relationships. The genetic characteristics of pathogens provide information about their sources and the paths they follow in transmission.

Materials and Methods

Sampling

In this study, a total of 212 samples (100 foods, 45 hand, 27 cutting board and 40 knife handle surface) taken from six different canteens inside university campus were examined during the period of 2017-2018. The food samples studied were consisted of 10 grilled chicken (Ready to eat; RTE), 5 meatball (raw), 5 chicken meat (raw), 5 chicken saute (raw), 5 chicken shish (raw), 5 chicken skewers (raw), 10 soujouk (RTE), 10 Adana kebab (raw), 10 Urfa kebab (raw), 20 chicken doner (RTE), 10 vegetables (RTE) and 5 pancake (RTE). At least 100 gr food samples were taken into sterile bags. Forefingers and thump samples from 45 food handlers were taken during working hours without previous notification.

Cutting board and knives were sampled by swaps (premoistened sterile swab in 10 mL of sterile 0.1%-peptone water) after bordering the surface of sampling area by a 15-cm^2 sterile template. The food contact surfaces were wiped three times in three directions with the swaps (14). All samples were transported to the laboratory in a cool box under 2 °C and were immediately analyzed.

Isolation of Salmonella from Samples

RODAC plates containing selective agar (XLD, CM 0469) was used to sample the thumb and forefinger of both hands of the personnel.

Swaps taken from cutting boards and knife handles were placed in sterile tubes containing 10 ml buffer peptone water (OXOID, CM0509) and used directly for pre-enrichment and enrichment stage.

The isolation and phenotipic identification of *Salmonella* from all samples were carried out as referred by ISO 6579 (15). Presumptive *Salmonella* isolates were verified with polyvalent O (somatic) and H (flagellar) antisera (Difco 2264-47-2).

PCR and Sequencing

The total genomic DNA was exctracted by using the commercial spin column kit (Thermo Fisher Scientific, K0722) according to the manufacturer's recommendations. *rrsE 16S rRNA* and *sun 16S rRNA* (cytosine (967)-C(5))-methyltransferas) genes were used to identify *Salmonella* strains. The isolates were analysed for *qacE*, *qacEΔ1*, and *sugE* genes for the determination of disinfectant resistance (DR). Fast PCR Professional 6.1.2 package program was used for primers design (16) as shown in table 1.

Melting temperature (Tm) was determined using gradient PCR with the following PCR mixture (each 20 µl) consisted of 1X PCR buffer, 2.0m M $MgCl_2$, 0.2Mm dNTP, 0.25mM forward and reverse primer, 1U Platinium Taq DNA polymerase (Invitrogen,10966034) and 20ng template DNA. All PCR amplification was carried out initial denaturation at 95°C for 2 min, 35 cycles of denaturation 45 sec at 94°C, 1 min primer annealing at 60-62°C, 1 min extension at 72°C and a final extension at 72°C for 10 min. Amplified PCR products were analyzed by gelelectrophoresis on 2% agarose gel followed by Red Safe (Intron, 21141) staining.

Subsequently, all PCR products were purged with exonucleaseI (Thermo Fisher Scientific, EN0581) and Fast AP thermosensitive alkaline phosphatase

Table 1. Primers designed to determine *Salmonella* strains and DR genes

Gene	Forward (5'→3')	Revers (5'→3')	Tm(°C)	Base pair	GenBank No
rrsE16sRNA	ACCAAGTCTCAAGAGTGAACACG	TCACAAAGTGGTAAGCGCCCTC	60	1540	**NC_003197.2**
sun16sRNA	ATGCTTACCCCACACAGTGGCA	AGGTGGCGTAAACCAGCGTCC	62	660	**NC_003197.2**
sugE	TTCTTCCGGGCAAAAATGCCA	TCCTTTCACGGACCCCTACTA	62	528	NC_010259.1
qacE	AACAATTCGTTCAAGCCGACG	GATCCGACTCGCAGCATTTCG	62	615	**NC_013437.1**
qacEΔ1	GCACATAATTGCTCACAGCCA	GATCCGACTCGCAGCATTTCG	62	552	**NC_003292.1**

