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REVIEW ARTICLE Open Access

Prevalence of MRSA Genes in Kurdistan Region: Systematic Review

Heshu Jalal Ahmed [1]*, Dana Luqman Qadir[1], Khanda Tareq Salim [1], and Elaf Jalal Tahir[1]
Mardin Farsat Ghazali [1]

[1] Biology Education Department, Tishk International University, Erbil, Iraq.

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**Email address:*
heshu.jalal@tiu.edu.iq
**Corresponding Author*

Abstract: Antibiotic resistance, particularly Methicillin-resistant Staphylococcus aureus (MRSA) is a trending global threat associated with severe infections and high morbidity and mortality rates. This study was carried out to systematically review the prevalence and distribution of MRSA in the Kurdistan region. A comprehensive search identified 244 studies, but only 14 meeting the inclusion criteria. Studies from Zakho, Duhok, Erbil, Sulaimani, and Kirkuk revealed varying MRSA rates, with high rates among urinary tract patients, diabetic foot patients, and healthcare workers. The genetic analysis highlighted the presence of the mecA gene as a predominant resistant gene. The distribution of MRSA was unequal, as Duhok had the highest incidence. These findings emphasize the urgent need for intervention and surveillance strategies to overcome this combat with MRSA and antibiotic resistance in the Kurdistan region.

Keywords: *MRSA; Kurdistan; mecA.*

1. Introduction

Antibiotic resistance is an increasing global health crisis that threatens the effectiveness of many medications due to different mechanisms evolved by bacteria [1].

Staphylococcus aureus, one of the top threatening strains reported by the CDC, is resistant to methicillin due to mechanisms that confer resistance to many antibiotics. It presents a global challenge, making traditional antimicrobial treatments ineffective. Consequently, the proliferation of these strains in hospitals and community settings has heightened the need for effective methicillin-resistant staphylococcus aureus (MRSA) infection management and control [2, 3]. First labeled in the 1960s, MRSA was originally thought to be a hospital-acquired strain. The bacteria are correlated with significant morbidity and death rates. The challenge of antibiotic resistance, especially methicillin resistance, complicates the treatment and prevention of MRSA infections [4].

The global prevalence of MRSA varies across regions, a recent meta-analysis shows that the prevalence of MRSA colonization among residents of elderly care centers globally is 14.7% [5] with different rates in specific regions such as 22.27% in the Americas while records show lower incidence in European countries, showing 10.93% [5].

The resistance of S. aureus to multiple antibiotics is due to the possession of mobile genes, this features the significance of knowing the predominance of MRSA and its variations comprehensively and creating unused treatment procedures instead of depending exclusively on conventional methods [6]. MRSA strains found in both health centers and communities is resistant to different antimicrobials, including imipenem, nafcillin, oxacillin, cephalosporins, and beta-lactamase inhibitors [7]. Methicillin resistance happens through the integration of a foreign gene that integrates into the chromosomal DNA, changing the binding location of penicillin-binding proteins (PBP) and inhibiting the liking for beta-lactam antibiotics [3]. The significant lack of data on the prevalence of Methicillin-resistant Staphylococcus aureus (MRSA) and its causative genes in the Kurdistan region is a key factor in the resistance to various modern medications. Despite the general concern over this issue, which encompasses multidrug-resistant bacteria, there remains a scarcity of knowledge regarding MRSA, its strains, and the responsible genes in this region, to systematically investigate and evaluate the prevalence, distribution, and characteristics of MRSA genes among bacterial isolates.

2. Methods

2.1 Search strategy

This review was performed following the Preferred Reporting Items for Systematic Reviews and Meta-analysis (PRISMA) guidelines. The search was performed on the following databases and other publishers: PubMed, Science Direct, and Google Scholar. We aimed to identify studies that reported the prevalence of MRSA in the Kurdistan region. We used the following keywords: methicillin-resistant *Staphylococcus aureus*, 'MRSA', 'antibiotic resistance', and 'Kurdistan region'.

2.2 Study selection

Studies were included in the study if they met the following criteria: 1) studies published in the English language. 2) Reported extractable data from clinical specimens from the Kurdistan region. 3) studies that provide data on prevalence, frequency, proportion

Exclusion criteria as detailed in Figure 1 were as follows: 1) Studies with bias. 2) Studies with overlapping data. 3) studies with insufficient data.

