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RESEARCH ARTICLE

Molecular Detection of Some Virulence Genes of Salmonella Typhymurium and Salmonella Enteritidis Isolated from Patients Suffering Watery Diarrhea

Abdul Aziz Thamer A.1, Lamees A. Abdul-Lateef 2*, Moshtak A. Wtwt 3

- ^{1.} Al Hashemia Hospital, Babylon health Directorate, Iraq.
- ² Department of Microbiology, College of Medicine, University of Babylon, Iraq.
- ^{3.} College of Medicine, University of Babylon, Iraq.

*Corresponding Author: Lamees A. Abdul-Lateef

Abstract

Salmonella enterica virulence factors can be divided into chromosomal, plasmid and bacteriophages encoded virulence factors. Many of the Salmonella virulence factors, such as adhesion, invasion, and toxin genes are clustered in certain areas of the chromosome known as "Salmonella pathogenicity islands" (SPI). A total of 200 clinical stool samples were collected during this study which obtained from patient Suffering from watery diarrhea who a dmintted to three main hospitals of Babylon Governorate: Merjan Medical city, Al-Hillah Surgical Teaching Hospital and Babil Teaching Hospital for Women and Children during a period of three months (from july 2018 to September 2018). Out of 200 specimens 35(17.5%) were detected by culture and vitek2 compact, 24 (12%) of them were confirmed by PCR using target gene, (17) Salmonella typhimurium and (7) Salmonella enteritidis. PCR was conducted to determine the some virulence genes of the isolates by using primers inv A, sdiA and sifA. The PCR amplification products were visualized by electrophoresis on 1% agarose gels for 35min at 70v. The sizes of the amplicons were determined by comparison to the 200 bp allelic ladder. Among isolates studies it was found that invA gene present in 13(54)% isolates of S. enterica, (9) isolates of S. typhimurium and (4) isolates of S. enteritidis, sdiA gene it was found in all isolates (100)% while sifA gene it was found in all isolates only isolate number 18 not contained this gene 23(96)%.

Keywords: Salmonella typhimurium, S. enteritidis, invA, sdiA and sifA.

Introduction

Salmonella enterica infections remain a major public health concern worldwide, contributing to the economic burden of both industrialized and under developed countries through the costs associated with surveillance, prevention and treatment of disease [1]. Salmonella enterica is a Gramnegative, facultative rod-shaped bacterium belonging to the family Enterobacteriaceae [2].

Members of this genus are generally motile with peritrichous flagella, aerogenic, non-lactose fermenting, oxidase-negative, urease-negative, citrate-utilizing, acetyl methyl carbinol-negative and potassium cyanide-negative [3]. The invA gene usually codes for protein in the inner bacterial membrane that is responsible for invasion of intestinal cells

of the host [4]. The invA gene contains unique sequences specific to the genus Salmonella and has been proved as a specific PCR target with important diagnostic applications [5]. The invA target gene of Salmonella is located on the pathogenicity island 1 (SPI-1), it is important for the invasion of host epithelial cells. This gene is highly specific in most Salmonella serotypes and has been used as an important target for detection of Salmonella [6].

In Salmonella enterica serovar Typhimurium, SdiA positively regulates two loci, (1) the rck (resistance to complement killing)operon located on the virulence plasmid, pSLT [7] and (2) srgE (sdiA-regulated gene), a single gene horizontal acquisition that encodes an effector protein

that is secreted by type III secretion system 2 (T3SS2) [8]. Quorum sensing (QS) is a density dependent regulatory mechanism mediated by the accumulation of signaling molecules produced by bacteria and is related to transcriptional regulation of several genes, including those involved in biofilm formation, bacterial adhesion, host colonization and virulence factors [9].One of the most significant regulators of bacterial pathogenicity and especially of Salmonella intestinal virulence seems to be QS[10], and SdiA as a QS system product is the sole LuxR-type receptor in S. enterica [11].

The potential roles of sdiA may be construed from the recognized functions of genes known to be regulated by SdiA [11]. Existence and expression of the sdiA and sdiA-regulated genes would be beneficial to Salmonella within the gastrointestinal environment, and the observed upregulation of sdiA in the population brings the relevance of the differentiated state closer to the milieu of the host environment [12]. The T3SS-2 effector protein SifA [13] plays a significant role in Salmonella virulence and several phenotypes are linked to the translocation of SifA.

