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Occurrence and molecular characterization of *Salmonella* Typhimurium and *Salmonella* Enteritidis isolates from contaminated food samples from Palestine

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ABSTRACT: *Salmonella* is one of the most frequently isolated foodborne pathogens. It is of major public health concern worldwide. Poultry meat and eggs represent important sources of Salmonellae organisms with an impact on consumers' health. This study aims to evaluate the occurrence of *Salmonella* Typhimurium and *Salmonella* Enteritidis using multiplex PCR (mPCR) among isolates collected from samples of the local food market and to assess genetic relationships between isolates of *S. Typhimurium*, which was the only serotype isolated from the tested food samples. This was achieved using virulence factors profiling and fingerprint profiling, which were assessed by random amplified polymorphic DNA (RAPD-PCR) and repetitive sequence PCR (REP-PCR). Both enterobacterial repetitive intergenic consensus (ERIC-PCR) and interspersed repetitive DNA sequence BOXAIR-PCR were used for this purpose. The overall occurrence percentage of *S. Typhimurium* and *S. Enteritidis* out of 51 isolates was 54.9% and 0.0%, respectively. Only 13 out of 17 virulence genes were detected in these isolates. The occurrence of the detected virulence genes among these isolates was 100%, 50.0%, 46.4%, 39.3%, 35.7%, 35.7%, 32.1%, 25.0%, 25.0%, 17.6%, 14.3%, 14.3%, 3.6% for *invA*, *sopB*, *prgH*, *sitC*, *pefA*, *tolC*, *cdtB*, *msgA*, *sifA*, *iroN*, *spiA*, *ipfC* and *pagC*, respectively. The remaining virulence genes were absent in all of the isolates. Based on the combination of the presence and absence of virulence genes, eight profiles were detected among these isolates, the most common genetic profile was V5 (each 32.1%). Based on this genetic profile at cut-off point 96.0%, both ERIC and BOX primers allowed for discrimination into 4 and 6 clusters or clones of 16 *S. Typhimurium* isolates, respectively. Results of PCR typing methods showed that, three strains clustered together using both ERIC-PCR and BOX-PCR typing methods and they had the same virulotype (V1), while other four strains also clustered together by both typing methods and had the same virulotype (V4). Contamination of food with Salmonellae, especially with *S. Typhimurium*, was high and affected the microbiological quality of food. This emphasizes the need for rigorous public health and food safety control methods to lower the human health hazard and risk associated with Salmonellae infection.

Keywords: foodborne pathogens, *Salmonella* Typhimurium, *Salmonella* Enteritidis, molecular characterization, Palestine.

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INTRODUCTION

Foodborne microorganisms are major pathogens affecting food safety and causing human illness worldwide. These foodborne infections and intoxications result from the consumption of various food-stuffs, mainly contaminated animal products. Most of these food-borne pathogens have zoonotic nature, resulting in a significant impact on both human public health and the economic sector (Abebe et al., 2020). In the developed countries, the annual incidence of foodborne illnesses is estimated to be around 30.0% of the population (De Giusti et al., 2007).

According to the WHO, *Salmonella* spp. are among the 31 pathogenic agents showing the highest ability of provoking intestinal or systemic disease in humans among diarrheal and/or invasive pathogens, and the third causative agent of death among food-borne diseases (Ferrari et al., 2019). Salmonellosis is an important zoonotic infection seen in all animal species (Seifi et al., 2019). It is considered the second major cause of food-borne diseases worldwide (Jeníková et al., 2000; Scallan et al., 2011; EFSA 2019; Abuseir et al., 2020). Non-typhoid *Salmonella* accounts for 93.8 million foodborne infections and 155,000 deaths per year (Eng et al., 2015).

Salmonella enterica serotype Typhimurium (*S. Typhimurium*), *S. Enteritidis*, *S. Heidelberg*, and *S. Newport* are epidemiologically important non-typhoidal *Salmonella* serotypes, which have been responsible for the majority of human *Salmonella* disease-burden worldwide (Jajere, 2019). In the European Union, the second most frequently involved bacterial genus in gastrointestinal outbreaks in humans is *Salmonella* and more particularly the subspecies *S. Enteritidis* and *S. Typhimurium* (Paniel and Noguera, 2019). Contaminated poultry products such as meat and eggs continue to play a central role in spreading the infection of the *S. Enteritidis* and *S. Typhimurium* serovars to humans (Tarabees et al., 2017; Ferrari et al., 2019;

Paniel and Noguera, 2019; Wang et al., 2019).

Among more than 2,500 serovars of *Salmonella enterica*, *S. Typhimurium* was also one of the most frequently isolated serovars worldwide (Medeiros et al., 2015), and it is one of the leading serovars that cause salmonellosis globally (Medeiros et al., 2015).

In 2015, *S. Enteritidis* was representing 45.7% of all reported serovars in confirmed human cases (EFSA 2016) and accounted for 57.9% of all *Salmonella* outbreaks and 48.7% of human cases in all *Salmonella* outbreaks in the EU countries (EFSA 2021).

