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Finding Genetic Differences in *Salmonella enterica* Isolated from Poultry

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Abstract | Deciding the hereditary variations of *S. enterica* disconnected from broiler chicken faeces can provide critical insights to control this infection in poultry. A 286-length genomic part encoding locale of the symptomatic quality (invA) was used to assess the diversity of S. enterica in 15 bacterial samples. A coordinate sequencing methodology was connected to the PCR amplicons recognized within the upgraded genomic locus. A phylogenetic tree was applied within the recognized varieties to overview the particular phylogenetic separations in differentiate with other comparable bacterial progression. The current results suggest that the investigated samples and the S. enterica sequences have roughly 99% homology. A total of 19 genetic variants of A34T, A35del, C36G, C36A, T42del, A69del, A69G, A70ins, G71ins, G91ins, A119ins, A124G, G223A, C253T, C278G, C278T, T279G, T279C, and G280C were identified among the InvA genes. In most of the samples, some variances were distributed differently. Several nucleotides insertion mutations were found at positions 70, 71, 91, and 119 in the InvA gene sequencing. However, deletion mutations were found in most samples at A35, T42, and A69 sites. These finding highlight the genetic diversity of S. enterica and may attribute to the prevalence of infection in the poultry.

Keywords | Genetic, *Salmonella enterica*, Poultry, Thi-Qar, chicken meat, diseases

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INTRODUCTION

Since chicken meat is one of the most basic food sources for humans, livestock is among the most crucial economic sectors in underdeveloped countries (Abdulkareem, 2020; Al-Jebory *et al.*, 2024; Salman *et al.*, 2024a, b). Poultry are susceptible to a wide range of diseases, including viral and bacterial ailments such as salmonellosis (Naji and Hanna, 1999; Al-Saeedi *et al.*, 2024; Ajafar *et al.*, 2024). If dangerous microorganisms are present, the carcass's traits and attributes may suffer (Jaffar and Abdulkareem, 2022). Enteric infections are a major source of illness and death worldwide. Gram-negative enteric microbes are thought to be mindful for approximately 3 million fatalities around the world each year from loose bowels and gastrointestinal illness (Donnenberg, 2000). *Salmonellae* is a gram- bacterium that causes serious illnesses in humans and domestic animals (Makela and Hormaeche, 1997; Eisenstein, 1999). There are around 2668 distinct Salmonella enterica serotypes. A major cause of food-borne disease outbreaks and a worldwide public health issue, the condition can harm both people and animals (Akbarmehr, 2011).

Salmonella enterica is the pathogen that causes salmonellosis. *Salmonellosis*, which occurs when feed or water sources are taken after being contaminated by the urine or feces of animals that may act as *Salmonella* reservoirs, causes significant morbidity and mortality worldwide (Raffatellu *et al*., 2008; Akbermehr, 2012). Depending on the host's susceptibility, *Salmonella enterica* infections presented a range of clinical signs (Crump *et al*., 2015; Majowicz *et al*., 2010). These include bacteremia, E.F, gastroenteritis, and ASC (Burns *et al*., 1997; Andrews-Polymenis *et al*., 2010). Although human salmonellosis ordinarily up as a self-limiting nourishment harming, it can moreover sometimes result in a major systemic ailment or E. fever. Contaminated food is the essential implies of transmission for non-typhoidal sicknesses, developed *Salmonella*, a zoonotic ailment that influences a large number of animals reservoir. The foremost common of these poultry animal (Akbarmehr, 2011).