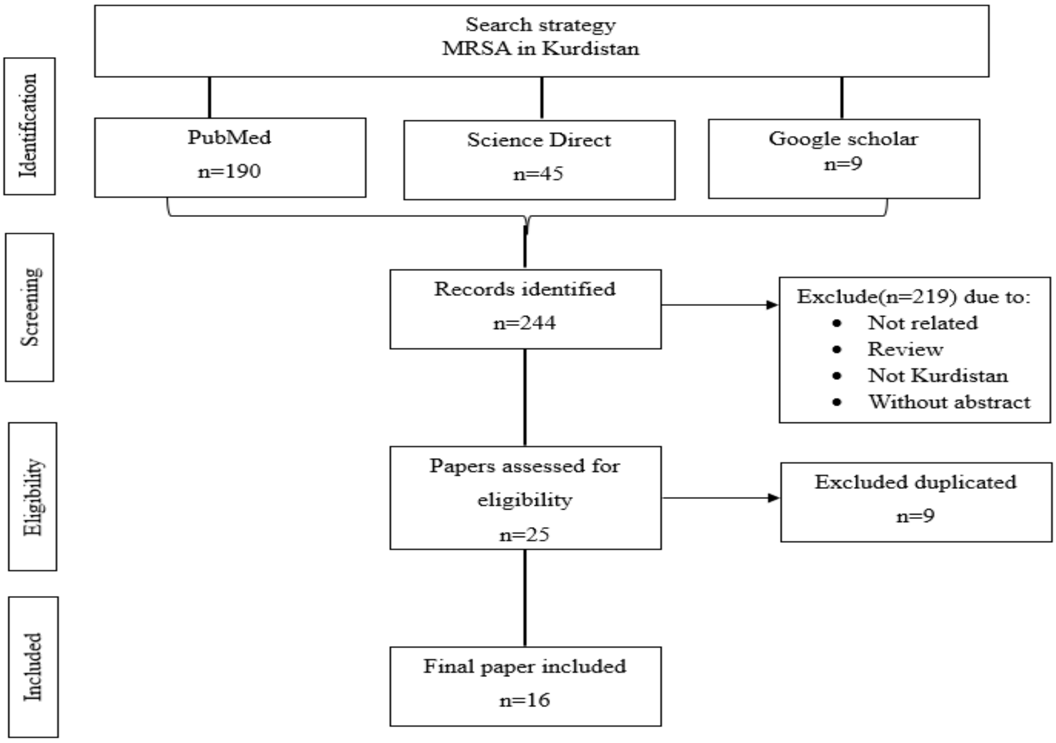

Figure 1: Schematic diagram of the literature search and study selection.

2.3 Data extraction

The extracted variables of each study included the following: the specific city of Kurdistan where the study was conducted, the duration over which the study was conducted, the demographic or group of individuals from whom samples were collected, the total number of MRSA cases identified in the study, the type of clinical specimen collected, gene detection results.

3. Results

3.1 General findings

This systematic review identified and analyzed 244 studies from PubMed, Google Scholar, and Science Direct databases. After excluding 219 studies, 25 were assessed for eligibility. Nine of these were excluded due to duplication, resulting in only 16 studies being included in the final analysis. These studies provided necessary data on the prevalence and genetic characteristics of MRSA in various cities within the Kurdistan region.

In Zakho, many studies showcased the incidence of MRSA among different populations. One study conducted over 8 months involving urinary tract infection (UTI) revealed that out of 402 urine samples, 37 (12.6%) were identified as Staphylococcus aureus, among which 28 (75.7%) were MRSA. The study reported a comparably higher infection rate among females, particularly those with chronic conditions and married individuals, genetic analysis showed 14 (50%) of the MRSA isolates harbored all three resistance and virulence genes (mecA, icaA, and luk-PV), while other isolates had a combination of these genes with mecA present in all [8].

In Duhok multiple studies are conducted over periods ranging from 6 to 13 months focused on different populations including scholars, clinical patients, preoperative patients, and students. Nasal swabs from scholars aged 14-23 years showed an MRSA prevalence of 2.04% in urban areas and 21.95% in rural areas, additionally, hospitalized patients had a 77.42% MRSA prevalence, with genes such as nuc, PVL mecA, and eta detected [9].

In Sulaimani, a 3-month study focusing on diabetic foot infection patients found that MRSA was present in 43 out of 46 diabetic foot abscesses, with the mecA gene detected in 41.6% of Staphylococcus aureus isolates.

