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Molecular investigation of Tsst, Eta, and Etb Genes in Staphylococcus aureus isolated from impetigo patients among children in Al-Diwaniyah city, Iraq

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Abstract

Objective

Staphylococcus aureus is a versatile and opportunistic pathogen responsible for a broad spectrum of human diseases ranging from superficial skin infections to life-threatening systemic situations. Among its many clinical manifestations, impetigo—a contagious skin infection primarily affecting children is commonly related with *S. aureus* as a principal causative agent. The prevalence of *S. aureus* in skin and soft tissue infections has become a growing public health concern, especially in pediatric populations and in regions with restricted access to advanced healthcare resources. The current investigation aimed to investigate the molecular presence of the *tsst*, *eta*, and *etb* genes in *S. aureus* isolates achieved from children diagnosed with impetigo in Al-Diwaniyah City, Iraq. By combining 16S rRNA gene amplification with virulence gene profiling, this research contributes to a deeper understanding of the molecular epidemiology and pathogenic traits of *S. aureus* in a vulnerable patient population.

Materials and methods

This investigation was managed on clinical isolates achieved from children diagnosed with impetigo and attending dermatology clinics in Al-Diwaniyah City, Iraq. A total of 21 swab samples were gathered from infected skin lesions applying sterile cotton swabs. Genomic DNA was extracted from affirmed *S. aureus* isolates. To affirm the identity of the isolates, PCR was carried out targeting the 16S rRNA gene. The presence of *tsst*, *eta*, and *etb* genes was identified by conventional PCR applying gene-specific primers.

Results

All *Staphylococcus aureus* isolates demonstrated a distinct 1,500 bp band upon PCR amplification of the 16S rRNA gene, affirming successful amplification of the target gene. This result also indicated the high quality of the extracted bacterial DNA and the specificity of the primers applied. The conserved nature of the 16S rRNA gene reinforces its reliability as a molecular marker for bacterial identification. In addition, the presence of exfoliative toxin genes (*eta*, *etb*, and *tsst-1*) was evaluated applying PCR. Each gene generated a distinct amplification pattern. Among the 21 clinical isolates, 11 (52.4%) were positive for the *tsst-1* gene. The *eta* and *etb* genes were also detected but in varying frequencies, suggesting differential distribution of these virulence factors among the isolates.

Conclusions

This investigation highlights the molecular presence of key virulence genes (*tsst-1*, *eta*, and *etb*) in *Staphylococcus aureus* isolates from impetigo cases in children. The detection of these toxin genes, particularly the high prevalence of *tsst-1*, underscores the pathogenic potential of circulating strains and reinforces the importance of molecular screening in clinical diagnostics and infection control strategies.

Keywords: Children, impetigo, PCR, *Staphylococcus aureus*, virulence genes

Paper Type: Research Paper.