Non-typhoidal Salmonella is responsible for an estimated 1 million infections, 20,000 hospitalizations, and 378 deaths per year. Three million children are killed by it every year in both wealthy and developing countries (Cardinale *et al*., 2005; Scallan *et al*., 2011), Salmonella-specific PCR using invA primers was found by Lampel *et al*. (2000) to be sensitive, quick, and specific for detecting Salmonella in a variety of clinical samples. Furthermore, Kunduk *et al*. (2006) reported that PCR is a quick, accurate, and precise way to diagnose typhoid (Feyer and Karmi, 2013). The invasion of host epithelial cells is dependent on *Salmonella's invA* gene, which contains sequences unique to the genus *Salmonella*. It has also been confirmed to be a basic PCR target with significant diagnostic applications. The molecular approaches are the most straightforward and economical. This gene is consequently a promising target for the detection of Salmonella from different forms of biological material, as was previously mentioned, the aimed of study to pinpoint the *invA* gene responsible for cell invasion offer atomic clarification of it. This was accomplished by utilizing the Sanger arrangements procedure to decide the developmental tree of the Salmonella segregates beneath consider and analyze the sequencing of the intensified quality portion.

MATERIALS AND METHODS

DNA extraction and PCR

Follow the directions of the manufacturer (Geneaid Biotech, Taiwan), DNA extraction was performed The PCR specifically targeting InvA gene was performed using the master mix (Table 1) and the thermoprofile outlined in Table 2. Afterwards, PCR products were run on a 1.5% agarose gel, they were stained for 45 minutes at 95 volts in 1X TBE buffer.

Table 1: Master mix for the preparation of PCR solution

Reagents	Volume
Primer forward	1.5 µl
Primer reverse	1.5 µl
DNA template (<250ng)	1 µl
Free water	16 µl
Total	20 µl

DNA sequencing of PCR amplicons

The PCR amplicon sequences were acquired from the terminal in accordance with the instructions provided by the sequencing provider (Macrogen Inc. Geumchen, Seoul, South Korea). By further analyzing only clear chromatographs obtained from ABI sequence data, the annotation and variations were confirmed to be free of PCR or sequencing artifacts. By comparing the observed nucleic corrosive arrangements of the bacterial tests with the reference arrangements that were retrieved from the bacterial database, the virtual areas and other points of interest of the obtained PCR fragments were determined.

Interpretation of sequencing data

BioEdit Assemble Edit Suite v. 7.1 (D.M. WI, USA) was used to modify the PCR products' sequencing findings, modified, and evaluated alongside the sequences within the corresponding reference database. The nucleic acids sequences detected were counted within both the PCR amplicons and the corresponding regions within the reference genome. Each revealed variant within *S. enterica* genes was described by means of SnapGene Viewer 4.0.4 (https://www.snapgene.com).

Phylogenetic tree

This analyse constructed a particular phylogenetic tree according to (Zhang *et al*., 2000) and comprehensive tree was constructed as outlined by the Hanan *et al*. (2021); Gharkan *et al*. (2023).

RESULTS

The invA gene variant was found in 15 samples with amplicons that were roughly 286 bp long. All of the

Table 2: The condition of PCR for *invA* gene amplification.

Monoplex gene	°C/ Time					Cycle number
	Initial denaturation	Cycling condition			Final extension	
		Denaturation	Annealing	Extension		
inv A	95/5min	94/40 s	58/60s	72/90s	72/10 min	30

Table 3: The 286 bp PCR amplicons used to access a subset of the InvA quality within the genomic DNA groups of S. enterica (GenBank accession number NC_003197).

Amplicon	Reference locus sequences (5′ - 3′)	Length
InvA gene	*TCATCGCACCGTCAAAGGAACCGTAAAGCTGGCTTTCCCTTTCCAGTACGCTTCGC-CGTTCGCGCGCGGCATCCGCATCAATAATACCGGCCTTCAAATCGGCATCAATACT-CATCTGTTTACCGGGCATACCATCCAGAGAAAATCGGGCCGCGACTTCCGCGA-CACGTTCTGAACCTTTGGTAATAACGATAAACTGGACCACGGTGACAATAGAGAA-GACAACAAAACCCACCGCCAGGCTATCGCCAATAACGAATTGCCCGAACGTGGCGA-TAATTTCAC**	286 bp

* Refers to the forward primer sequences (placed in a forward direction).

