Original Article

Isolation and Characterization of Stenotrophomonas Maltophilia from Hospital Environments and Clinical Specimens in Duhok City, Kurdistan Region, Iraq

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ABSTRACT

Background: Stenotrophomonas maltophilia represents a multidrug-resistant, opportunistic pathogen that is frequently related to healthcare-associated infections, particularly in immunocompromised individuals.

Aim: This study aimed to assess the prevalence and antibiotic susceptibility of the S. maltophilia isolated from hospital environmental and clinical specimens in Duhok, Iraq.

Methodology: A total of 155 hospital environmental samples and 126 clinical specimens were collected between November 2024 and February 2025. The isolates were identified through cultural characteristics, biochemical testing, and molecular identification via PCR.

Results: A total of 25 environmental isolates (16.1%) as well as 12 clinical isolates (9.5%) were identified as S. maltophilia. The primary sources were sink drains, as well as sputum specimens. The highest rate of infection was found amongst infants in the age group of less than one year. Antibiotic susceptibility tests demonstrated high resistance rates, with ceftazidime showing 100% resistance and ticarcillin-clavulanic acid exhibiting over 90% resistance. Trimethoprim/sulfamethoxazole demonstrated the highest susceptibility.

Conclusion: The findings underscore the necessity for rigorous infection control protocols and emphasize the importance of ongoing surveillance and targeted antibiotic therapy to effectively address S. maltophilia infections within healthcare settings.

Key Words: Antibiotic, hospital environment, iraq, resistance, stenotrophomonas maltophilia.

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INTRODUCTION

Stenotrophomonas maltophilia (S. maltophilia) is a Gram-negative, aerobic, motile, rod-shaped, non-fermentative microorganism. It can survive in nutrient-deficient aquatic habitats, including water, soil, and plant surfaces. S. maltophilia is an opportunistic nosocomial pathogen, particularly in immunocompromised patients and those with prior exposure to broad-spectrum antibiotics, prolonged intensive care unit stays, mechanical ventilation, and the utilization of intravascular devices[1, 2]. Healthcare-associated infections may occur via direct touch, ingestion, inhalation, aerosolization of drinkable water, or the hands of healthcare workers[3]. This bacterium may induce severe infections, including urinary tract infections, pneumonia, bacteremia, sepsis, meningitis, especially following neurosurgical procedures, endocarditis, septic arthritis, and endophthalmitis[4]. It has a wide variety of putative virulence factors[5, 6]. Antibiotic resistance has become a growing global public health concern[7-9]. A major clinical challenge posed by S. maltophilia is its intrinsic and acquired resistance to many antibiotics, including aminoglycosides, carbapenems, beta-lactams, and fluoroquinolones[10].

S. maltophilia mostly resists β-lactam antibiotics through blaL1 and blaL2 genes. Through establishing biofilms, S. maltophilia can cause pulmonary and urinary tract infections as well as infections related to indwelling medical devices, including catheters and ventilatory equipment. This ability increases its resistance to disinfection and extends its persistence in healthcare settings. The prevalence of S. maltophilia in clinical specimens and hospital settings in Duhok, Iraq, has not been assessed. The current research aimed to isolate S. maltophilia from diverse healthcare samples and to investigate its antibiotic resistance patterns.

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METHODOLOGY

Study design and sample collection:

The study was conducted between October 2024 and May 2025 in Duhok City, Kurdistan region, Iraq. 155 environmental samples from sink drains, medical devices, device containers (Luken trap or bronchoalveolar lavage trap), and surfaces, tap water were collected. 126 different clinical specimens, which included sputum, bronchial washings, blood, urine, and CSF. The study was carried out in the intensive care unit (ICU), medical administration ward (MAW), burn ward (BW), surgical ward, oncology ward, hemodialysis ward, and neurological wards of the Duhok hospitals in Duhok City, Iraq. Sterile cotton swabs (Cultiplast, Italy) were used and were transferred to the lab, using transport medium (Amies media)[11]. The specimens were cultured on blood, MacConkey, and S. maltophilia selective agar, then incubated at 37°C for 24-48 hours[12]. Except for blood samples, which were inoculated in brain heart infusion broth for 24 to 48 hours before being transferred to cultivation media[13]. One hundred milliliters of tap water were collected in sterile containers and subsequently filtered through a 0.45 µm filter membrane. The filter was subsequently positioned on the surface medium and then incubated at 37°C for a duration of 24 to 48 hours[14].