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Introduction

Impetigo is a very common bacterial skin infection that affects children globally. It shows in two clinical forms: non-bullous impetigo, which results from direct inoculation of bacteria into minor skin abrasions, and bullous impetigo, which arises from the action of exfoliative toxins generated by Staphylococcus aureus. These toxins disrupt the skin's protective barrier, making it vulnerable to further infection and damage. The exfoliative toxins, particularly exfoliative toxin A (ETA) and exfoliative toxin B (ETB), play a destructive role in the epidermis. These toxins target intercellular adhesion molecules like desmoglein-1 and desmocollin-1, leading to epidermal splitting and characteristic blister formation (Medugu et al., 2023). Staphylokinase, another key virulence factor, acts by cleaving plasminogen to form plasmin, which in turn dissolves fibrin deposits at the site of infection, thereby facilitating bacterial spread and nutrient acquisition. The molecular characterization of these virulence genes is crucial for understanding the pathogenic mechanisms of methicillin-resistant Staphylococcus aureus (MRSA) strains involved in impetigo. This situation is most frequently created by S. aureus (Brazel et al., 2021), which can express a range of virulence factors responsible for numerous clinical manifestations. One of the major virulence factors generated by S. aureus is the toxic shock syndrome toxin-1 (TSST-1). This superantigen leads to a cascade of immune responses resulting in systemic symptoms like diffuse rash, desquamation, and hyperemia of the mucous membranes—containing the conjunctiva, mouth, and vaginal epithelium. Furthermore, exfoliative toxins like ETA and ETB create persistent injury to the skin. The eta gene, once expressed, creates intraepidermal cleavage by targeting desmoglein-1, whereas the etb gene acts on desmocollin-1 in the stratum granulosum. Clinical symptoms like fatigue and skin peeling often emerge a few days after toxin production. Improper food handling in neonatal incubators or unsanitary situations may also expose ETB to heat and sunlight, further enhancing its production (Schmitt et al., 2025; Chen et al., 2022). Impetigo is typically created by Staphylococcus aureus, but Group A beta-hemolytic Streptococcus pyogenes can also be involved. It remains a major public health concern in low-resource settings, especially in rural or underserved regions where poor hygiene, overcrowding, and lack of healthcare facilities prevail (Yassin et al., 2022). In such environments, S. aureus strains carrying virulence genes like tst, eta, and etb are of particular concern. These strains are often related with severe forms of impetigo, containing the bullous type. S. aureus is capable of producing different toxins and enzymes, like alpha-toxin, TSST-1, Panton-Valentine leukocidin (PVL), exfoliative toxins, enterotoxins, hemolysins, and coagulase—each playing distinct roles in disease progression. Some of these, like TSST-1 and enterotoxins, have systemic effects, leading to situations like toxic shock syndrome and food poisoning, respectively. Besides systemic illness, S. aureus contributes to localized infections through the production of

extracellular proteins that act at the infection site. Certain strains generate ETA and ETB toxins, which have been directly linked to the development of impetigo. In hot and humid climates, like Iraq, impetigo remains one of the most prevalent superficial bacterial skin infections among children. Reports indicate that in Iraq, impetigo is one of the most commonly registered pediatric dermatological situations (Yassin et al., 2022; Ahmad-Mansour et al., 2021). The emergence of antibiotic resistance in S. aureus, particularly MRSA strains, has further complicated impetigo treatment. The relevance of quinolone resistance in impetigo has been documented, with a high prevalence of resistant phenotypes announced even before quinolone therapy is initiated. Treatment failures due to non-beta-lactam-resistant MRSA strains have become increasingly common, particularly in regions with restricted access to alternative therapies (Alfeky et al., 2022). In central Iraq, especially in Al-Diwaniyah City, impetigo has become an important pediatric health concern due to socioeconomic challenges and inadequate healthcare infrastructure. The situation is particularly prevalent among children, many of whom live in crowded and unsanitary environments. Recent investigations have also announced zoonotic transmission of S. aureus, with similar strains causing impetigo in both humans and animals. These strains often carry multiple virulence genes, containing tst, eta, and etb, denoting a complex pattern of transmission and pathogenicity (Kadhum & Abood, 2022; Al-Kahfaji, 2022). To date, different investigations in southern Iraq have investigated the molecular prevalence of these virulence genes in S. aureus isolates from numerous clinical sources. This investigation builds upon previous research concerning the prevalence of MRSA in wound infections among children in Al-Diwaniyah City, expanding the investigation to include isolates from impetigo cases in children. In addition, recent advancements in molecular biology and epigenetics suggest that gene expression in S. aureus may be modulated by numerous environmental and epigenomic factors. These include DNA methylation, histone modifications, chromatin remodeling, microRNAs, and long non-coding RNAs. Such mechanisms interact with external factors, like nutrition, climate, and pathogen exposure—to influence gene expression and disease phenotypes (Mousavizadeh et al., 2009; Mohammadabadi et al., 2021). Complex multi-level interactions between the genome, epigenome, and environment may explain the variability in virulence and clinical outcomes (Sulimova et al., 2007; Mohammadabadi et al., 2024b). The expression of eukaryotic genes is both temporally and spatially regulated, with specific genes expressed in a tissue- and development-stage-specific manner (Shahsavari et al., 2023; Mohammadabadi et al., 2024a). Furthermore, gene expression is influenced by the quantity of gene products needed in different tissues (Hajalizadeh et al., 2022). Therefore, the cellular or chromosomal investigation of virulence-related genes is essential for understanding bacterial pathogenicity at the molecular