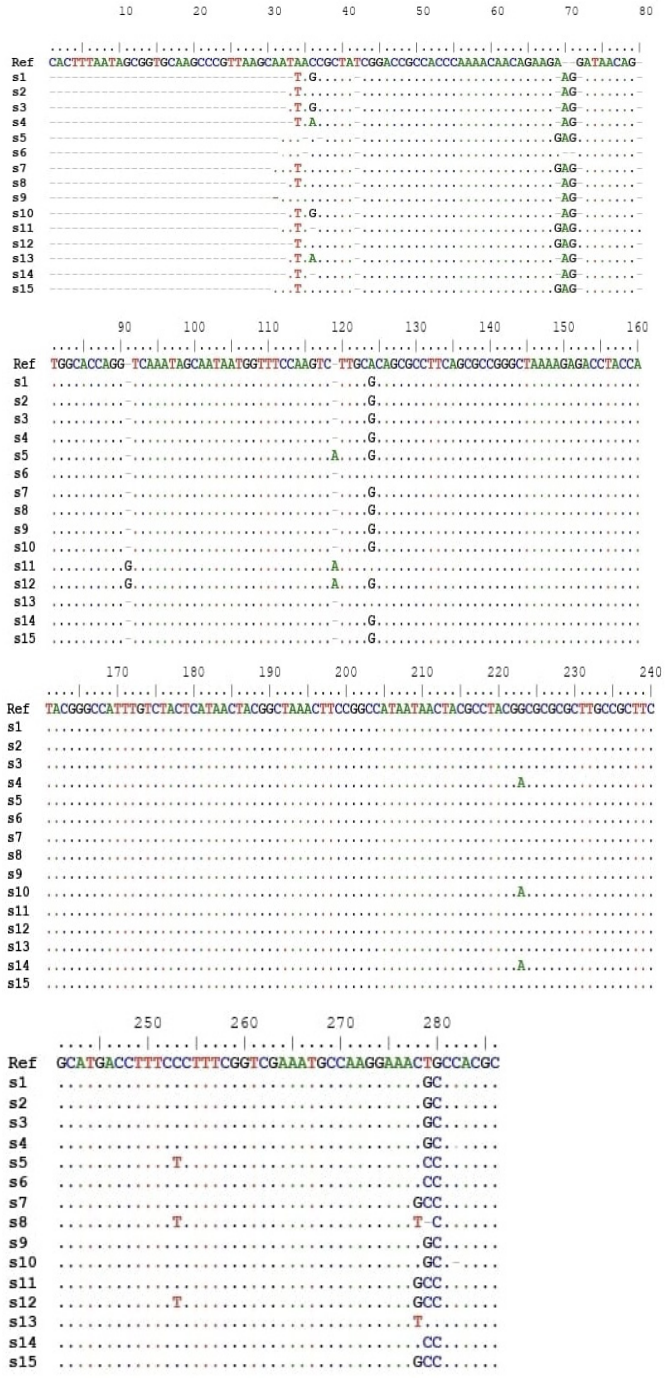

Figure 1: Nucleic destructive course of action course of action of 15 bacterial tests with its comparing reference groupings of the InvA insides the *S. enterica* genomic DNA courses of action. The picture ref: implies to the NCBI reference courses of action, whereas "S: implies to test numbers.

amplified amplicons were checked for clean, distinct, and sharp bands before sending for sequencing. By utilizing NCBI impact, the sequencing responses illustrated the intensified products confirmed manually. The NCBI BLASTn motor uncovered a tall degree of arrangement closeness between the sequenced tests and *S. enterica* arrangements with respect to the 286 bp PCR amplicons of the as of now focused on InvA arrangements. The NCBI BLASTn motor appeared that the InvA quality sequences coding locale was mostly secured by roughly 99% homology with the expecting target. The highlights of these groupings were underscored inside the increased groupings (Table 3) by differentiating the gotten DNA groupings (GenBank acc. NC_003197) with the watched DNA arrangements of the tests beneath examination.

The 286 bp PCR amplicons used to access a subset of the InvA quality within the genomic DNA groups of *S. enterica* (GenBank accession number NC_003197) as are displayed in Table 3 along with their length and location. A total of 19 nucleic acid differences were found in the alignment findings of the 286 bp samples when compared to the matching *S. enterica* referencing sequences (Figure 1). These sequences were created by matching the most related sequences that were deposited in the NCBI database (GenBank accession NC_003197) with the samples that we examined.