(Thermo Fisher Scientific, EF0652). PCR Sequencing was performed according to Big Dye Therminator 3.1 kit protocol. The products obtained at the end of the sequenced PCR were purified by ethanol/EDTA/sodium acetate precipitation method. Hi Diformamide was added to15µl to each well and loaded onto the DNA Sequence Analyzer (ABI3500). Sequence chromatograms were edited and defined by alignment of forward and reverse *sequences* using Sequencher®5.4.6 DNA sequence analysis software (Gene Codes Corporation, Ann Arbor, MIUSA) and Bioedit sequence alignment editor analysis program (17). All sequences were edited (GeneCode, Sequencher 5.4.6) and aligned with the Bioedit sequence alignment editor analysis program (17) and amplification product was read 360 bp. Genotypic results were compared, and similarity searches were performed using MEGA 4 (18).

Antimicrobial susceptibility testing

The isolates were tested against 24 antimicrobial agents including Imipenem (10 µg, Bioanalyse), Marbofloxacin (5 µg, Bioanalyse), Vancomycin (30 µg, Bioanalyse), Erythromycin (15 µg, Bioanalyse), Streptomycin (10 µg, Bioanalyse), Rifampin (5 µg, Bioanalyse), Cloxacillin (5 µg, Oxoid), Lincomycin/Neomycin (75 µg, Oxoid), Tetracycline (30 µg, Oxoid), Cefoperazone (75 µg, Oxoid), Ceftrofur (30 µg, Bioanalyse), Chloramphenicol (30 µg, Oxoid), Amoxicillin/Clavulanic acid (20/10 µg, Bioanalyse), Gentamicin (10 µg, Bioanalyse), Ciprofloxacin (5 µg, Oxoid), Neomycin (10 µg, Oxoid), Penicillin/Novobiocin (10/30 µg, Bioanalyse), Sulphamethoxazole/Trimethoprim (25 µg, Oxoid), Kanamycin (30 µg, Oxoid), Amoxycillin (25 µg, Oxoid), Ceftazidime (30 µg, Oxoid), Tobramycin (10 µg, Oxoid), Amikacin (30 µg, Oxoid), Nalidixic acid (30 µg, Oxoid) by using the Kirby-Bauer disc diffusion method (19). The resistance levels were defined as described by the Clinical and Laboratory Standards Institute (20).

Results

Overall, 6 (2.7%) of 212 samples yielded *Salmonella* including 1(1%) grilled chicken, 4 (8.8%) food handlers' hand and 1 (2.5%) knife handle samples. A total of 4 serotypes were identified from *Salmonella* contaminated samples and the serotype distrubition of the isolates are listed in table 2.

According to sequencing results; two Newport (knife handle and hand) from Canteen 4 and Canteen 6 were found 100% identic and were also 100% identic to *S. Newport* obtained from Genbank. Moreover, 16S rRNA sequence of other strains obtained from this study also showed similar pattern (99.0–100.0%) with five other sequences provided from GenBank (Table 2).

Among the DR genes, *sugE* was detected in one hand and one grilled chicken isolates while *qacEΔ1* was detected in 2 hand isolates. None of the isolates found to harbour *qacE* gene (Table 3).