level (Mohammadinejad et al., 2022; Mohammadabadi et al., 2024c). Thus, the aim of this investigation was to investigate the molecular presence of the tst, eta, and etb genes in Staphylococcus aureus isolates from children with impetigo in Al-Diwaniyah City, Iraq, to better understand their role in disease pathogenesis and inform potential therapeutic strategies.

Materials and methods

Sample collection: Clinical specimens were achieved from pediatric patients showing with impetigo at healthcare centers in Al-Diwaniyah, Iraq. Swab samples were gathered from numerous body regions containing the face, hands, feet, and genital area applying sterile cotton swabs. To maintain sample integrity and minimize contamination, aseptic techniques were strictly followed through collection. The swabs were immediately placed into sterile transport media and transported to the laboratory under refrigerated situations for microbial analysis.

Bacterial isolation and identification: Samples were cultured on Mannitol Salt Agar and Blood Agar plates and incubated at 37°C for 24–48 hours under aerobic situations. Colonies exhibiting typical morphology of *Staphylococcus aureus*, containing golden-yellow pigmentation, smooth convex shape, and beta-hemolysis were sub-cultured to obtain pure isolates. Standard biochemical tests containing catalase, coagulase, and Gram staining were carried out in accordance with protocols outlined in the Clinical and Laboratory Standards Institute (CLSI) guidelines to affirm bacterial identity.

DNA Extraction and 16S rRNA Gene Amplification: Genomic DNA was extracted from affirmed *S. aureus* isolates applying a commercial bacterial DNA extraction kit (e.g., Qiagen, Germany), following the manufacturer's protocol. The 16S rRNA gene was amplified by polymerase chain reaction (PCR) applying a gradient thermal cycler (Eppendorf, Germany). The primers applied were adopted from Srivastava et al. (2008) as below:

Forward primer: 5′-AGAGTTTGATCCTGGCTCAG-3′ and Reverse primer: 5′-CTTGTGCGGGCCCCCGTCAATTC-3′. PCR reaction mixture (50 µL total volume) for 16S rRNA gene amplification is shown in Table 1 and PCR thermocycling situations for 16S rRNA gene amplification are shown in Table 2.

Diagnosis of exfoliative toxin genes (Tsst, Eta, Etb): The presence of toxin genes (*tsst*, *eta*, *etb*) in the *S. aureus* isolates was evaluated applying specific primers (Table 3) in 50 µL reaction mixture (Table 4) with standard situations (Table 5).

Agarose gel electrophoresis: Amplified PCR products were resolved applying 0.8% agarose gel electrophoresis prepared with 1× TBE (Tris-Borate-EDTA) buffer. Agarose was dissolved by heating and cooled to approximately 50°C before adding RedSafe™ nucleic acid

staining solution (iNtRON Biotechnology, Korea). The gel was poured into a casting tray with combs and permited to solidify at room temperature. A molecular weight marker (100–1500 bp DNA ladder) was run alongside the samples. Electrophoresis was carried out at 100 volts for 1 hour. DNA bands were visualized applying a UV transilluminator, and amplicon sizes were compared with the DNA ladder.

Table 1. PCR reaction mixture (50 µL total volume) applied in this investigation for 16S rRNA gene amplification

Component	Final concentration / volume
Genomic DNA	10 ng
Taq DNA Polymerase	2.5 U
10× PCR Buffer	5 µL
dNTPs (each)	200 µM
Forward Primer	10 pmol
Reverse Primer	10 pmol
$MgCl_2$	1.5 mM
Nuclease-free water	To 50 µL total

Table 2. PCR thermocycling situations applied in the current investigation for 16S rRNA gene amplification

Step	Temperature	Time	Cycles
Initial Denaturation	94°C	3 minutes	1
Denaturation	94°C	30 seconds	
Annealing	55°C	30 seconds	30
Extension	72°C	1 minute	
Final Extension	72°C	10 minutes	1

Results and discussion

16S rDNA gene amplification: The amplification of the 16S rDNA gene was successfully achieved, as evidenced by distinct and bright bands observed under a UV transilluminator following agarose gel electrophoresis. The expected amplicon size of approximately 1500 base pairs (bp) was clearly visible in all bacterial isolates, affirming effective PCR amplification (Figure 1). The consistency of band intensity across the gel lanes indicates good DNA quality and successful amplification across all samples.