Salmonella spp. can establish an infection and cause illness through the expression of several virulence genes that interact with host cells (Elemfareji and Thong, 2013; Borges et al., 2013; Mezal et al., 2014; Rowlands et al., 2014; Gharieb et al., 2015; Tarabees et al., 2017; Srisanga et al., 2017; Thung et al., 2018; Liaquat et al., 2018; Elkenany et al., 2019). Virulence genes play a very important role in the broad spectrum of pathogenic mechanisms. These mechanisms include invasion, adhesion, toxin production, systemic infection, antibiotic resistance, fimbrial expression, intracellular survival, and iron and Mg²⁺ uptake (Hensel, 2004). The genes *prgH*, *invA*, *spaN* (*invJ*), *spiA*, *tolC*, *orgA*, *sipB*, *pagC*, *pefA*, *msgA*, *sopB*, *spvB*, *lpfC* and *sifA* are expressed to produce certain proteins associated with invasiveness traits, such as cellular invasion/survival and adhesion or pili production. Other genes encode certain proteins thought to be very important virulence factors. These factors include *iroN* and *sitC*, which are involved in iron acquisition, and *cdtB* gene, a putative toxin-encoding gene (Skyberg et al., 2006). The function of these virulence factors are presented in table 1.

The main aim of this study was to estimate the occurrence of the main *Salmonella* strains found in food samples, namely *S. Typhimurium* and *S. Enteritidis*. In addition, the fingerprinting of the main strain,

Table 1. Function of virulence factors of *Salmonellae* used in this study in virulence genotyping (Skyberg et al., 2006).

Virulence factor	Virulence-related function
<i>invA</i> , <i>orgA</i> , <i>prgH</i> , <i>tolC</i> , <i>sopB</i> , <i>lpfC</i> , <i>cdtB</i> , <i>pefA</i>	Host recognition/invasion
<i>spaN</i>	Entry into non-phagocytic cells, killing of macrophages
<i>sipB</i>	Entry into non-phagocytic cells, killing of macrophages
<i>iroN</i> , <i>sitC</i>	Iron acquisition
<i>pagC</i> , <i>msgA</i> , <i>spiA</i>	Survival within macrophage
<i>sifA</i>	Filamentous structure formation
<i>spvB</i>	Growth within-host

recovered by random amplified polymorphic DNA (RAPD-PCR) and repetitive sequence PCR (REP-PCR) using enterobacterial repetitive intergenic consensus (ERIC-PCR) and interspersed repetitive DNA sequence BOXAIR-PCR primers was accomplished. The genetic relationships between the strains, and the pathogenic potential of the recovered isolates were assessed by using virulotyping PCR assay, targeting 17 virulence gene sequences.

MATERIALS AND METHODS

Samples collection

A total of 51 *Salmonella* isolates were recovered from different types of food samples, which were collected from the local retail market in different governorates and areas in the West Bank, Palestine during 2019. These samples were fresh chicken meat (24), Kebab (1), fresh turkey meat (3), cheese (1), beef burger (11), Hummus (1), Parsley (1), Tahini (4), restaurant's salad (1), Halawa (1), fish-Fillet (1) and beef meat (2). All *Salmonella* isolates were collected and identified by the Analysis, Poison Control and Calibration Center, An-Najah National University, and the Central Laboratories, Ministry of Health, Palestine. Identification of these isolates was done according to ISO 6579-1: 2017, by conventional methods using enrichment, selective and differential media, Gram staining, and biochemical tests. All cultures that were negative for Lactose/Sucrose, positive for Glucose, produce H₂S, and motile were kept for serological confirmation. The serological confirmation used is genus-specific, to confirm the *Salmonella* isolates. The positive isolates were stored at -70°C.

DNA extraction

DNA of *Salmonella* isolates was prepared for PCR according to the method described previously (Adwan et al., 2013). The concentration of the DNA sample was determined using a nanodrop spectrophotometer (Genova Nano, Jenway), and the DNA samples were

stored at -20°C for further analysis.

Salmonella spp. confirmation and *S. Typhimurium* and *S. Enteritidis* identification by multiplex PCR (mPCR)

For mPCR detection, three primer pairs were used to identify specific target genes, including *invA* for *Salmonella* spp. identification, *STMO159* for *S. Typhimurium* identification, and *SEN1383* for *S. Enteritidis* identification. Target gene, primer sequence; and amplicon size for these primer pairs are presented in table 2.

The mPCR reaction mix was carried according to the method described previously (Ranjbar et al., 2017). A final volume of 25 µl PCR reaction mix was performed as follows: 12.5 µl of PCR premix (Ready-Mix™ Taq PCR Reaction Mix with MgCl₂, Sigma), 0.3 µM of each primer and 3 µl (50-70 ng) of target DNA template. DNA amplification was carried out using a thermal cycler (Mastercycler Personal, Eppendorf, Germany) according to the following conditions: initial denaturation at 94°C for 3 min; followed by 30 cycles of denaturation at 94°C for 1 min, annealing at 57°C for 1 min and extension at 72°C for 1 min. Then, these cycles were followed by a single final extension step at 72°C for 5 min. The PCR amplicons were then detected by electrophoresis through 1.5% agarose gels to determine the size of amplicons after staining with a final concentration of 0.5 µg/ml of ethidium bromide dye. The sizes of the PCR products were determined by comparing them with a 100-bp DNA ladder. Live attenuated vaccines for *S. Typhimurium* and *S. Enteritidis* (Biovac Company), were used as positive controls and *E. coli* ATCC 25922 strain was used as a negative control.