As shown in table 4, all six isolates were found 100% resistant to penicillin/novobiocin, tetracycline, cloxacillin and rifampin. Also, evident resistance to sulphamethoxazole / trimethoprim (83.3%), vancomycin,

Table 2. Genetic similarity of the isolates

Sample	Source	Closest 16S rRNA NCBI isolate and accession	Sequence similarity to isolate (%)	Canteen
43	Hand	*Salmonella supsb. enterica serovar* Infantis strain L41/ CP038516.1	100	Canteen 1
6a	Hand	*Salmonella supsb. enterica serovar* Infantis strain L41/ CP038516.1 *strain* NCTC8272/ LR134149.1	100	Canteen 2
6b	Grilled chicken	*Salmonella enterica supsb. enterica serovar* Koessen strain S-1501/ CP019412.1	99	
39a	Hand	*Salmonella enterica supsb. enterica serovar* Newport strain USDA-ARS-USMARC-1925/ CP025232.1	100	Canteen 4
39b	Hand	*Salmonella enterica supsb. enterica serovar* Newport *strain* NCTC129/ LR134140.1	99	
45	Knife handle	*Salmonella enterica supsb. enterica serovar* Newport strain USDA-ARS-USMARC-1925/ CP025232.1	100	Canteen 6

Table 3. DR genes of *Salmonella* isolates

Source	Species	Disinfectant resistance genes		
		sugE	***QacEΔ1***	***qacE***
Hand	*Salmonella supsb. enterica serovar* Infantis	-	-	-
Hand	*Salmonella supsb. enterica serovar* Infantis	+	+	-
Grilled chicken	*Salmonella enterica supsb. enterica serovar* Koessen	+	-	-
Hand	*Salmonella enterica supsb. enterica serovar* Newport	-	-	-
Hand	*Salmonella enterica supsb. enterica*	-	+	-
Knife handle	*Salmonella enterica supsb. enterica serovar* Newport	-	-	-

Table 4. Antimicrobial resistance percentages of *Salmonella* isolates tested

Antibiotics	No. of *Salmonella* spp. isolates (n= 6)	
	S (%)	**R (%)**
Imipenem (10 µg)	100	0
Marbofloxacin (5 µg)	100	0
Vancomycin (30 µg)	66.7	66.7
Erythromycin (15 µg)	33.3	66.7
Streptomycin (10 µg)	33.3	66.7
Rifampin (5 µg)	33.3	100
Cloxacillin (5 µg)	0	100
Lincomycin/Neomycin (75 µg)	0	33.3
Tetracycline (30 µg)	66.7	100
Cefoperazone (75 µg)	0	0
Ceftrofur (30 µg)	100	0
Chloramphenicol (30 µg)	100	0
Amoxicillin/ Clavulanic acid (20/10 µg)	100	16.7

Antibiotics	No. of *Salmonella* spp. isolates (n= 6)	
	S (%)	R (%)
Gentamicin (10 µg)	83.3	0
Ciprofloxacin (5 µg)	100	0
Neomycin (10 µg)	100	0
Penicillin/Novobiocin (10/30 µg)	100	100
Sulphamethoxazole/Trimethoprim (25 µg)	0	83.3
Kanamycin (30 µg)	16.7	33.3
Amoxicillin (25 µg)	66.7	66.7
Ceftazidime (30 µg)	33.3	33.3
Tobramycin (10 µg)	66.7	33.3
Amikacin (30 µg)	66.7	33.3
Nalidixic acid (30 µg)	66.7	0

Table 5. Multidrug-resistant (MDR) *Salmonella* isolates from canteens in Afyon –Turkey

Serotype	Source	Antibiotics (n)	Antimicrobial resistance percentages
Infantis	C1-Hand	VA, E, S, RA, CX, TE, P/NV, SXT, K, CAZ, TOB, AK (12)	50
	C2-Hand	VA, E, S, RA, CX, TE, P/NV, SXT, K, CAZ, TOB, AK (12)	
Koessen	C2-Grilled chicken	VA, E, S, RA, CX, L/N, TE, AM/C, N, P/NV, SXT, AX (12)	
Newport	C4-Hand	RA, CX, TE, P/NV, AX (5)	20.8
	C4-Hand	VA, E, S, RA, CX, L/N, TE, P/NV, SXT, AX (10)	41.6
	C6-Knife handle	RA, CX, TE, P/NV, SXT, AX (6)	25