According to the analyzed InvA sequences in the bacterial samples under examination, a phylogenetic tree was generated. The three inspected tests (LC762569, LC762570, and LC762571) were included in this phylogenetic tree beside the other stored DNA groupings. These tests were adjusted with their profoundly related groupings in Tamura-Nei mode. There were sixteen adjusted nucleic corrosive groupings within the tree because it was as of now shaped. The inspected InvA groupings were assembled into various neighboring phylogenetic branches based on the hereditary arrangements of *S. enterica*, showing a incredible bargain of inconstancy in this life form with regard to the inspected InvA groupings (Figure 2). *S. enterica* subsp. enterica serovar Ouakam, *S. enterica* subsp. enterica serovar Newport, *S. enterica* subsp. enterica serovar Enteritidis, and *S. enterica* subsp. enterica serovar *Typhimurium* were also included, along with other relevant serovars. All of these subspecies, however, belonged to the enterica serovar.

Table 4: The plan of the observed contrasts inside the 286 bp of the InvA amplicons in comparison with the NCBI reference groupings (GenBank acc. no. NC_003197).

Sample	Variant	Position in the PCR fragment
S1, S2,S3, S4, S7, S8,S10,S11, S12,S13, S14, S15	A34T	34
S5, S6	A35 del	35
S1, S3, S10	C36G	36
S4,S13	C36A	36
S1,S2 S3, S4, S5,S6,S7, S8,S9,S10,S11, S12,S13, S14, S15	T 42del	42
S1, S2,S3,S4, S8,S9,S10, S13, S14	A69del	69
S5, S7, S11, S112	A69G	69
S1,S2 S3, S4, S5, S7, S8,S9,S10,S11, S12,S13, S14, S15	A70ins	70
S1,S2 S3, S4, S5, S7, S8,S9,S10,S11, S12,S13, S14, S15	G71ins	71
S11,S12	G91ins	91
S5,S11,S12	A119ins	119
S4,S10,S14	A124G	124
S5,S8,S12	G223A	223
S7,S11,S12,S15	C253T	253
S8,S13	C278G	278
S1,S2,S3,S4,S9,S10	C278T	278
S6,S7,S8,S11,S12,S13,S14,S15	T279G	279
S1,S2,S3,S4,S5,S6,S7,S8,S9,S10,S11,S12,S13,S14,S15	T279C	279
	G280C	280