Diagnosis of genes involved in impetigo: PCR assays targeting the exfoliative toxin genes **ETA**, **ETB**, and **TSST-1** in *Staphylococcus aureus* isolates demonstrated the presence of these virulence factors with distinct amplicons visualized on agarose gels. Each gene showed specific

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and consistent banding patterns denoting successful amplification (Figures 2, 3, and 4).

Table 3. Primers for diagnosis of exfoliative toxin genes in the current investigation

Gene	Primer	Sequence (5′→3′)	Product Size	Reference
tsst	F	ATGGCAGCATCAGCTTGATA	350 bp	Becker et al., 1998
	R	TTTCCAATAACCACCCGTTT		
eta	F	CTAGTGCATTTGTTATTCAA	119 bp	Mehrotra et al., 2000
	R	TGCATTGACACCATAGTACT		
etb	F	ACGGCTATATACATTCAATT	200 bp	Mehrotra et al., 2000
	R	TCCATCGATAATATACCTAA		

Table 4. PCR reaction mixture (50 µL total) for diagnosis of exfoliative toxin genes

Component	Final Concentration / Volume
Genomic DNA	10 ng
Taq DNA Polymerase	2.5 U
10× PCR Buffer	5 µL
dNTPs (each)	200 µM
Forward Primer	10 pmol
Reverse Primer	10 pmol
$MgCl_2$	1.5–2 mM
Nuclease-free water	To 50 µL total

Table 5. PCR thermocycling situations for diagnosis of exfoliative toxin genes

Gene	Initial Denaturation	Cycles	Denaturation	Annealing	Extension	Final Extension	Reference
eta	94°C, 3 min	30	94°C, 30 sec	52°C, 30 sec	72°C, 30 sec	72°C, 5–10 min	Mehrotra et al., 2000
etb	94°C, 3 min	30	94°C, 30 sec	52°C, 30 sec	72°C, 30 sec	72°C, 5–10 min	Mehrotra et al., 2000
tsst	94°C, 3 min	30	94°C, 30 sec	55°C, 30 sec	72°C, 30 sec	72°C, 5–10 min	Becker et al., 1998

Molecular characterization of *S. aureus* via 16S rRNA: Amplification of the 16S rRNA gene in all *S. aureus* isolates affirmed the presence of this conserved bacterial marker. Gel electrophoresis revealed the expected ~1500 bp band across all samples, validating the DNA extraction quality and specific binding of the primers. The 16S rRNA gene is commonly applied for bacterial taxonomy and species-level identification due to its high conservation and phylogenetic informativeness. This result aligns with previous investigations, like AlMosawi et

al. (2024), who highlighted the evolutionary utility of 16S rRNA in classifying *S. aureus* strains.