SifA is required to maintain the integrity of the Salmonella-containing vacuole (SCV) [14] and in epithelial cells promotes the formation of tubular membranous structures connected which SCVs, have been to named Salmonella-induced filaments (Sifs) [15,16].In absence of SifA, the molecular motor kinesin-1, which is directly recruited by the T3SS-2 effector PipB2 [17,18], accumulates on the SCV. This accumulation on the SCV is also visible for PipB2 and other membrane bound T3SS-2 effectors such as SifA or SseJ. We have suggested that these accumulations result from a slow formation of SCV-derived vesicles [19].

Materials and Methods

Samples Collection

Two hundred fecal samples were collected from Persons suffering from diarrhea, from both sexes in Merjan Medical city, Al-Hillah Surgical Teaching Hospital and Babel Teaching Hospital for Women and Children in Babylon province during the period from july 2018 to September 2018. Fecal samples (1gm) were put immediately in a sterile tube contained buffered peptone water, and transmitted immediately to the laboratory of Collage of Medicine in Babylon university with cooling box [20].

Culturing of Samples

Spread a 10 µl(loop full) from the inoculated and incubate tetrathionate broth on XLD ,S.S. Agar and on BGA agar plates and incubate at 37°C overnight (18-24 hours) and read the XLD plates and BGA plate Salmonella suspect colonies on XLD ,S.S. Agar and BGA agar onto non-selective media, (nutrient agar)plates for morphology and biochemical confirmation of Salmonella .After culturing of sample used vitek 2 compact system to detection of Salmonella enterica.

DNA Extraction for Gram Negative Bacteria

DNA extraction was carried out according to the genomic DNA purification kit supplemented by manufactured company (Gene aid, UK).

Confirmed Detection of S. typhimurium and S. enteritidis by Multiplex PCR using Specific Primer

For Salmonella enterica ser. Enteritidis specific motifs were found in the target gene SEN1383 - hypothetical protein, the primers flanking portion length 304 bp were selected. The target gene STM0159 - restriction endonuclease demonstrated specificity for Salmonella enterica ser. Typhimurium, the primers flanking region 224 bp were choose [21].

Molecular Detection of Salmonella Typhimurium and Salmonella Enteritidis Group using Multiplex PCR

PCR mixture was prepared by adding 12.5 µl of Green master mix (2x) promaga, 2.5 µl template DNA, 1.5 µl from forward primer and 1.5 µl from each four revers primer, final volume was completed to 25 µl by adding nucleuse free water.

Table 1: The primer sequences and PCR conditions of S.typhimurium and S.enteritidis

Genes	P	Primer sequence (5'-3')	bp	PCR condition	Refer ence
Salmonella	F	TGTGTTTTATCTGATGCAAGAGG		95 °C 5min	
enterica ser.	R	TGAACTACGTTCGTTCTTCTGG	304	$95^{\circ}\mathrm{C}$ $60\mathrm{Sec}$	[21]

Enteritidis				57 °C 60Sec 30x
Salmonella	F	ATGATGCCTTTTGCTGCTTT		72 °C 5min
enterica ser.	R	TCCCAGCTCATCCAAAAA	224	72 °C 7min
Typhimurium				

Detection of Some Virulence Gene Markers by PCR

The primers and PCR conditions used to amplify genes encoding virulence factors with PCR are listed in Table (2). The primer includes *invA* gene, *sdiA* gene and *sifA* gene.

Each 25µl of PCR reaction contained 5µl of each upstream and downstream primer, 5 µl of free nuclease water, 2.5µl of DNA extraction and 12.5 µl of master mix. The PCR amplification products were visualized by electrophoresis on 1% agarose ladder (promega, USA).