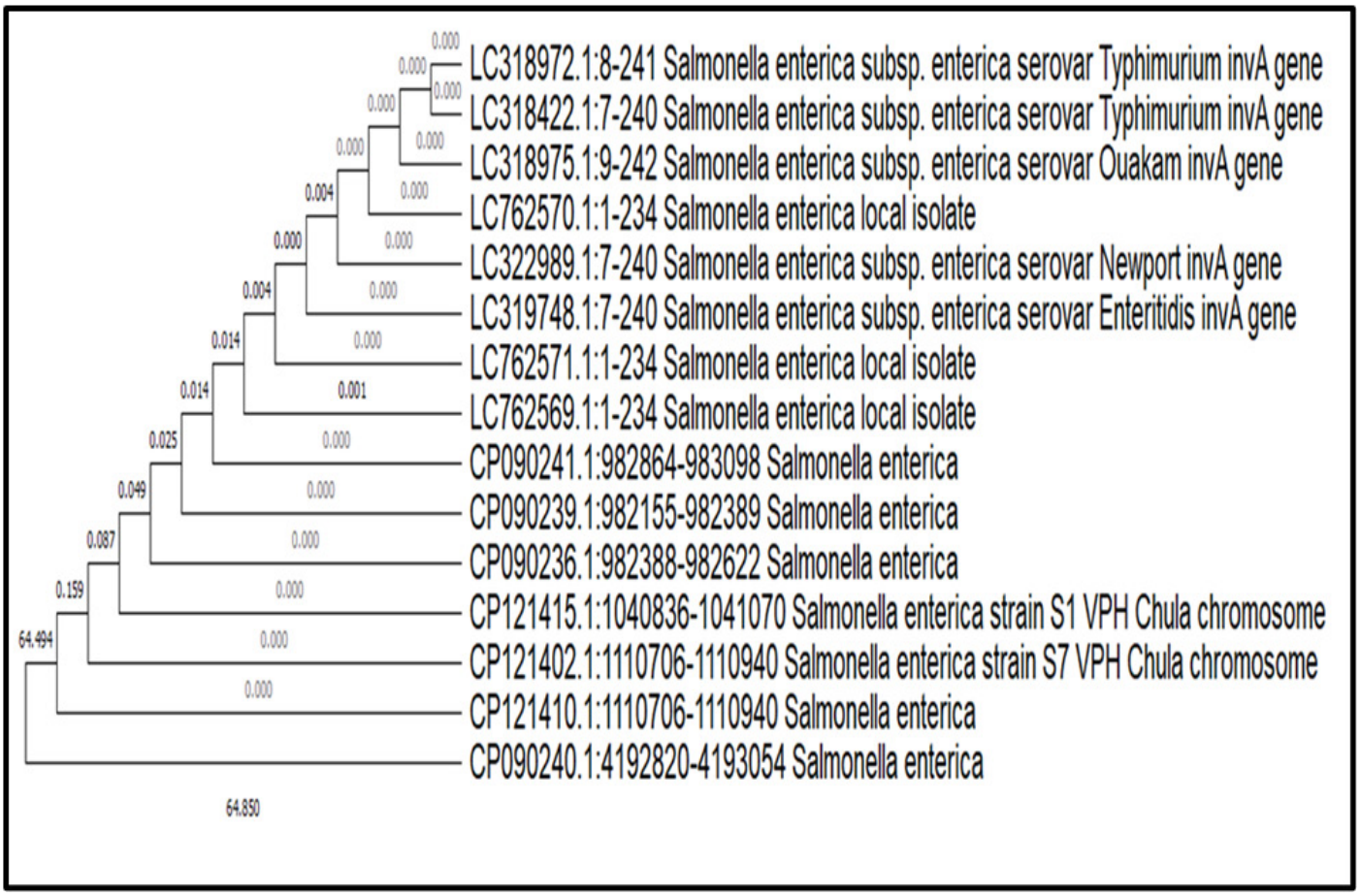

Figure 2: Using the Neighbor-Joining approach, the developmental history was collected, and the perfect tree emerged (moving on to the branches later). The developmental separations were calculated using the Most Extreme Composite Probability approach and were within the units of the number of base substitutions per place. This study included sixteen nucleotide configurations, including first, second, third, and noncoding codon positions. All ambiguous positions were eliminated for each arrangement combine (pairwise erasure alternative), resulting in 290 positions in the final dataset.

Submission in NCBI

InvA gene sequences were submitted in NCBI's Gene Bank and are available under accession numbers: LC762569, LC762570, and LC762571.

DISCUSSION

Investigating *S. enterica's* genetic variants was the aim of the most recent study. To do this, 15 bacterial samples (designated S1 to S15) were collected from grill chicken, ROSE 308 faeces, and were analysed for the InvA sequences. Salmonella's invasion of intestinal epithelial cells depends on the invA gene, which codes for a protein in the bacterial inner cell wall (Al-Kaaby *et al*., 2014; Sharma and Das, 2016; Shanmugasamy *et al*., 2011). *Salmonella's invA* gene is also utilised in the molecular diagnostics of the bacterium because it comprises a distinct sequence of this genus (Karim *et al*., 2020).

One of the numerous chromosomal virulence genes that were utilised to detect Salmonella in poultry faecal samples was the invA gene. The PCR assay of Salmonella serovar also targeted the invA gene (Jamshidi *et al*., 2009), and the invA gene was grouped in the islands of Salmonella species' pathogenicity (Daigle, 2008). The virulent *invA* gene, which encoded a protein present in the inner layer of the bacterial membrane and had sequences that were specific to all salmonella serovars, is what allowed the bacteria to infiltrate the host's epithelial cells (Daigle, 2008).