Molecular typing by ERIC-PCR and BOX-AIR-PCR

S. Typhimurium isolates that were the only *Salmonella* strain recovered from different food samples in

Table 2. Oligonucleotide primers used for *Salmonella* spp. confirmation, *S. Typhimurium*, and *S. Enteritidis* detection.

Target gene	Primer Sequence 5'→3'	Amplicon size (bp)	Reference
<i>invA</i> - secretory protein (<i>Salmonella</i> spp.)	<i>invA</i> F: GTATTGTTGATTAATGAGATCCG <i>invA</i> R: ATATTACGCACGGAAACACGTT	404	Ranjbar et al., 2017
<i>SEN1383</i> -a hypothetical protein (<i>S. Enteritidis</i>)	<i>SEN1383</i> F: TGTGTTTTATCTGATGCAAGAGG <i>SEN1383</i> R: TGAACACGTTTCGTTCTTCTGG'	304	Ranjbar et al., 2017
<i>STMO159</i> -a putative restriction endonuclease (<i>S. Typhimurium</i>)	<i>STMO159</i> F: ATGATGCCTTTTGCTGCTTT' <i>STMO159</i> R: TCCCAGCTCATCCAAAAA	224	Ranjbar et al., 2017

this study were fingerprinted to assess genetic relationships between the strains of *S. Typhimurium* from different sources, using ERIC-PCR primers and interspersed repetitive DNA sequence (BOX) primers as shown in table 3.

Each PCR reaction mix (25 µl) was composed of 10 mM PCR buffer pH 8.3, 3 mM MgCl₂, 0.4 mM of each dNTP, 0.8 µM of each primer, 1.5 U of Taq DNA polymerase and 3 µl of DNA template. The DNA amplification for ERIC-PCR was carried out using a thermal cycler (Master-cycler Personal, Eppendorf, Germany) according to the following conditions: initial denaturation for 2 min at 94°C, followed by 40 cycles of denaturation at 94°C for 50 s, annealing at 50°C for 40 s and extension at 72°C for 1 min. Then, these cycles were followed with a final extension step at 72°C for 5 min. For BOXAIR-PCR, the thermal conditions were: initial denaturation at 94°C for 2 min, followed by 30 cycles of denaturation at 94°C for 50 s, annealing at 50°C for 40 s and extension at 72°C for 2 min. After that, these cycles were followed with a final extension step at 72°C for 5 min.

The PCR products were analyzed by electrophoresis on 1.5% agarose gels. The bands in gel images were analyzed using a binary scoring system, which recorded the absence and presence of bands as 0 and 1, respectively. The binary matrix was analyzed by the unweight pair group method for arithmetic averages (UPGMA), using SPSS statistical software version 20 (IBM). The clusters of the fingerprints in the constructed dendrogram were described at a 96% similarity level. The number of different bands in each fingerprint was considered for comparison between *S. Typhimurium* strains as previously described (Adwan et al., 2016; Adwan et al., 2016; Adwan and Rabaya, 2016; Adwan and Haya, 2018), based on the following criteria: identical clones (no different bands), “closely related clones” (have 1 different band), “possibility different clones” (have two different bands), “different clones” (have three or more different bands).

Molecular typing by RAPD-PCR

Recovered *S. Typhimurium* isolates were fingerprinted by RAPD-PCR using the RAPD primer OPP-16 (Table 3) to assess genetic relationships between the strains of *S. Typhimurium* from these sources (Albufera et al. 2009).

RAPD-PCR was carried as described previously with some modification (Hashemi and Baghbani-Arani, 2015). PCR reaction mix was carried out as in ERIC-PCR mix and BOXAIR-PCR mix. DNA amplification for RAPD-PCR was carried out using a thermal cycler (Mastercycler Personal, Eppendorf, Germany) according to the following thermal conditions: initial denaturation for 3 min at 94°C, followed by 40 cycles of denaturation at 94°C for 1 min, annealing at 35°C for 1 min and extension at 72°C for 2 min. Then, these cycles were followed with a final extension step at 72°C for 5 min. The PCR products were analyzed as well as the ERIC-PCR, and BOXAIR-PCR.

Virulotyping of *S. Typhimurium* isolates by mPCR

Three mPCR reactions were used to amplify the seventeen virulence genes. Pools of reaction, target gene, primer sequence, amplicon size for these primers are presented in table 4.

The mPCR was carried as described previously with some modification (Skyberg et al., 2006). Each PCR reaction mix (25 µl) was composed of 10 mM PCR buffer pH 8.3, 6 mM MgCl₂, 0.3 mM of each dNTP, 0.3 µM of each primer, 1.5 U of Taq DNA polymerase, 3% DMSO, and 3 µl of target DNA template. DNA amplification for mPCR was carried out using a thermal cycler (Master-cycler Personal, Eppendorf, Germany) according to the following thermal conditions: initial denaturation for 3 min at 94°C, followed by 25 cycles of denaturation at 94°C for 40 s, annealing at 62°C for 40 s and extension at 72°C for 2 min. After that, these cycles were followed with a

Table 3. The primers for ERIC-PCR, BOXAIR-PCR and RAPD-PCR used in this study.