VA: Vancomycin; E: Erythromycin; S: Streptomycin; RA: Rifampin; CX: Cloxacillin; L/N: Lincomycin/Neomycin; TE: Tetracycline; AMC: Amoxicillin/ Clavulanic acid; P/NV: Penicillin/Novobiocin; N: Neomycin; SXT: Sulphamethoxazole/Trimethoprim; K: Kanamycin; AX: Amoxycillin; CAZ: Ceftazidime; TOB: Tobramycin; AK: Amikacin

erythromycin, amoxycillin and streptomycin (66.7%), lincomycin, kanamycin, ceftazidime, tobramycin and amikacin (33.3%) and amoxicillin / clavulanic acid (16.7 %) were observed.

All isolates exhibited resistance to at least five or more antimicrobial agents used and considered as multidrug resistant (MDR) (Table 5).

Discussion

Causes of most of food-borne diseases are commonly related to cross-contanmination caused by unsanitary food handling, contaminated raw material, inadequate cooking, heating and cooling as well as insufficient cleaning of food contact surfaces and manipulators hands (21). In this study, 2.8 % of samples found to be contaminated with *Salmonella*; 1(1%) grilled chicken, 4 (8.8%) food handlers' hand and 1 (2.5%) knife handle samples. *Salmonella* strains can be transmitted to the food chain by food-handler with asymptomatic disease, especially during catering practices (22, 23). It was noteworthy that among the six positive samples obtained from this study, 4 (66.6%) were isolated from maniplators hands. Food-handlers are reported to be the potential cause of serious outbreaks of food-borne diseases due to lack of hygiene knowledge (24). Food handlers, unconsciously and perhaps habitually touching their own body parts, can transfer pathogenic microorganism to food. Regarding

the food contact surfaces, in mass consumption places, one of the leading causes of foods contamination is reported to be peeling, slicing, shredding and chopping (25, 26, 27).

Although S. Typhimurium and S. Enteritidis are the most prevalent *Salmonella* serotypes in the global health arena with over 70% of human infections, (28, 29, 30) in our study, S. Newport, S. Infantis and S. Koessean Serovars were obtained. S. Newport was listed among the top ten serovars in human salmonellosis across the EU, causing 1.0% of all reported cases in 2015 (31). This change in serotype distribution noted in this study could be related to the implementation of several *Salmonella* control programmes including vaccination against S. Typhimurium and S. Enteritidis, which may have support new serotypes. These *Salmonella* diversities of different serotypes highlight the importance of periodic monitoring of this agent in food environments.

In the present study, the isolates indicated 100% resistance to penicillin/novobiocin, tetracycline, cloxacillin and rifampin. In addition, evident resistance to sulfamethoxazole/trimethoprim (83.3%), vancomycin, erythromycin, amoxycillin and streptomycin (66.7%) was observed. It was noteworthy that the resistance pattern of *Salmonella* Infantis and Koessen isolates from food handlers and grilled chicken, respectively were higher (50%) than Newport isolates in our study. Overall, we observed MDR among all *Salmonella* isolates with resistance to at least five or more antibiotics. The increase in the prevalence of MDR *Salmonella* could cause this pathogen to become a super bacteria (32) that cause public health concern. The circulation of MDR *Salmonella* strains in food environments not only complicate the control of the pathogen, but also contribute to the transmission of antimicrobial resistance to other *Enterobacteriaceae* (33). Our results, indicating frequent involvement of antibiotic-resistant *Salmonella* in food chain, underlines the necessity of the exploration of novel non-antibiotic interventions to combat against pathogens.