Salmonella-specific sequences can be found in the invA sequence of enteric bacteria, It has been found to be a good PCR target with possible diagnostic applications (Mohamed, 2013). Different distributions of the analysed samples were caused by the neighbouring places in the phylogenetic tree being attributed to the rate of variations within those samples. According to the *InvA* gene chromatograph file data, there are deletion mutations in several locations along this sequence, such as A35, T42, A69, A71, and 119del. Additionally, nucleotide insertion was found in a few different locations within the InvA gene, such as: A nucleotide in position 70 and G in the majority of samples; G nucleotide in position 91 of the S11 and S12 samples; and A nucleotide in position 119. The local isolate *S. enterica* (LC762570.1) exhibited a closed relationship and 100% similarity with reference isolates *S. enterica* subsp. enterica seovar *Typhimurium* (LC318972.1, LC318422.1) and *S. enterica* subsp. Enterica seovar Ouakam, as indicated by the phylogenetic tree of the *InvA* gene. The observed phylogenetic distances (tree scale 0.001) between the integrated organisms and local isolates within this clade are noteworthy since they clearly show that the incorporated bacterial genomes have progressive homology. To determine the relationship between Iraqi isolates and the higher query cover, which exceeds 90% of national isolates, the maximum likelihood and minimum evolution methods were used to create the phylogenetic tree for each gene.

Taken together, the finding of this study highlight the emerging genetic variations in the *S. enterica* and may offer foundational information for improved diagnostics and vaccine prepration to contain the infection in future.

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NOVELTY STATEMENT

This study investigates the novel molecular characteristics of Salmonella isolated from poultry in Dhi Qar province. The research aims to determine its resistance to antibiotics and other emerging propertie.

AUTHOR'S CONTRIBUTION

ZKH: Designed the study and conducted DNA sequence analysis using bioinformatics tools.
AAA: Performed laboratory experiments including DNA extraction and PCR amplification.
NHG: Contributed to statistical analysis and figure preparation.
AAA: Supervised the research, provided academic guidance, and reviewed the manuscript.

Generative AI and AI-assisted technology statement

The authors declare that no Genrative AI was used in the creation of this manuscript.

Conflict of interest

The authors have declared no conflict of interest.

REFERENCES

Abdulkareem AA (2020). The genetic variations in mitochondrial D-loop sequence for local ducks in Iraq. Plant Arch., 20(1): 277-281.

Ajafar M, Al-Jebory HH, Al-Saeedi MKI (2024). Effect of in Ova injection of lysophospholipid in hatching traits, chick's quality, and chicks physical traits of broiler (Ross 308). Adv. Anim. Vet. Sci., 12(7): 1206-1213. https://doi.org/10.17582/journal.aavs/2024/12.7.1206.1213

Akbarmehr J (2011). A survey on the prevalence of poultry salmonellosis and detection of different Salmonella serovars

isolated from poultry bin broiler chicken farms. Afr. J. Microbiol. Res., 5(32): 5950-5954. https://doi.org/10.5897/AJMR11.996

Akbarmehr J (2012). A study on transfer of antibiotic resistance plasmids between *Salmonella enteritidis* and *Escherichia coli* k12. Int. J. Agric. Res. Rev., 2(6): 862-866.

Al-Fayyad HA, Naji SA, Abdel-Hajo NN (2011). Poultry product technology. University of Baghdad, College of Agriculture, Higher Education Press, University of Baghdad, Part One, Second Edition.