Target gene	Primer Sequence 5'→3'	Reference
Enterobacterial repetitive intergenic consensus (ERIC)	ERIC1: ATGTAAGCTCCTGGGGATTAC ERIC2: AAGTAAGTGACTGGGGTGAGC G	Fendri et al., 2013
Interspersed repetitive DNA sequence (BOX)	BOXAIR: CTACGGCAAGGCGACGCTGACG	Dombek et al., 2000 Hashemi and Baghbani-Arani, 2015
Random amplified polymorphic DNA (RAPD-PCR)	OPP-16: CCAAGCTGC C	Albufera et al., 2009

Table 4. Virulence gene primers used in this study (Skyberg et al., 2006).

Target gene	Primer sequence (5'→3')	Amplicon size (bp)	pool
<i>spvB</i>	spvB F: CTA TCA GCC CCG CAC GGA GAG CAG TTT TTA	717	1
	spvB R: GGA GGA GGC GGT GGC GGT GGC ATC ATA		
<i>spiA</i>	spiA F: CCA GGG GTC GTT AGT GTA TTG CGT GAG ATG	550	1
	spiA R: CGC GTA ACA AAG AAC CCG TAG TGA TGG ATT		
<i>pagC</i>	pagC F: CGC CTT TTC CGT GGG GTA TGC	454	1
	pagC R: GAA GCC GTT TAT TTT TGT AGA GGA GAT GTT		
<i>cdtB</i>	cdtB F: ACA ACT GTC GCA TCT CGC CCC GTC ATT	268	1
	cdtB R: CAA TTT GCG TGG GTT CTG TAG GTG CGA GT		
<i>msgA</i>	msgA F: GCC AGG CGC ACG CGA AAT CAT CC	189	1
	msgA R: GCG ACC AGC CAC ATA TCA GCC TCT TCA AAC		
<i>invA</i>	invA F: CTG GCG GTG GGT TTT GTT GTC TTC TCT ATT	1070	2
	invA R: GTT TCT CCC CCT CTT CAT GCG TTA CCC		
<i>sipB</i>	sipB F: GGA CGC CGC CCG GGA AAA ACT CTC	875	2
	sipB R: ACA CTC CCG TCG CCG CCT TCA CAA		
<i>prgH</i>	prgH F: GCC CGA GCA GCC TGA GAA GTT AGA AA	756	2
	prgH R: TGA AAT GAG CGC CCC TTG AGC CAG TC		
<i>spaN</i>	Span F: AAA AGC CGT GGA ATC CGT TAG TGA AGT	504	2
	span R: CAG CGC TGG GGA TTA CCG TTT TG		
<i>orgA</i>	orgA F: TTT TTG GCA ATG CAT CAG GGA ACA	255	2
	orgA R: GGC GAA AGC GGG GAC GGT ATT		
<i>tolC</i>	tolC F: TAC CCA GGC GCA AAA AGA GGC TAT C	161	2
	tolC R: CCG CGT TAT CCA GGT TGT TGC		
<i>iroN</i>	Iron F: ACT GGC ACG GCT CGC TGT CGC TCT AT	1205	3
	iron R: CGC TTT ACC GCC GTT CTG CCA CTG C		
<i>sitC</i>	sitC F: CAG TAT ATG CTC AAC GCG ATG TGG GTC TCC	768	3
	sitC R: CGG GGC GAA AAT AAA GGC TGT GAT GAA C		
<i>lpfC</i>	lpfC F: GCC CCG CCT GAA GCC TGT GTT GC	641	3
	lpfC R: AGG TCG CCG CTG TTT GAG GTT GGA TA		
<i>sifA</i>	sifA F: TTT GCC GAA CGC GCC CCC ACA CG	449	3
	sifA R: GTT GCC TTT TCT TGC GCT TTC CAC CCA TC		
<i>sopB</i>	sopB F: CGG ACC GGC CAG CAA CAA AAC AAG AAG AAG	220	3
	sopB R: TAG TGA TGC CCG TTA TGC GTG AGT GTA TT		
<i>pefA</i>	pefA F: GCG CCG CTC AGC CGA ACC AG	157	3
	pefA R: GCA GCA GAA GCC CAG GAA ACA GTG		

final extension step at 72°C for 5 min. The PCR products were then detected by electrophoresis through 1.5% agarose gels to determine the size of amplified fragments after staining with a final concentration of 0.5 µg/ml of ethidium bromide dye. The sizes of the amplicons of these genes were determined by comparing them with a 100-bp DNA ladder.

RESULTS

Salmonella spp. confirmation and *S. Typhimurium* and *S. Enteritidis* detection

All *Salmonella* isolates were subjected to mPCR using specific primers to confirm that these isolates belonged to a *Salmonella* genus and to determine the occurrence of *S. Typhimurium* and *S. Enteritidis* serotypes among these isolates. PCR confirmation of

conventional and serological methods positive strains was documented by the appearance of the amplified DNA fragment of 404-bp for the *invA* gene, a target for *Salmonella* genus, in all 51 (100%) *Salmonella* isolates examined and confirmed. In addition, 28 (54.9%) isolates were *S. Typhimurium* serotype and produced amplified DNA fragment of 224-bp for *STMO159* gene (a putative restriction endonuclease), while amplified DNA fragment of 304-bp for *SEN1383* gene (a hypothetical protein) for *S. Enteritidis* serotype was not detected among the *Salmonella* isolates. Multiplex PCR profile specific for genes responsible for detection of *Salmonella* genus (*invA* gene; 404-bp), *S. Typhimurium* serotype (*STMO159* gene; 224-bp), and *S. Enteritidis* serotype (*SEN1383* gene; 304-bp) is shown in figure 1.