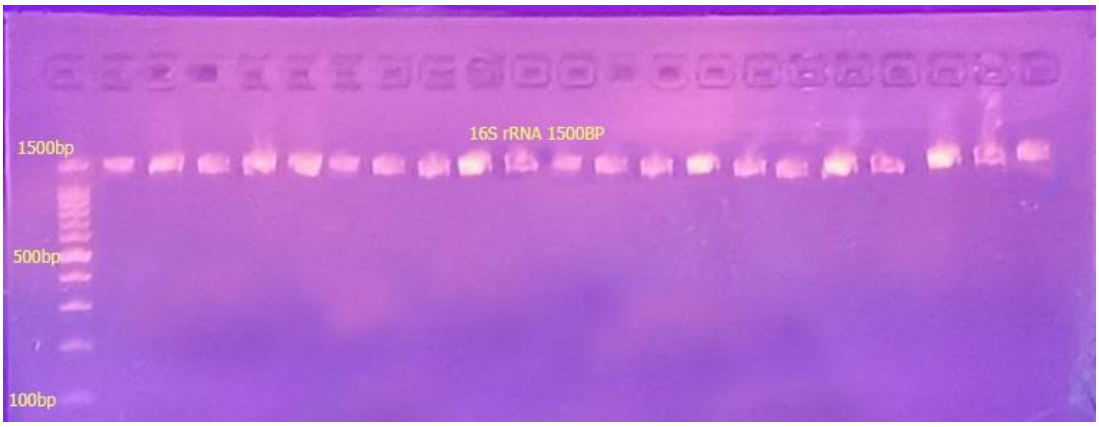

Figure 1. Agarose gel electrophoresis results of 16S rDNA gene amplification from bacterial isolates. Amplified bands (~1,500 bp) are shown for isolates 1–21. Electrophoresis was carried out at 80 V. Lane M: molecular weight marker (100–1500 bp DNA ladder)

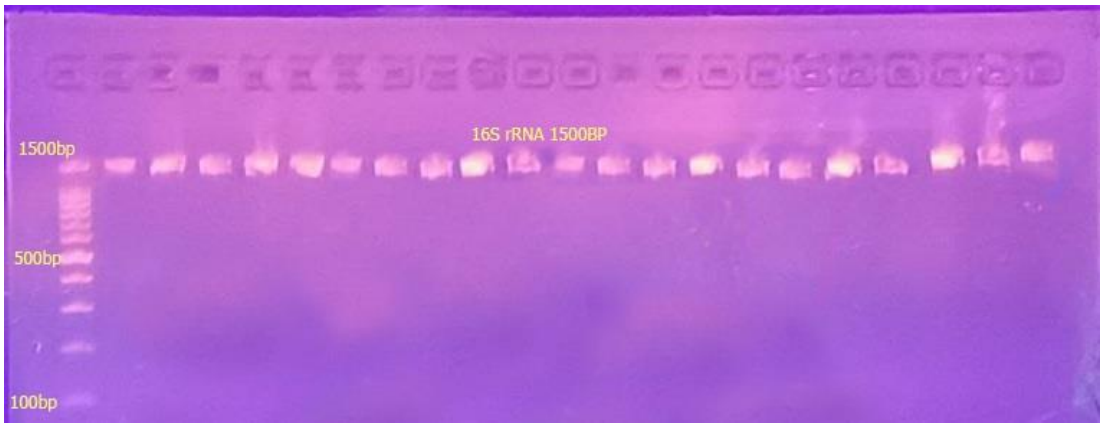

Figure 2. Agarose gel electrophoresis for ETB gene amplification. Bands were observed at ~119 bp across isolates 1–21. Lane M: DNA ladder (100–1500 bp)

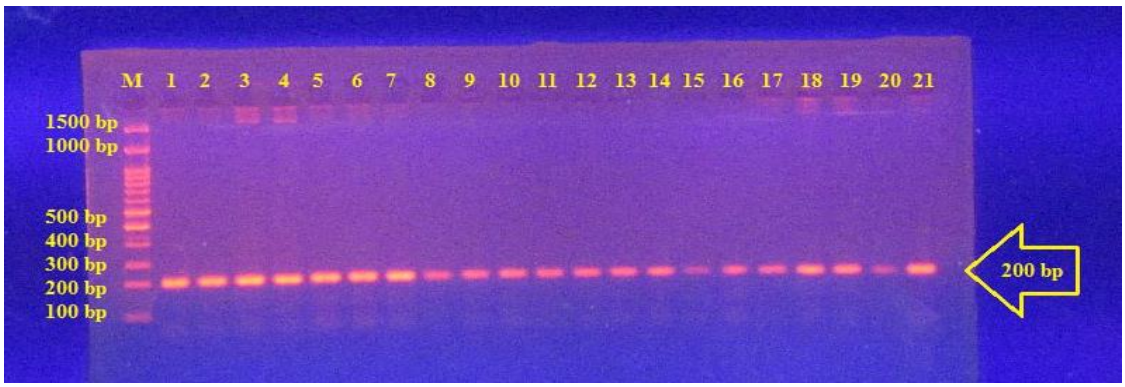

Figure 3. Agarose gel electrophoresis of the Exfoliative Toxin A (ETA) gene. Amplified bands were observed at ~200 bp for all isolates (1–21). Lane M: DNA ladder (100–1500 bp)