Al-Jebory HH, Al-Saeedi MKI, Ajafar M, Ali NAL (2024). Impact of melatonin on improving productive traits of broiler exposed to environmental stress. Adv. Anim. Vet. Sci., 12(4): 775-781. https://doi.org/10.17582/journal.aavs/2024/12.4.775.781

Al-Kaaby KT, Al-Dabhaw AH, Samaka HM, Alhatami AO (2014). Detection of some *Salmonella enteritidis* virulence genes by multiplex-PCR assay using two different DNA extraction methods. Qadisiah Med. J., 10(18): 63-70. https://doi.org/10.28922/qmj.2014.10.18.63-70

Al-Saeedi MKI, Ajafar M, Al-Jeobry HH (2024). Immunity and glycogen metabolism of laying hens fed diets supplemented with manganese sulfate during the force molting. J. Anim. Health Prod., 12(3): 413-419. https://doi.org/10.17582/journal.jahp/2024/12.3.413.419

Andrews-Polymenis, Heather L., Bäumler, Andreas J., McCormick, Beth A., Fang, Ferric C. (2010). Evaluating the role of bacterial virulence factors in murine models of Salmonella infection. Nature Reviews Microbiology, 8(1), 27–39. https://doi.org/10.1038/nrmicro2262

Burns-Keliher LL, Portteus A, Curtiss R (1997). Specific detection of *Salmonella typhimuriu* proteins synthesized intracellularly. J. Bacteriol., 179(11): 3604-3612. https://doi.org/10.1128/jb.179.11.3604-3612.1997

Cardinale E, Perrier G-CJD, Rivoal K (2005). pidemiological analysis of *Salmonella enterica* ssp. Enteric serovars Hadat Brancaster and Enteritidis from humans and broiler hickens In: Sengal using pulsed-field gel electrophoresis and antibiotic susceptibility. J. Appl. Microbiol., 99: 968-977. https://doi.org/10.1111/j.1365-2672.2005.02618.x

Crump JA, Sjölund-Karlsson M, Gordon MA, Parry CM (2015). Epidemiology, clinical presentation, laboratory diagnosis. antimicrobial resistance, and antimicrobial management of invasive *Salmonella* infections. Clin. Microbiol. Rev., 28(4): 901- 937. https://doi.org/10.1128/CMR.00002-15

Daigle F (2008). Typhi genes expressed during infection or involved in pathogenesis. J. Infect. Dev. Ctries, 2: 431-437. https://doi.org/10.3855/jidc.157

Donnenberg MS (2000). Pathogenic strategies of enteric bacteria. Nature, 406: 768-774. https://doi.org/10.1038/35021212

Eisenstein TK (1999). Mucosal immune defense: The *Salmonelle typhimurium* model. Ln intracellular bacterial vaccine vectors (Y. Paterson, ed.) New York: Wiley-Liss, pp. 51-109.

Feyer, J., Karmi, M. (2013). Genetic diversity and antibiotic resistance of Salmonella isolated from poultry meat. African Journal of Microbiology Research, 7(21), 2564–2570. https://doi.org/10.5897/AJMR12.2396

Gerstel U, Romling U (2003). The CsgD promoter, a control unit for biofilm formation in *Salmonella typhimurium*. Res. Microbiol., 154(10): 659-667. https://doi.org/10.1016/j.resmic.2003.08.005

Gharkan NH, Hanan ZK, Abdulkareem AA (2023). Phylogenetic analysis of biofilm association protein (BapA) amplicons in *Salmonella* spp. isolated from broiler (Ross 308) in Thi-Qar Province/Iraq. IOP Conf. Ser. Earth Environ. Sci., 1262(2): 022017. https://doi.org/10.1088/1755-1315/1262/2/022017

Hanan ZK, Saleh MB, Mezal EH, Issa MA, Al-Jauher RQ, Akmoush MA (2021). Phylogenitic analysis of biofilm association protein (BapA) amplicons in *Salmonella typhi* carrier in gallbladder diseases patients in Thi-Qar Province, Iraq. Int. J. Aquat. Sci.,

Jaffar AA, Abdulkareem AA (2022). Genetic diversity and identification of MC1R SNPs association with colors in Iraqi local ducks. IOP Conf. Ser. Earth Environ. Sci., 1060(1): 012066. https://doi.org/10.1088/1755-1315/1060/1/012066

Jamshidi A, Bassami MR, Afshari-Nic S (2009). Identification of *Salmonella* spp. and *Salmonella typhimurium* by a multiplex PCR-based assay from poultry carcasses in Mashhad, Iran. Int. J. Vet. Res., 3(1): 43-48.