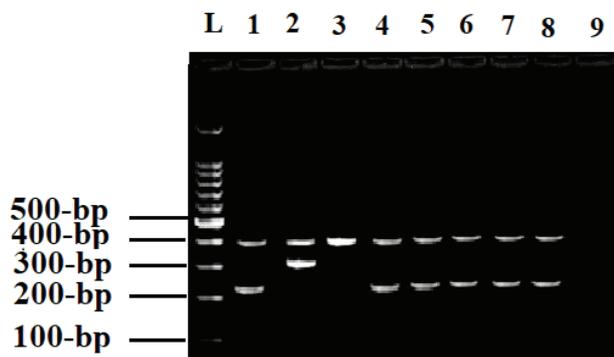


Fig. 1: Multiplex PCR profile specific for genes responsible for detection isolates of *Salmonella* genus, (*invA* gene; 404-bp) *S. Typhimurium* serotype (STMO159; 224-bp) and *S. Enteritidis* (SEN1383; 304-bp). Lanes: L represents 100 bp ladder, lanes 4, 5, 6, 7 and 8 represent *S. Typhimurium* serotype, lane 3 represents *Salmonella* genus, lane 9 represents *E. coli* as a negative control; Lanes 1 and 2 represent live attenuated vaccine strains for *S. Typhimurium* and *S. Enteritidis* serotypes (Biovac Company) as a positive control, respectively.

Virulotyping of *S. Typhimurium* serotype isolates by mPCR

As shown in table 5, only 13 genes among the targeted 17 genes were detected in the 28 *S. Typhimurium* isolates. The occurrence of the detected genes among these isolates was 100%, 50.0%, 46.4%, 39.3%, 35.7%, 35.7%, 32.1%, 25.0%, 25.0%, 17.6%,

14.3%, 14.3%, 3.6% for *invA*, *sopB*, *prgH*, *sitC*, *pefA*, *tolC*, *cdtB*, *msgA*, *sifA*, *iroN*, *spiA*, *ipfC* and *pagC*, respectively. The remaining virulence genes (*spvB*, *sipB*, *spaN* and *orgA*) were absent from all *S. Typhimurium* isolates.

Table 5. Presence and occurrence percentage of the virulence genes in the 28 *S. Typhimurium* isolates.

Present genes	Occurrence %	Absent genes
<i>spiA</i>	14.3%	<i>spvB</i>
<i>pagC</i>	3.6%	<i>spaN</i>
<i>cdtB</i>	32.1%	<i>orgA</i>
<i>msgA</i>	25.0%	<i>sipB</i>
<i>invA</i>	100%	
<i>prgH</i>	46.4%	
<i>tolC</i>	35.7%	
<i>iroN</i>	17.6%	
<i>sitC</i>	39.3%	
<i>ipfC</i>	14.3%	
<i>sifA</i>	25.0%	
<i>sopB</i>	50.0%	
<i>pefA</i>	35.7%	

Based on the combination of presence and absence of virulence genes, 7 profiles were detected among these isolates, the most common genetic profile was V5 (each 32.1%). Figure 2 and table 6 showed the data about virulence gene profiles detected in this study.

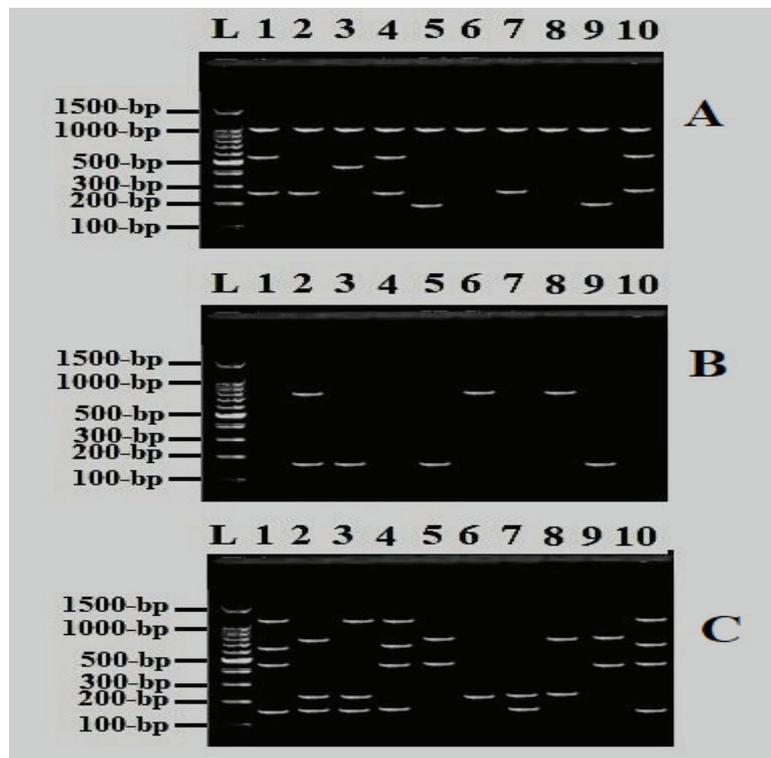


Fig. 2: Multiplex PCR profiles specific for *S. Typhimurium* virulence factors. Figure A: *spiA* gene (550-bp), *pagC* gene (454-bp), *cdtB* gene (268-bp) and *msgA* gene (189-bp). Figure B: *prgH* gene (756-bp) and *tolC* gene (161-bp). Figure C: *iroN* gene (1205-bp), *sitC* gene (768-bp), *ipfC* gene (641-bp), *sifA* gene (449-bp), *sopB* gene (220-bp) and *pefA* gene (157-bp).