Table 2: Virulence factor primers sequences with their amplicon size Base pair (bp) and their condition

Genes	Primer sequence (5'-3')	Size bp	PCR condition	Reference
Sdi A1	AATATCGCTTCGTACCAC	274	94 °C 5min	[22]
			94 °C 30Sec	
Sdi A2	GTAGGTAAACGAGGAGCAG		52 °C 40Sec 30x	
			72 °C 60Sec	
			72 °C 7min	
Inv F	ACAGTGCTCGTTTACGACC	244	94 °C 3min	[23]
	TGAAT		94 °C 60Sec	
Inv R			58 °C 60Sec 30x	
	AGACGACTGGTACTGATCG		72 °C 60Sec	
	ATAAT		72 °C 10min	
SifA F	TTTGCCGAACGCGCCCC	449	95 °C 5min	[24]
	CACACG		95 °C 60Sec	
SifA R			60 °C 40Sec 35x	
	GTTGCCTTTTCTTGCGCT		72 °C 60Sec	
	TTCCACCCATCT		72 °C 10min	

Results and Discussion

Molecular Detection of *invA* gene, *sdiA* gene and *sifA* gene in Salmonella enterica:

To confirmation of diagnosis for Salmonella enterica ser.typhimurium depend on STM0159- restriction endonuclease and Salmonella enterica ser. enteritidis depend on SEN1383- hypothetical protein in Multiplex PCR, the results revealed that only 24(12) % out of 35 were positive for culture and biochiemical test, these 24 isolates were 17 (48.57) % S. typhimurium and 7 (20) % S. enteritidis as show in Figure (1). The results

was obtained in this study by molecular methods were 24 (12) % out of 35 samples positive results and this study agreement with results obtained by [25] who found that (10%) were identified as carriers of Salmonella typhimurium and Salmonella enteritidis on the basis of the molecular methods .Multiplex PCR is considered as a rapid molecular approach for simultaneous detection of several targets a single amplification reaction. This technique is frequently evaluated in order to assess the possible presence of microbial pathogens causing foodborne diseases [26].

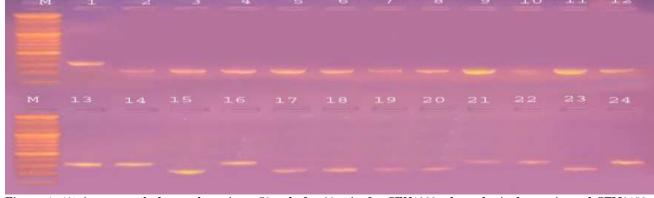


Figure 1: 1% Agarose gel electrophoresis at 70 volt for 30 min for SEN1383 - hypothetical protein and STM0159 - restriction endonuclease *PCR* products visualized under U.V light at 280 nm after staining with ethidium bromide. L: 1500 bp ladder;lane(1-24) were positive for these genes, the size of product is 304 bp for SEN1383 target gene(S. enteritidis) and 224 bp for STM0159 - restriction endonuclease target gene (S. typhimurium)

304 224

224

304

Molecular detection of *invA* gene was done by using specific primer. It was found that *invA* gene observed in 13 isolates (54%) of *S. enterica* strains with long length (244 bp) as shown in Figure (2). The result of this study was dis agreement with the result obtained by [27] and [28] who were found that the percentage of invA gene in *Salmonella* is 100%.

This gene encodes a protein in the inner membrane of bacteria which is responsible for invasion to the epithelial cells of the host [29]. The gene may not also always be present in all *Salmonella* spp. While it may be possible to state that the species that showed the *invA* band may be virulent, penetrate and cause infection in host cells. The detection of the gene in the *Salmonella* isolated implies the organisms are virulent and will be able to

penetrate host epithelia cells, causing infection.

Absence of the gene in the confirmed Salmonella isolates can lead to lack of invasiveness by those isolates [30]. However, our study, this gene cannot be used for diagnosis because some isolates do not have this gene, the differences between presence the virulence genes in S. enterica isolates in our study and other studies may be influence of geographic conditions, dietary factors, movement the virulence genes by transposon and integron in addition to plasmids are a major mechanism for the spread of virulence genes in bacterial populations by conjugation, and/or host genetic factors. Other studies showed that the failure of the PCR detection was due to naturally occurring deletions in the centisome 63 PAI. Interestingly, the strains that were not associated with disease were shown to lack invA sequences [31].