Isolation and identification of S. maltophilia

Suspected colonies with smooth, round, green colonies with a dark green center and a blue halo[5] on the S. maltophilia selective agar base medium (contains 5 mg/L vancomycin, 32 mg/L imipenem, 2,500 mg/L amphotericin, mannitol, and a bromothymol blue indicator) underwent biochemical tests, which included Gram stain, TSI testing, oxidase, catalase, DNase, and identification using the BIOMÉRIEUX VITEK ® 2 system[14].

Molecular identification:

The genomic DNA extraction kit (Favorgen, Taiwan) was used for the extraction of DNA. The DNA of all suspected S. maltophilia isolates was extracted, following the manufacturer's guidelines. The genome was stored at -20°C. The isolates were screened for the presence of species-specific PCR primers (SM1-F 5′-CAGCCTGCGAAAAGTA-3′ and SM4-R 5′-TTAAGCTTGCCACGAACAG-3′), which detect signature sequence of the 23S rRNA gene[15]. The PCR conditions involved an initial denaturation at 95°C for 5 minutes, followed by 30 cycles that include denaturation at 95°C for 10 seconds, annealing at 58°C for 10 seconds, and extension at 72°C for 1 minute, and a final extension at 72°C for 3 minutes. Amplification was performed in a 20 µl reaction utilizing 10 µl of 2× GoTaq orange master mix, 2 µl genomic DNA, 1 µl for each primer and the volume adjusted to 20 µl using sterile injection water. The gel apparatus (VILBER LOURMAT, Germany) has been utilized to express PCR products (513 bp), molecular weight of the gene using 1% agarose (Servicebio, China), followed by the use of SYBR™ Safe DNA Gel Stain (addbio, Korea)[16].

Antibiotic susceptibility testing

The susceptibility of S. maltophilia isolates was tested against six antibiotic agents (belonging to different classes) in accordance with the guidelines of the Clinical Laboratory Standards Institute[17] as presented in (Table 1) using the disk diffusion method on Muller-Hinton agar. The antibiotics were supplied from (HiMedia, India) and (Bioanalyse, Turkey).

Table 1: The antibiotics used in this study.

Antimicrobial Class	Name	Abbreviation	Concentration (µg/ml)
β -Lactam Combination	Ticarcillin -clavulanic acid	TCC	75/10
Cephalosporin	Ceftazidime	CAZ	30
Sulfonamide	Trimethoprim/sulfamethoxazole	SXT	1.25/23.75
Fluroquinolones	Levofloxacin	LE	5
Tetracycline	Minocycline	MI	30
Phenicol	Chloramphenicol	C	10

Statistical Analysis:

Statistical analysis of findings was conducted using SPSS software version 26 with Microsoft Excel (2021), employing the Chi-square test. The probability value (*p-value*) of 0.05 or lower was considered statistically significant.

ETHICAL STATEMENT

This study and methodology received approval from the ethics committee of the Ministry of Health, Duhok Directorate General of Health, Kurdistan Region, Iraq (ID: 30/10/2024/ 9-42).

RESULTS

S. maltophilia identification

Morphology and biochemical diagnosis

Colonies of S. maltophilia grown on blood agar exhibited a slight lavender color without hemolysis and emitted an ammonia-like odor. On MacConkey agar, isolates produced colorless, transparent, flat colonies with irregular margins and non-lactose fermenting. On S. maltophilia selective agar base medium, colonies appeared smooth and spherical with an olive-green center and a lighter edge, occasionally surrounded by a blue halo (Figure 1). Biochemically, the strains exhibited positive results for oxidase (indicated by a distinctive purple or dark blue), catalase (characterized by gas bubble formation), and DNase (shown by a clear zone surrounding the bacterial growth following the addition of HCl). On triple-sugar iron agar, they exhibited non-fermentative behavior—both the slant and butt remained red, signifying an alkaline/alkaline reaction with no gas or H_2S formation.