Table 6. Virulence gene profile of the 28 *S. Typhimurium* isolated from different types of food samples

Virulotypes (V)	Gene combinations	No. of strains (%)
V1	<i>invA, spiA, cdtB, iroN, ipfC, sifA, pefA</i>	4 (14.3)
V2	<i>invA, cdtB, prgH, tolC, sitC, sopB, pefA</i>	2 (7.1)
V3	<i>invA, pagC, tolC, iroN, sopB, pefA</i>	1 (3.6)
V4	<i>invA, msgA, tolC, sitC, sifA</i>	7 (25.0)
V5	<i>invA, prgH, sopB</i>	9 (32.1)
V6	<i>invA, cdtB, sopB, pefA</i>	3 (10.7)
V7	<i>invA, prgH, sitC, sopB</i>	2 (7.1)

Genotyping of *S. Typhimurium* serotype by PCR-based methods

In the present study, ERIC and BOX primers allowed for discrimination into 4 and 6 clusters or clones of 16 *S. Typhimurium* serotype isolates respectively, based on their genetic profile at a cut-off point of 96.0%.

RAPD-PCR using the RAPD primer OPP-16 did not allow for discrimination between *S. Typhimurium* isolates, as it did not produce any amplified fragments

during PCR amplification.

According to the ERIC-PCR profile, strains of cluster C1 and C2, C3 and C4, and C3 and C2 are closely related clones. Strains of C4 and C1, and C3 and C1 are different clones, while strains of C4 and C2 are possibly different clones. ERIC-PCR DNA fingerprint pattern, dendrogram, and the relationship between the clones of 16 *S. Typhimurium* strains recovered from different food samples are presented in figure 3 and table 7.

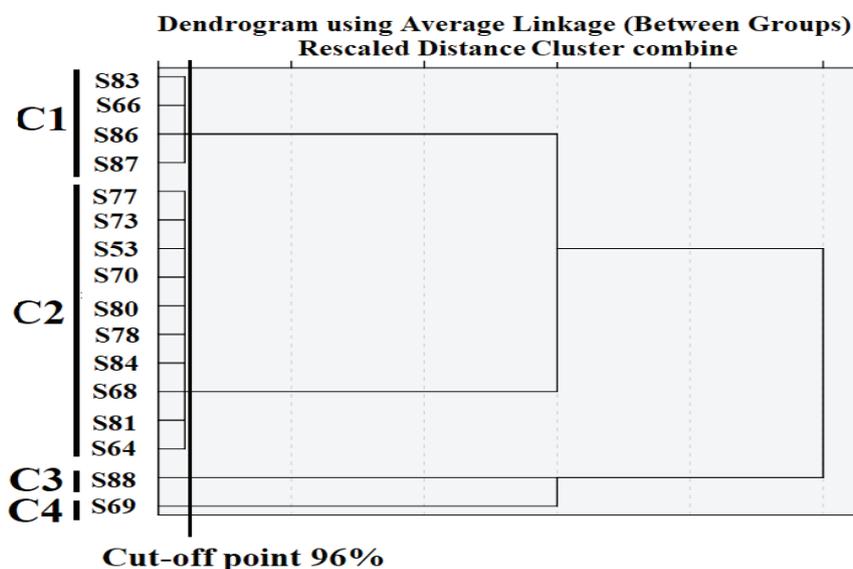


Fig. 3: Dendrogram of 16 *S. Typhimurium* serotype isolates based on the UPGMA method using the average group linkage/squared Euclidean distance by SPSS software version 20 derived from analysis of the ERIC-PCR-profiles at a 96.0% similarity level. C: Cluster.

Table 7. Relationship between the clones or the clusters depending on the number of different bands based on ERIC-PCR profile of 16 *S. Typhimurium* serotype isolates.

Cluster or clone	Cluster relationship			
	C1	C2	C3	C4
C1	1	2	4	4
C2		1	2	3
C3			1	2
C4				1

1: Identical clones. 2: Closely related clones. 3: Possibility different clones. 4: Different clones.

C: cluster or clone.

According to the BOX-PCR profile, strains of cluster C1 and C2, C3 and C4, C4 and C5, and C4 and C6 are closely related clones. Strains of cluster C2 and C3, C5 and C2, C5 and C3, C6 and C2, C6 and C3, and C6 and C5 are possibility different clones, while strains of C3 and C1, C4 and C1, C4 and C2, C5 and C1, and C6 and C1 are different clones. BOX-PCR DNA fingerprint pattern, dendrogram, and the relationship between the clusters or clones of 16 *S. Typhimurium* serotype isolates recovered from different food samples are presented in figure 4 and table 8.

Results of PCR typing methods showed that strain S83 (isolated from chicken wings) and strains S86 and S87 (isolated from chicken) are clustered together using both ERIC-PCR and BOX-PCR typing methods and they had the same virulotype pattern (V1). How-

ever, strains S78 and S80 (isolated from beef burger) and strains S53 and S73 (isolated from chicken) also clustered together by both typing methods and had the same virulotype pattern (V4).