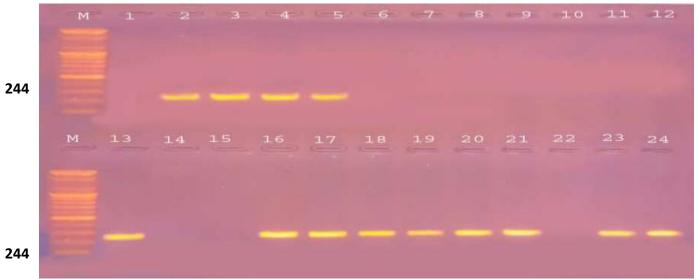


Figure 2: 1% Agarose gel electrophoresis at 70 volt for 30 min for *invA PCR* products visualized under U.V light at 280 mm after staining with ethidium bromide. L: 1500 bp ladder; lane(2,3,4,5,17,18,19,20,23) S. typhimurium(13,16,21,24) S. enteritidis for this gene, the size of product is 244 bp for *invA* gene

The quorum sensing gene (sdiA) was investigated by PCR technique using specific primers for this gene. The results of this experiment indicate for positive amplification as shown in figure (3). It was found that sdiA marker was observed in 24 isolates, (100%). This result was correlated with the results obtained by [22], [32] who were found that sdiA gene at similar frequencies 100% respectively. [32] Were showed that the sdiA quorum sensing gene can be used as a target gene for detection of Salmonella spp. by PCR. Quorum sensing (QS) is a density dependent regulatory mechanism mediated by the accumulation of signaling molecules

produced by bacteria and is related to transcriptional regulation of several genes, including those involved in biofilm formation, bacterial adhesion, host colonization and virulence factors [9]. Signaling mechanisms, like sdiA in Salmonella, control those pathways which are responsible expressing various virulence factors. There are over 2,600 serovars of S. enterica, and it is likely that the SdiA regulon is different among the serovars. SdiA regulates accessory factors that may contribute to intestinal survival or colonization [33]. For example, the sdiA gene of S. typhimurium regulates two loci, the rck operon and the srgE gene [34].

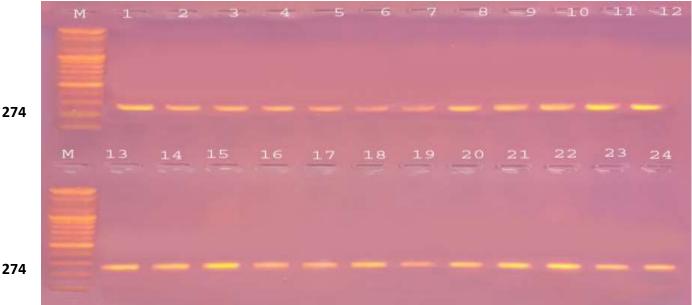


Figure 3: 1% Agarose gel electrophoresis at 70 volt for 30 min for sdiA PCR products visualized under U.V light at 280 nm after staining with ethidium bromide. L: 1500 bp ladder;lane(1-24) were positive for this gene, the size of product is 274 bp for sdiA gene

Salmonella-induced filament (sifA) gene was investigated by PCR technique using specific primers for this gene. The results of this experiment indicate for positive amplification

449

449

as shown in figure (4). It was found that sifA marker was observed in 23 isolates only isolate number 18 not contained this gene, (96%).



Figure 4: 1% Agarose gel electrophoresis at 70 volt for 30 min for sifA PCR products visualized under U.V light at 280 nm after staining with ethidium bromide. L: 1500 bp ladder;lane(1-24) only isolate No. 18 not contained for this gene, the size of product is 449 bp for sifA gene

This result was closly correlated with the results obtained by [24], [35] who were found that sifA gene at similar frequencies 100% respectively. is SalmonellaSifA a typhimurium effector that protein translocated across the membrane of the Salmonella-containing vacuole Salmonella pathogenicity island 2-encoded type III secretion system. SifA is necessary for the formation of Salmonella induced filaments and for the maintenance of the vacuolar membrane enclosing the pathogen

[36]. SIF are tubular aggregations of late endosomal/lysosomal vesicles. Presence of glycoproteins lysosomal (lgp) such lysosome-associated membrane protein 1 (LAMP1) is characteristic for membranes. The Salmonella SPI2-T3SS effector protein SifA is crucial for formation of SIF [37] and stability of SCV during intracellular replication [38]. The T3SS-2 effector protein SifA3 plays a significant role in Salmonella virulence and several cellular phenotypes are linked to its translocation.

SifA is required to maintain the integrity of the *Salmonella*-containing vacuole (SCV) [38]. It promotes the formation of tubular

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membranous structures connected to SCVs that are named *Salmonella*-induced tubules [39].

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