Among the DR genes tested in our study, *sugE* and *qacEΔ1* genes were detected from 33.3% of isolates (Table 4). *sugE* and *qacEΔ1* genes in *Salmonella* isolates have also been reported in previous studies (34, 35, 36, 37). Although *qacE*, is reported to be very common in gram-negative bacteria[13] none of the isolates tested in our study is found to harbour *qacE* gene. However, Fernandez Marquez et al. (36) detected *qacE* gene in 9.5% of *Salmonella* isolates. The development of disinfectant resistance in pathogenic bacteria is related to their common applications in human medicine and the food industry (38). The widespread use of disinfectants has led to their dissemination into the environment which could lead to bacterial adaptation and result in cross-resistance to antibacterial agents (39, 40). Likewise, hand and grilled chicken isolates found to harbour *sugE* and *qacEΔ1* genes and were MDR in our study. Similarly, Deng et al. (37) reported that 92.8% of 152 *Salmonella* isolates obtained from retail foods of animal origin were resistant to at least one antibiotic among which 8.6% contained *qacEΔ1*gene. Tetracycline and sulfonamide resistance genes (*tet*, *sul*) are reported to be highly correlated with disinfectant resistance genes of *qacF* and *qacEΔ1* (37).

In this study phylogenetic analysis revealed that Infantis (hand) and Koessen (grilled chicken) isolates were genetically identic. Furthermore, close genetic relationship between Newport strains obtained from hand and knife handle were observed, indicating food-handler to be the source of contamination. FDA recommends avoiding bare-hand contact to RTE food as washed hands still could transmit the pathogens to food or food environments (41).

Conclusion

This study demonstrates that food-handlers and food preparation equipments may serve as reservoirs for cross-resistant *Salmonella* in food chain. Increased tolerance to disinfectants could probably facilitate the survival of pathogenic organisms and contribute to the emergence of persistent strains. The increasing prevelance of disinfectant and MDR *Salmonella* strains isolated from food environments could pose potential risk for public health. Therefore, periodic food safety training programmes should effectively be implemented for food handlers and cross-resistant patogens should be monitored in food environments. As disinfectant tolerance could facilitate the antibiotic resistant strains in food related areas, attention should be paid while

selecting appropriate disinfectant for food preparing surfaces.

Acknowledgments: This research was supported by the University of Afyon Kocatepe, Project code of 16 VF 13.

Ethical Statement: This study was approved by the Afyon Kocatepe University Animal Ethics Committee (2016-49533702-68).

Conflict Of Interest: No potential conflict of interest relevant to this article was reported by the authors