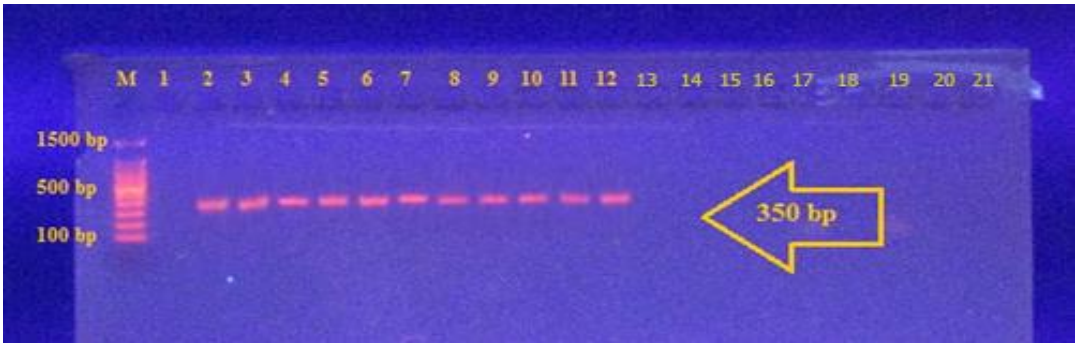

Figure 4. Agarose gel electrophoresis of the TSST-1 gene showing amplification at ~350 bp for 11 of 21 isolates. Electrophoresis managed at 80 V. Lane M: DNA ladder (100–1500 bp)

Similarly, Gumaa et al. (2023) observed 100% sequence similarity between foodborne *S. aureus* isolates and database references, reinforcing its diagnostic accuracy. Alsanie et al. (2018) further noted that while 16S rRNA is reliable for genus-level classification, complementary markers are recommended for distinguishing closely related species like coagulase-negative staphylococci. Thus, the consistent presence of this gene in all isolates affirms its value as a foundational diagnostic marker.

Diagnosis of exfoliative toxin genes (ETA, ETB, TSST-1): PCR analysis affirmed the presence of exfoliative toxin genes ETA and ETB in 100% of isolates (21/21), while TSST-1 was detected in 11 of 21 isolates (52.4%). The amplification patterns corresponded with known product sizes, affirming successful gene identification and potential virulence. This investigation centralized on characterizing toxin genes of *S. aureus* from impetigo-infected children in Al-Diwaniyah City, Iraq. The universal presence of ETA and ETB genes suggests their meaningful contribution to pathogenesis in this region. Impetigo, a common pediatric skin infection, is strongly related with exfoliative toxins that degrade desmoglein-1, leading to intraepidermal blistering and skin desquamation. Our results mirror those announced by Muhammad et al. (2024), who emphasized pediatric vulnerability to toxin-producing *S. aureus*, and Neamah (2024), who proposed molecular surveillance of virulence genes for effective infection control.

Impact of the ETA gene: The universal diagnosis of the ETA gene highlights its epidemiological importance. ETA, a serine protease, specifically cleaves desmoglein-1, a cadherin involved in epidermal cell-cell adhesion, resulting in blister formation and the characteristic skin peeling seen in staphylococcal scalded skin syndrome (SSSS). Mohseni et al. (2018) and Taher & Othman (2024) similarly announced high prevalence (up to 80%) of ETA in pediatric skin infections. Recent investigations, containing Díaz-Formoso et al. (2023), have linked gene regulatory mutations at the eta locus with improved toxin expression and

pathogenicity. Furthermore, Del Barrio-Tofiño et al. (2020) announced higher ETA prevalence in hospital-acquired strains in South America, while Bazghandi et al. (2021) found ETA to be less common in community-acquired isolates. These variations underscore the influence of environmental, antimicrobial, and host-related factors on gene distribution.