In Erbil city, the period of studies ranged from 9 months to 4 years, and many clinical samples and patients were examined. In clinical specimens, there was a high prevalence of virulence genes, with 228 samples testing positive for MRSA. Among cancer patients, 100 isolates showed multidrug resistance.

In Kirkuk City, a one-year study conducted on a population of healthy individuals reported 236 MRSA carriers, representing a 4.5% prevalence of community-acquired MRSA nasal carriage among the healthy population. These findings suggest that MRSA is not confined to hospital environments and highlight the importance of public health surveillance to address community-acquired MRSA.

Table 1: Summary of included studies on the prevalence of MRSA in the Kurdistan region

S/N	**Study Period**	**City**	**Number of MRSA**	**Population Sample**	**Finding**	**Ref.**
1	8 months	Zakho	104	Urinary tract infections (UTIs)	Out of 402 urine samples collected, 37 (12.6%) were identified as S. aureus, with a high prevalence of MRSA (75.7%). **Method of detection:** Disc diffusion test confirmed by molecular identification of gene markers of MRSA. Females showed a higher infection rate than males, with most cases being chronic and in married individual.	[8]
2	6 months	Duhok	78	Nasal swabs were found in the nostrils of scholars between 14-23 years old.	Methicillin-resistant S. aureus (MRSA) prevalence was 2.04% in urban and 21.95% in rural districts. Urban areas had a higher S. aureus carriage rate, while more MRSA strains were found in rural regions. **Method of detection:** Kirby-Bauer disc diffusion and agar dilution assay, confirmed by molecular detection of MRSA genes	[9]
3	12 months	Duhok	104	Clinical samples	The study found MRSA with one strain was resistant to vancomycin, and another strain showed high-level resistance to mupirocin. **Method of detection:** Kirby-Bauer disc diffusion and agar dilution assay were then tested by molecular methods for the presence of *mecA, pvl,* and *luk*-PV-1.	[10]
4	one year	Duhok	41	Nasal swabs were obtained from the patient	The study conducted at Azadi Teaching Hospital in Duhok Province, Iraq, found that 27.3% of preoperative patients were carriers of MRSA in their nasal bone passages. **Method of detection:** MRSA was detected using disc diffusion by the Kirby Bauer method.	[11]

5	7 months	Zakho	27	Adult urinary tract pathogens	The study identified MRSA in adults affected by urinary tract illnesses (UTIs) in Zakho City. All S. aureus isolates were confirmed to have both *nuc* and *mecA* genes.	[12]
6	6 months	Duhok	56	Hospital staff and community students	The study found that all healthcare labors in Duhok, Kurdistan, Iraq were carriers of S. aureus. **Method of detection:** MRSA was detected using disc diffusion by Kirby Kirby-Bauer method.	[13]
7	3 months	Sulaimani	43	Diabetic foot infection (DFI)	*MRSA* was detected in diabetic foot abscesses, with the mecA gene present in 41.6 of *Staphylococcus aureus* isolates. **Method of detection:** For the detection of MRSA disc diffusion method was used, and genotypic detection was carried out by detecting two genes (*mecA* and *PVL*)	[14]
8	9 months	Erbil	228	Human specimens	The research highlighted the manifestation of resistance genes in the insulates, indicating the genetic basis of antibiotic resistance in the samples studied. **Method of detection:** The disk diffusion method was carried out to detect MRSA from wounds and burn infection clinical samples.	[15]
9	4 years	Erbil	100	Cancer patients	Identified 100 S. aureus isolates from various clinical samples, showing multidrug resistance. Antibiotic susceptibility tests revealed resistance to more than six antibiotics. **Method of detection:** Disc diffusion was used.	[16]
10	One year	Erbil	114	Various clinical specimens	All MRSA separates examined confirmed the mecA gene, associated with methicillin fighting. MRSA strains exhibited resistance to β-lactam antibiotics, highlighting the challenge of treating MRSA infections effectively **Method of detection:**	[17]