References

1. Dao HTA, Yen PT. Study of *Salmonella*, *Campylobacter*, and *Escherichia coli* contamination in raw food available in factories, schools, and hospital canteens in Hanoi, Vietnam. Ann NY. Acad Sci 2006; 1081(1): 262–265.
2. Kirk MD, Pires SM, Black RE, et al. World Health Organization estimates of the global and regional disease burden of 22 foodborne bacterial, protozoal, and viral diseases, 2010: a data synthesis. PLoS Med 2015; 12(12): e1001921.
3. Langridge GC, Wain J, Nair S. Invasive salmonellosis in humans. Eco Sal Plus 2012; 5(1).
4. Bula-Rudas FJ, Rathore MH, Maraqa NF. *Salmonella* infections in childhood. Adv Pediatr 2015; 62(1): 29–58. https://doi.org/10.1016/j.yapd.2015.04.005.
5. Hawkey J, Edwards DJ, Dimovski K, et al. Evidence of microevolution of *Salmonella* Typhimurium during a series of egg-associated outbreaks linked to a single chicken farm. BMC Genomics 2013; 14(1): 1–15. https://doi.org/10.1186/1471-2164-14-800.
6. Padungtod P, Kadohira M, Hill G. Livestock production and foodborne diseases from food animals in Thailand. J Vet Med Sci 2008; 70(9): 873–879.
7. McKee SR, Townsend JC, Bilgili S.F. Use of a scald additive to reduce levels of *Salmonella* Typhimurium during poultry processing. Poult Sci J 2008; 87(8): 1672–1677.
8. Arguello H, Carvajal A, Collazos JA, García-Feliz C, Rubio P. Prevalence and serovars of *Salmonella* Enterica on pig carcasses, slaughtered pigs and the environment of four Spanish slaughterhouses. Food Res Int 2012; 45(2): 905–912.
9. Hernández M, Gómez-Laguna J, Luque, I, et al. *Salmonella* prevalence and characterization in a free-range pig processing plant: tracking in trucks, lairage, slaughter line and quartering. Int J Food Microbiol 2013; 162(1): 48–54.
10. Steenackers H, Hermans K, Vanderleyden J, De Keersmaecker SC. *Salmonella* biofilms: an overview on occurrence, structure, regulation and eradication. Food Res Int 2012; 45(2): 502–531.
11. Gerba CP. Quaternary ammonium biocides: efficacy in application. Appl Environ Microbiol 2015; 81(2): 464–469.
12. Zhang C, Cui F, Zeng GM, et al. Quaternary ammonium compounds (QACs): a review on occurrence, fate and toxicity in the environment. Sci. Total Environ 2015; 518: 352–362.
13. Morente EO, Fernández-Fuentes MA, Burgos MJG, Abriouel H, Pulido RP, Galvez A. Biocide tolerance in bacteria. Int J Food Microbiol 2013; 162(1): 13–25.
14. Sveum WH, Moberg LJ, Rude RA, Frank JF. Microbiological monitoring of the food processing environment. In: Vanderzant C, Splittstoesser DF (Ed): Compendium of methods for the microbiological examination of foods. 51–74. Public Health Association, Washington, 1992.
15. International Standard Organization (ISO) 6579, Microbiological of food and animal feeding stuffs-horizontal method for the detection of *Salmonella* spp. International Standards Organization. 1–50. Geneva, Switzerland, 2002.
16. Kalendar R, Lee D, Schulman AH. Fast PCR software for PCR primer and probe design and repeat search. G3 2009; 3(1): 1–14.
17. Hall TA. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. In Nucleic Acids Symp Ser 1999; 41: 95–98.
18. Tamura K, Dudley J, Nei M, Kumar S. MEGA4: molecular evolutionary genetics analysis (MEGA) software version 4.0. Mol Biol Evol 2007; 24(8): 1596–1599.
19. Bauer AW, Kirby WMM, Sherris JC, Turck M. Antibiotic susceptibility testing by a standardized single disc method. Am J Clin Pathol 1966; 45(4): 493–6.
20. Clinical and Laboratory Standards Institute (CLSI). Performance standards for antimicrobial susceptibility testing. Twentieth Informational Supplement, M100-S20, 2010.
21. World Health Organization (WHO). Food Hygiene, Food and Agriculture Organization. Pan European Conference on food safety and quality, Italy, 2002.
22. Birhaneselassie M, Williams D. A study of *Salmonella* carriage among asymptomatic food-handlers in southern Ethiopia. Int J Nutr Food Sci 2013; 2(5): 243–245.https://doi: 10.11648/j.ijnfs.20130205.15
23. Woh PY, Thong KL, Behnke JM, Lewis JW, Zain SNM. Characterization of nontyphoidal *Salmonella i*solates from asymptomatic migrant food handlers in Peninsular Malaysia. J Food Prot 2017; 80(8): 1378–1383.
24. Santos M, Nogueira JR, Patarata L, Mayan O. Knowledge levels of food handlers in Portuguese school canteens and their self-reported behavior towards food safety. Int J Environ Health Res 2008; 18(6): 387–401.
25. Wirtanen G, Storgards E, Mattila-Sandholm T. Biofilms. In: Caballero B, Trugo L, Finglas P. (Ed): Encyclopedia of Food Sciences and Nutrition. 484–9. Academic Press, London, 2003.
26. Santana NG, Almeida RC, Ferreira JS, Almeida PF. Microbiological quality and safety of meals served to children and adoption of good manufacturing practices in public school catering in Brazil. Food Control 2009; 20(3): 255–261.