ETB gene diagnosis and clinical implications: Interestingly, all 21 isolates also tested positive for the **ETB** gene, a result that deviates from prior research. Kot et al. (2022) noted that ETB is less frequently detected than ETA and is typically related with more invasive or systemic infections. The universal diagnosis of ETB in our samples may reflect unique regional strain dynamics or enhanced virulence within this population. Investigations by Tam & Torres (2019) suggest that ETB-expressing strains are more likely to form persistent biofilms and evade host immune responses. Camaione (2025) also proposed that co-expression of ETB with other virulence factors might contribute to both immune evasion and antimicrobial resistance, increasing the complexity of infection management.

TSST-1 gene and broader implications: The **TSST-1** gene was detected in 11 of 21 isolates (52.4%), a result consistent with Omar & Mohammed (2021), who announced 46.7% prevalence in impetigo isolates. Although presence does not affirm active toxin production, TSST-1 is a potent superantigen capable of inducing systemic inflammation and toxic shock syndrome (Brosnahan & Schlievert, 2011). Zhao et al. (2019) found strong associations between TSST-1 and methicillin-resistant *S. aureus* (MRSA) strains. Merriman et al. (2016) proposed applying TSST-1 as a biomarker for disease severity in staphylococcal infections due to its impact on cytokine dysregulation. Its partial distribution in this investigation suggests that TSST-1 contributes to virulence in a subset of more invasive or systemic strains circulating locally.

Broader context: virulence, resistance, and biofilm formation: The diagnosis of all three major toxin genes underscores the pathogenic potential of *S. aureus* isolates from impetigo cases in children. However, virulence is not identified by toxin genes alone. As highlighted by Al-Bukhalifa & Tameemi (2024) and Chen et al. (2022), resistance profiles and biofilm-forming capacity are equally important for understanding clinical outcomes. Therefore, future investigations should integrate toxin gene profiling with antimicrobial resistance patterns and biofilm assays to fully characterize *S. aureus* epidemiology in pediatric skin infections.

Conclusions: This investigation revealed a high prevalence of ETA and ETB genes and moderate occurrence of TSST-1 among *Staphylococcus aureus* isolates from impetigo-infected children in Al-Diwaniyah, Iraq. The consistent presence of exfoliative toxins suggests their critical role in disease pathogenesis. The diagnosis of TSST-1 in a subset of isolates implies strain heterogeneity and varying virulence potential. These results support the implementation of

molecular diagnostics for early identification of virulent *S. aureus* strains and inform regional public health strategies aimed at improving infection control, particularly in pediatric populations.

Author contributions

Conceptualization and design: A.A.J.; Data acquisition: A.A.J.; Data analysis: M.S.; Data interpretation: M.S.; Manuscript drafting: M.S.; Critical revision of the manuscript: A.A.J.; Final approval of the manuscript: A.A.J.; Writing—original draft preparation: M.S.; Writing—review and editing, supervision: A.A.J. All authors have read and approved the final version of the manuscript.

Data availability statement

The datasets generated and analyzed through the current investigation are available from the corresponding author upon reasonable request.

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Ethical considerations

This investigation was managed in accordance with the ethical principles outlined in the Declaration of Helsinki. It was approved by the Institutional Review Board and the Research Ethics Committee of the University of Al-Qadisiyah, Iraq. Informed consent was achieved from all participants. Participation was voluntary, and all subjects were informed about the purpose, procedures, and their right to withdraw from the investigation at any time without any consequences. Confidentiality of all personal data was ensured.

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Conflict of interest

The authors declare that there are no conflicts of interest related to this investigation.