					MRSA was detected using a PBP2a kit rapid assay.	
11	One year	Kirkuk	236	healthy individuals of various ages	The study found that the incidence of public-acquired S. aureus (CA-SA) nasal carriers was 16.6%, with 4.5% being carriers of community-acquired CA-MRSA. **Method of detection:** Oxacillin-screening test on Mueller-Hinton agar supplemented with 6 µg/mL oxacillin and 4% NaCl.	[18]
12	11 months	Duhok	62	Inpatients admitted	MRSA was discovered in 77.42% of S. aureus detaches, predominantly from skin swabs. The authorities of nuc, pvl, mecA, and eta genes were identified in varying proportions among the isolates. **Method of detection:** The Cefoxitin disk diffusion method, which assesses the inhibition zone around a cefoxitin disk, is a phenotypic detection for *mec*A-mediated resistance. Another method used is the VITEK2 system, as well as the molecular method.	[19]
13	13 months	Duhok	27	Student groups in various departments	The study contributes to understanding nasal transport patterns of *Staphylococcus aureus* and the importance of preventing nosocomial illnesses. **Method of detection:** MRSA was detected using the Mueller-Hinton agar method using methicillin or oxacillin disks.	[20]
14	N.M	Duhok	78	Health care workers with non HCWs	The study found a high prevalence of MRSA among healthcare staff (HCWs) in Kurdistan, Iraq. **Method of detection:** The Kirby-Bauer disk diffusion method and agar dilution assay were used to detect MRSA.	[21]
15	5 months	Duhok	16 MRSA 2nmrMRSA	150 burn swabs, 50 wound swabs from	S. aureus was more predominant than P. aeruginosa in burns and wounds. 37.5% of S. aureus were mecA positive.	[26]

			30 MSSA	hospitalized patients	**Method of detection:** Disc diffusion and molecular methods were used.	
16	8 months	Duhok	76 from the community and 49 among Syrian refugees	Nasal swabs	MRSA carriage rate was not significantly different between the host community and refugees. SCCmec types IV (67.1%) and V (5.26%) were most common in the host community while IVa (49%) and V (2.04) were dominant among refugees. **Method of detection:** Disc diffusion and PCR (molecular method) were used to detect MRSA.	[27]

3.2 Prevalence of virulent genes

Methicillin-resistant Staphylococcus aureus is known to harbor different genes that are accountable for its resistant and virulence nature. The most common of these genes include a chart in Figure 2 (mecA genes, nuc genes, icaA genes, and PVL). According to the results accumulated from our review, the mecA gene is the most common gene and its prevalence across different cities in Kurdistan is 52%, It is followed by the nuc gene and PVL which are the second and third most common genes respectively, and they account for 24% and 21% of MRSA from all the research we reviewed. The least common gene reported is the icaA gene, which is reported to be only 3% of the detected genes.

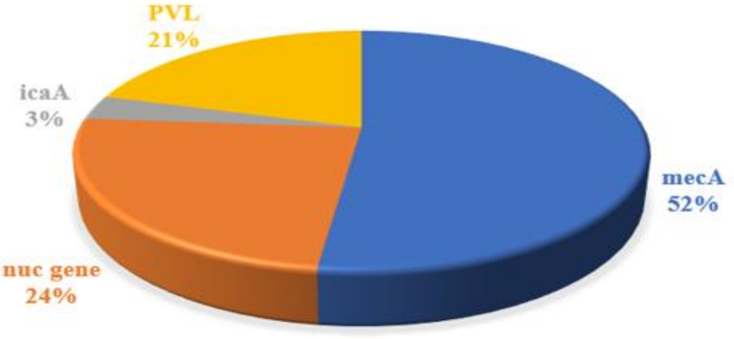

Figure 2: Prevalence of MRSA genes among methicillin-resistant Staphylococcus aureus.

MecA gene: Methicillin-resistance gene A, nuc gene: Thermo-nuclease gene, PVL: Panton-Valentine leucocidin, icaA: Intracellular Adhisin gene A

3.3 Distribution of MRSA across the Kurdistan region

The distribution of MRSA in Kurdistan varies among the cities, as is illustrated in Figure 3. In Erbil city, we see a significant presence of MRSA, and it’s the second highest rate among all cities as 442 cases of MRSA were reported in reviewed studies. The reported MRSA cases in Sulaymaniyah city are notably lower compared to the other cities as it shows around only 100 cases of MRSA. For Kirkuk city, the prevalence of MRSA is moderate in comparison with the other cities with nearly only 300 cases of MRSA reported based on the different samples and populations. The finding for Duhok city exhibits the highest prevalence of MRSA compared to the other cities which is about 700 cases of reported MRSA.