27. Nyenje ME, Odjadjare CE, Tanih NF, Green E, Ndip RN. Foodborne pathogens recovered from ready-to-eat foods from roadside cafeterias and retail outlets in Alice, Eastern Cape Province, South Africa: public health implications. Int J Environ Res Public Health 2012; 9(8): 2608-2619.
28. Velhner M, Potkonjak D, Stojanov I, Stojanović D, Petrović J, Kozoderović G. *Salmonella* control in poultry production and resistance monitoring in Serbia. Arch. Vet Sci 2011; 4(2): 11–22.
29. Campos J, Pichel M, Vaz TMI, et al. Building PulseNet Latin America and Caribbean Salmonella regional database: First conclusions of genetic subtypes of S. Typhi, S. Typhimurium and S. Enteritidis circulating in six countries of the region. Food Res Int 2012; 45(2): 1030–1036.
30. Luvsansharav UO, Vieira A, Bennett S, et al. *Salmonella* serotypes: A novel measure of association with foodborne transmission. Foodborne Pathog Dis 2020; 17(2): 151–155.
31. European Food Safety Authority, & European Centre for Disease Prevention and Control (EFSA). The European Union summary report on trends and sources of zoonoses, zoonotic agents and food-borne outbreaks in 2015. EFSA J 2016; 14(12): e04634.
32. Campioni F, Zoldan MM, Falcao JP. Characterization of *Salmonella* Enteritidis strains isolated from poultry and farm environments in Brazil. Epidemiol Infect 2014; 142(7): 1403–1410.
33. Davies R, Wales A. Antimicrobial resistance on farms: a review including biosecurity and the potential role of disinfectants in resistance selection. Compr Rev Food Sci Food Saf 2019; 18(3): 753–774.
34. Chuanchuen R, Khemtong S, Padungtod P. Occurrence of qacE/qacED1 genes and their correlation with class 1 integrons in *Salmonella* enterica isolates from poultry and swine. Southeast Asian J Trop Med Public Health 2007; 38: 855–862.
35. Long M, Lai H, Deng W, et al. Disinfectant susceptibility of different *Salmonella* serotypes isolated from chicken and egg production chains. J Appl Microbiol 2016; 121(3): 672–681.
36. Fernandez Marquez, ML, Burgos MJG, Pulido RP, Gálvez A, López RL. Biocide tolerance and antibiotic resistance in Salmonella isolates from hen eggshells. Foodborne Pathog Dis 2017; 14(2): 89–95. https://doi.org/10.1089/fpd.2016.2182.
37. Deng W, Quan Y, Yang S, et al. Antibiotic resistance in Salmonella from retail foods of animal origin and its association with disinfectant and heavy metal resistance. Microb Drug Resist 2018; 24(6): 782–791. https://doi.org/10.1089/mdr.2017.0127
38. Donaghy JA, Jagadeesan B, Goodburn K, et al. Relationship of sanitizers, disinfectants, and cleaning agents with antimicrobial resistance. J. Food Prot 2019; 82(5): 889–902.
39. Knapp L, Amézquita A, McClure P, Stewart S, Maillard JY. Development of a protocol for predicting bacterial resistance to microbicides. Appl. Environ. Microbiol 2015; 81(8): 2652–2659.
40. Paul D, Chakraborty R, Mandal SM. Biocides and healthcare agents are more than just antibiotics: Inducing cross to co-resistance in microbes. Ecotoxicol Environ Saf 2019; 174: 601–610.
41. Food and Drug Administration (FDA). Report of the FDA Retail Food Program Database of Foodborne Illness Risk Factors. US Food and Drug Administration, Center for Food Safety and Applied Nutrition, Washington DC, 2000.

Correspondence:
Şebnem Pamuk
Phone: +90 272 2182708
Fax: +90 272 2281422
E-mail: spamuk@aku.edu.tr
ORCID: 0000-0001-7227-3364