DISCUSSION

Salmonellosis remains a significant public health problem causing food poisoning in humans. Contamination with *Salmonella* in food products can occur at multiple steps along the food chain, including production, processing, distribution, retail marketing, handling, and preparation (Tarabees et al., 2017), and monitoring of *Salmonella* spp. along all these steps in food chain should be conducted (EFSA 2018).

The current study supported the ability of specific primer sets to detect *invA* gene which confirms the

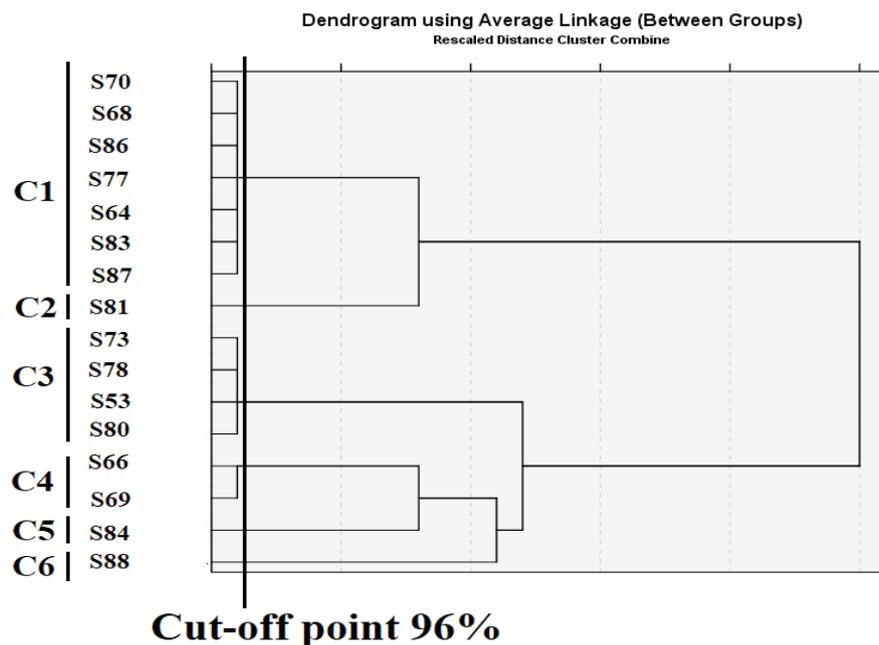


Fig. 4: Dendrogram of 16 *S. Typhimurium* serotype isolates based on the UPGMA method using average group linkage/squared Euclidean distance by SPSS software version 20 derived from analysis of the BOX-PCR-profiles at a 96% similarity level. C: Cluster.

Table 8. Relationship between the clones or the clusters depending on the number of different bands based on BOX-PCR profile of 16 *S. Typhimurium* serotype isolates.

Cluster or clone	Cluster relationship					
	C1	C2	C3	C4	C5	C6
C1	1	2	4	4	4	4
C2		1	3	4	3	3
C3			1	2	3	3
C4				1	2	2
C5					1	3
C6						1

1: Identical clones. 2: Closely related clones. 3: Possibility different clones. 4: Different clones.

C: cluster or clone.

isolates as *Salmonella* spp. The protein encoded by the *invA* gene is essential for the invasion of host epithelial cells (Darwin and Miller, 1999). Several studies had also proven the effective detection of all *Salmonella* isolates using specific primers for the *invA* gene (Helmy et al., 2009; Moussa et al., 2010; Shanmugasamy et al., 2011; Borges et al., 2013; Ammar et al., 2016; Ranjbar et al., 2017; Srisanga et al., 2017; Proroga et al., 2018), which was used as a target gene in PCR assays and a confirmatory test for *Salmonella* detection.

The use of PCR protocols for the recognition and the identification of *S. Typhimurium* and *S. Enteritidis* can be used as an alternative method to the conventional serotyping method according to ISO 6579-3:2014 that is highly expensive and time consuming.

Despite the results of many research work showing that *S. Enteritidis* was the main *Salmonella* serotypes isolated from food samples (El-Baz et al., 2017; Moussa et al., 2010; EFSA 2018; Magwedere et al., 2015), results of this research study showed that *S. Typhimurium* was the prevalent among the isolates, and no *S. Enteritidis* samples were detected. These results are similar to the results of other research work conducted on the prevalence of the main *Salmonella* serotypes in food samples (Abuseir et al., 2020; Ammar et al., 2016).

The previous studies and others may also indicate that *Salmonella* serovars vary geographically. *S. Enteritidis* and *S. Typhimurium* were considered the most common serovars recorded and clinically significant (EFSA 2015; Ammar et al., 2016). The differences in occurrence rates of *Salmonella* serotypes may be affected by different factors such as differences in the sampling method, sample types, *Salmonella* detection protocol, geographic region, and the housing and husbandry conditions (Busani et al., 2005; Nouichi et al., 2018).

Results of this study showed that using more than one molecular method is useful in epidemiological studies. Both ERIC and BOX primers allowed for discrimination into 4 and 6 clusters or clones of 16 *S. Typhimurium* isolates, respectively, based on their genetic profile at cut-off point 96.0%. RAPD-PCR using the RAPD primer OPP-16 did not allow for discrimination between *S. Typhimurium* isolates. On the other hand, a study conducted in Colombia (Lozano-Villegas et al., 2019) revealed that genotyping of *Salmonella* spp. using RAPD primers allowed the typing of

34 of 49 strains of *Salmonella* spp. The best discriminatory index was observed when GTG 5 (0.92) and OPP 16 (0.85) primers were used alone or combined with RAPD-PCR and BOX-PCR (0.99).