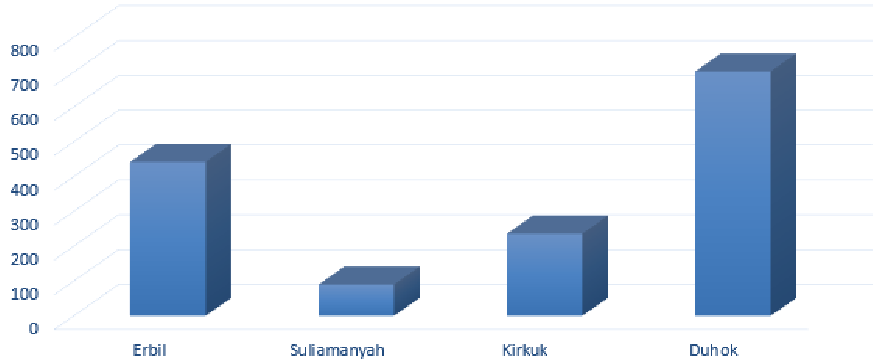

Figure 3: MRSA distribution across cities of Kurdistan region.

4. Findings and Discussion

Methicillin-resistant Staphylococcus aureus is a significant pathogen responsible for many illnesses, ranging from skin infection to other severe conditions such as septicemia; however, there is a great lack of collective data showing the incidence of this pathogen across our region. In this systematic review of MRSA in the Kurdistan region we aimed to study the prevalence of MRSA, distribution across regions, and specific virulence genes in MRSA isolates.

Studies in Kurdistan show different MRSA rates among different populations, such as secondary school students, healthcare workers, and community members, with rates ranging from 2.04% to 61% for instance a study in Zakho identified a high prevalence of MRSA among urinary tract infection patients (UTI) patients, with 75.7% of S.aureus isolates being MRSA. this high rate of MRSA incidence is by the rates reported in cities in the south of Iraq, for instance, a study in Al-Diwaniya reported 72 isolates of MRSA and another study from Nineveh reported 203 isolates of MRSA [22, 23], however, this trend can be seen more significantly in more recent studies from Basrah city, for example, a study conducted in March 2024 reported (91.67%) MRSA among (48) Staph. auerus isolates. These high ranges from Zakho, which is considered a relatively small city, are ringing alarms and must be taken into consideration.

In Duhok city studies that have been conducted among scholars, clinical samples, UTI patients, healthcare personnel, inpatients and students show very interestingly lower percentages than other cities, which ranges from (6.05% to 23.32%), compared to these results a study reported from southern Turkey showed 53.3% of their isolates to be MRSA which is interesting as these two areas are geographically close and influenced by each other. Compared to Zakho and Turkey, we see a moderately lower rate of reported MRSA, which could be attributed to various factors such as community awareness, infection control practices, and not enough reported cases. Similarly, in Erbil city high rates of MRSA are all much higher than in a study that was reported from Istanbul, Turkey, which stated that they isolated only 56 MRSA Strains [24]. This big difference ensures our need for surveillance and instant action against MRSA in our region.

In our review, we also noticed a high prevalence of the mec A gene which was responsible for up to half of the incidence of MRSA isolates, followed by the nuc gene at 24%, PVL 21%, and lastly icaA gene at 3%. This result aligns with another systematic review conducted in Iran which showed 52.7% of reported MRSA strains to be mecA positive [25].

The difference in rates of MRSA across our region could be due to multiple factors, such as different practices for infection control, antibiotic usage, population, study design, and the lack of studies representing all cities and areas.

5. Conclusion

Based on our systematic review we found several key findings, first the incidence of MRSA is different across different populations and cities reflecting diverse epidemiological patterns, we also found that there are high rates observed in certain areas with a small geographical surface area such as Zakho, underlining the urgency for targeted intervention. Comparatively low rates in Duhok suggest differences in healthcare and people's awareness.

Addressing these challenges is required as well as immediate action to manage and control MRSA infections and their virulence genes.

6. Limitations

This study focused on collecting papers that were conducted in the Kurdistan region, which may not be representative of a border trend in the country. Included studies had various methodologies and sample sizes which made direct comparison more challenging.

7. Significance of the study

Despite the limitations, our study appears to be the first comprehensive systematic review of MRSA prevalence in the Kurdistan region, as well as highlighting high-risk areas for specific virulence genes (mecA genes, nuc genes, icaA genes, and PVL) in MRSA isolates.

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