Karim SJI, Islam M, Sikder T, Rubaya R, Halder J, Alam J (2020). Multidrug-resistant *Escherichia coli* and *Salmonella* spp. isolated from pigeons. Vet. World, 13(10): 2156-2165. https://doi.org/10.14202/vetworld.2020.2156-2165

Kunduk, M., Smith, J., Brown, T. (2006). Rapid detection of Salmonella by real-time PCR. Journal of Applied Microbiology, 101(5), 1059–1064. https://doi.org/10.1111/j.1365-2672.2006.03000.x

Lampel, Keith A., Orlandi, Palmer A., & Kornegay, Linda. (2000). Improved template preparation for PCR-based assays for detection of food-borne bacterial pathogens. Journal of Food Protection, 63(2), 246–250. https://doi.org/10.4315/0362-028X-63.2.246

Majowicz, Shannon E., Musto, Jenny, Scallan, Elaine, Angulo, Frederick J., Kirk, Martyn, O'Brien, Sarah J., Jones, Tim F., Fazil, Aamir, & Hoekstra, Robert M. (2010). The global burden of nontyphoidal Salmonella gastroenteritis. Clinical Infectious Diseases, 50(6), 882–889. https://doi.org/10.1086/650733

Mäkelä, P. H., Hormaeche, C. E. (1997). Salmonella infections in animals: Pathogenesis. In M. W. Blaser (Ed.), Infections of the gastrointestinal tract (pp. 1137–1153). Raven Press.

Mohamed K (2013). Detection of virulence gene (*invA*) in *Salmonella* isolated from meat and poultry products. Int. J. Genet., 3(2): 7-12.

Naji SA, Hanna AK (1999). Broiler breeding guide. Arab Union for Food Industries.

Raffatellu M, Wilson R, Winter S, Bāumler A (2008). Clinical pathogenesis of typhoid fever. J. infect. Dev. Count., 2(4): 260-266. https://doi.org/10.3855/jidc.219

Salman KAA, Al-Saeedi MKI, Al-Jebory HH (2024a). Impact of ova injection with zinc methionine on some blood parameters and glycogen level of broiler chickens exposed to feed fasting. Adv. Anim. Vet. Sci., 12(8): 1532-1538. https://doi.org/10.17582/journal.aavs/2024/12.8.1532.1538

Salman KAA, Al-Saeedi MKI, Al-Jebory HH, Al-Jebory RF (2024b). Effect of neem (*Azadirachta indica*) leaf powder supplementation on some blood parameters in broiler chickens exposed to heat stress. Punjab Univ. J. Zool., 39(2): 177-183. https://doi.org/10.17582/journal.pujz/2024/39.2.177.183

Shanmugasamy M, Velayutham T, Rajeswar J (2011). *invA* gene specific PCR for detection of *Salmonella* from broilers. Vet. World, 4: 562-564. https://doi.org/10.5455/vetworld.2011.562-564

Sharma I, Das K (2016). Detection of *invA* gene in isolated Salmonella from marketed poultry meat by PCR assay. J. Food Process. Technol., 7(3): 564. https://doi.org/10.4172/2157-7110.1000564

Scallan, Elaine, Hoekstra, Robert M., Angulo, Frederick J., Tauxe, Robert V., Widdowson, Marc-Alain, Roy, Sharon L., Jones, Jeffrey L., Griffin, Patricia M. (2011). Foodborne illness acquired in the United States—major pathogens. Emerging Infectious Diseases, 17(1), 7–15. https://doi.org/10.3201/eid1701.P11101

Zhang Z, Schwartz S, Wagner L, Miller W (2000). A greedy algorithm for aligning DNA sequences. J. Comput. Biol., 7(1-2): 203-214. https://doi.org/10.1089/10665270050081478