PCR-based fingerprinting methods are considered as a simple and easily applicable typing technique and potentially available to any molecular laboratory. It was suggested that RAPD, ERIC-PCR, REP-PCR, BOXAIR-PCR are good discriminatory techniques to type the different clinical *Salmonella* isolates and these methods are sufficient to determine genetic relationships among *Salmonella* strains for epidemiological purposes when different techniques were combined (Hashemi and Baghbani-Arani, 2015). BOX-AIR-based repetitive extragenic palindromic-PCR (BOX-PCR) is considered to be the best method comparing to other repetitive element-based PCR typing methods, specifically, ERIC-, poly-trinucleotide (GTG) and REP-PCR. BOX-PCR provides a convenient molecular typing method to distinguish *Salmonella* spp. of the same and different serotypes according to genetic relatedness and should be proper for application in typing and tracking route of transmission in outbreaks. Similar results were reported by Poonchareon et al. (2019) and Lozano-Villegas et al. (2019), who showed that BOX-PCR can differentiate the genetic relationship between *Salmonella* isolates as well as grouping them into different clusters according to their origin.

The virulence of *Salmonella* is linked to a combination of chromosomal and plasmid factors (Yehia et al., 2020). Pathogenicity of *Salmonella* strains is controlled by a set of factors encoded by specific virulence genes that assist these types of pathogens to express the virulence in the host cells. This led to the appearance of typical symptoms of infection in an infected individual (Gharieb et al., 2015). In addition, virulotyping techniques are useful approaches to study *Salmonella* epidemiology. *S. Typhimurium* isolates have a range of virulence factors that play a role in *Salmonella* infection, diseases and interact with their host cells (Tarabees et al., 2017).

Results of the current study are in contrast to a previous study from Egypt, which reported that only 9 genes *sitC*, *iroN*, *sopB*, *sifA*, *lpfC*, *span*, *sipB*, *invA*, and *tolC* were successfully amplified in cases of *S. Typhimurium* isolated from chicken meat (Tarabees et al., 2017). The results of this research agree with many recent studies in Egypt (Awadallah and Abdelall, 2015) and Nigeria (Smith et al., 2015) conduct-

ed on *Salmonella* isolated from humans, animals, food, and water samples in which *invA* gene (284 bp) was prevalent at 96.0%. A wide prevalence of this gene (100%) had also been recorded earlier among *Salmonella* isolates, irrespective of their serovars or sample source by previously published works (Ammar et al., 2016; Ranjbar et al., 2017; Proroga et al., 2018; Thung et al., 2018; Elkenany et al., 2019).

The *Salmonella* outer protein encoded by *sopB* gene was found in 50.0% of *S. Typhimurium* isolates. A study from Malaysia reported that 50.0% of the *S. Typhimurium* isolates harbored *sopB* virulence gene (Thung et al., 2018). The obtained percentage was approximately similar to that reported from *S. Typhimurium* (44.4%) isolated from broilers in Egypt (Ammar et al., 2016). The occurrence of *sopB* factor in this study was less than that reported from *S. Typhimurium* isolated in India, which showed that all tested *S. Typhimurium* isolates carried *sopB* gene (Rahman, 2006).

Fimbriae in *Salmonella* spp. play a significant role in the pathogenicity, because they contribute to the attachment of these pathogens to the host epithelial cells. The plasmid-encoded fimbriae are encoded by the *pef* operon (Murugkaret al., 2003). Among the *S. Typhimurium* isolates tested, the *pefA* gene was detected in 35.7% of the isolates. These results were in similar to some studies and different from others (Ammar et al., 2016; Thunget al., 2018; Elkenany et al., 2019). A study conducted in Italy showed that the occurrence of *pefA* gene among *S. Typhimurium* isolates of human origin was 8.2% (Proroga et al., 2018). According to relevant studies, in Brazil, the occur-

rence of the virulence gene *pefA* was higher than that in Palestine; it was 66.7% among *S. Typhimurium* isolates, associated or not with foodborne Salmonellosis (Rowlands et al., 2014).

Virulotyping of *S. Typhimurium* serotype in this study showed that the occurrence of *prgH* gene was 46.4%. This result was, in contrast, to a study conducted by Srisanga et al., (2017), which showed that the occurrence of this gene among different *S. enterica* including *S. Typhimurium* serotype recovered from dogs and cats was 91.8% (Srisanga et al., 2017).

CONCLUSION

The preliminary data from this study have considerable epidemiological implications. Molecular assays using PCR-based methods for identification, virulotyping, and genotyping of *S. Typhimurium* is a useful approach for drawing up a group of genes to use in the epidemiological characterization of *S. Typhimurium* isolates. Early detection of the virulence gene provides many benefits for public health, especially for rapid diagnosis and control of contamination and infection.

The present study emphasizes the need for rigorous public health and hygienic measures throughout the food chain to minimize the human health hazard risk associated with *Salmonella* diseases. Moreover, the recovered *S. Typhimurium* isolates exhibit multiple virulence genes, which constitute a possible risk to humans from consumption of contaminated food products.

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