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مطالعه مولکولی ژن‌های Tsst، Eta و Etb در باکتری Staphylococcus aureus جدا شده از بیماران مبتلا به زردزخم در میان کودکان شهر دیوانیه عراق

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چکیده

هدف: Staphylococcus aureus یک پاتوژن فرصت‌طلب و همه‌کاره است که مسئول طیف وسیعی از بیماری‌های انسانی، از عفونت‌های سطحی پوست گرفته تا شرایط سیستمیک تهدیدکننده حیات است. یکی از تظاهرات بالینی رایج آن زردزخم است. عفونتی مسری در پوست که عمدتاً کودکان را تحت تأثیر قرار می‌دهد و معمولاً با S. aureus به‌عنوان عامل اصلی بیماری همراه است. شیوع این باکتری در عفونت‌های پوستی و بافت نرم به یک نگرانی رو به رشد در حوزه سلامت عمومی، به‌ویژه در جمعیت‌های کودکان و مناطقی با دسترسی محدود به خدمات درمانی پیشرفته تبدیل شده است. مطالعه حاضر با هدف بررسی حضور مولکولی ژن‌های tsst، eta و etb در جدایه‌های S. aureus به‌دست‌آمده از کودکان مبتلا به زردزخم در شهر دیوانیه عراق انجام شد. این تحقیق با ترکیب تکثیر ژن 16S rRNA و شناسایی ژن‌های ویرولانس، درک عمیق‌تری از اپیدمیولوژی مولکولی و ویژگی‌های بیماری‌زای S. aureus در یک جمعیت بیمار آسیب‌پذیر ارائه می‌دهد.

مواد و روش‌ها: این مطالعه بر روی جدایه‌های بالینی به‌دست‌آمده از کودکان مبتلا به زردزخم که به درمانگاه‌های پوست در شهر دیوانیه مراجعه کرده بودند انجام شد. در مجموع ۲۱ نمونه سواب از ضایعات پوستی آلوده با استفاده از سواب‌های پنبه‌ای استریل جمع‌آوری گردید. DNA ژنومی از جدایه‌های تأییدشده S. aureus استخراج شد. برای تأیید هویت جدایه‌ها، PCR هدفمند بر روی ژن 16S rRNA انجام گرفت. حضور ژن‌های tsst، eta و etb با استفاده از PCR معمولی و پرایمرهای اختصاصی بررسی شد.

نتایج: تمام جدایه‌های S. aureus باند مشخصی به اندازه ۱۵۰۰ جفت باز در PCR مربوط به ژن ۱۶S rRNA نشان دادند که بیانگر موفقیت‌آمیز بودن تکثیر این ژن هدف بود. این نتیجه همچنین کیفیت بالای DNA باکتریایی استخراج‌شده و اختصاصی بودن پرایمرهای مورد استفاده را نشان داد. ماهیت حفاظت‌شده ژن 16S rRNA آن را به یک نشانگر مولکولی قابل اعتماد برای شناسایی باکتری تبدیل کرده است. علاوه بر این، حضور ژن‌های tsst-1، eta و etb با استفاده از PCR بررسی شد و هر ژن الگوی تکثیر خاصی از خود نشان داد. از میان ۲۱ جدایه بالینی، ۱۱ مورد (۵۲.۴٪) برای ژن tsst-1 مثبت بودند. ژن‌های eta و etb نیز شناسایی شدند، اما با فراوانی‌های متفاوت، که نشان‌دهنده توزیع متفاوت این عوامل ویرولانس در بین جدایه‌هاست.

نتیجه‌گیری: این مطالعه حضور مولکولی ژن‌های ویرولانس کلیدی tsst-1، eta و etb را در جدایه‌های S. aureus از موارد زردزخم در کودکان برجسته می‌کند. شناسایی این ژن‌های سمی، به‌ویژه شیوع بالای tsst-1، پتانسیل بیماری‌زایی سویه‌های در گردش را برجسته کرده و اهمیت غربالگری مولکولی در تشخیص‌های بالینی و راهبردهای کنترل عفونت را تقویت می‌کند.

کلمات کلیدی: استافیلوکوکوس اورئوس، زردزخم، ژن‌های ویرولانس، کودکان، PCR

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