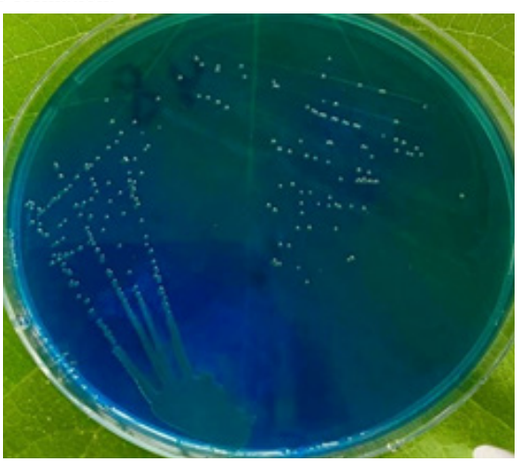

Fig. 1: S. maltophilia on the S. maltophilia selective agar medium.

Molecular detection by PCR

A total of 48 suspected S. maltophilia isolates that were phenotypically identified as S. maltophilia were confirmed molecularly using primers that targeted specific signature sequence regions of the 23S rRNA gene (SM1-F and SM4-R primers), amplified by PCR. Out of 48 isolates, 37 (77%) were confirmed positive, while 11 (22.9%) were negative. PCR reactions were loaded on 1% agarose gel electrophoresis with a molecular weight of (~513bp) as shown in (Figure 2).

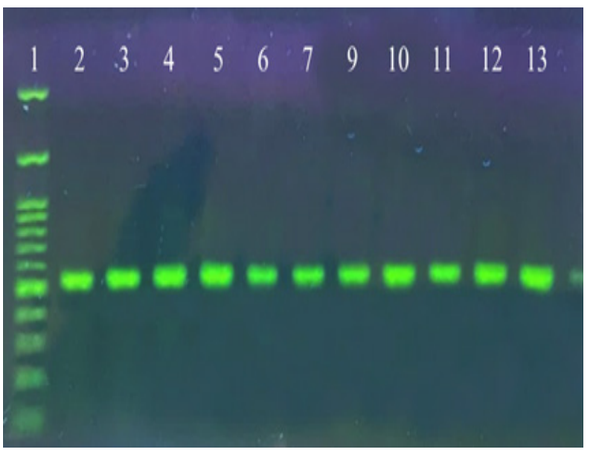

Fig. 2: Species-specific gene (513bp) on agarose gel electrophoresis. Lane 1; DNA marker. Lanes 2-13; positive samples for S. maltophilia.

Prevalence of S. maltophilia in the hospital environment:

A total of 155 environmental samples were examined for the presence of S. maltophilia. Among them, 25/155 samples (16.1%) had positive results (Table 2). The highest prevalence of positive samples was observed in sink samples (14/28; 50%), followed by device containers (9/37; 24.3%), devices (1/22; 4.5%), and humidifiers containing water (1/32; 3.1%). No growth was observed in surface samples (0/36; 0%). A chi-square analysis demonstrated a ($p < 0.05$).

Table 2: Isolation of S. maltophilia from various environmental sources.

Location*	Sink drain	Container	Surface	Humidifier & Water	Device	Total (%)
MAW	4/12(33%)	1/10(10%)	0/15(0%)	0/8(0%)	0/11(0%)	5/56 (8.9%)
BW	3/6 (50%)	0/2(0%)	0/0(0%)	1/11(9%)	0/0(0%)	4/19 (21%)
ICU	7/10(70%)	8/25(32%)	0/21(0%)	0/13(0%)	1/11(9%)	16/80 (20%)
Total	14/28(50%)	9/37(24%)	0/36(0%)	1/32(3%)	1/22(4%)	25/155(16.1%)

* MAW: medical administration ward, BW: burn ward, ICU: intensive care unit

Prevalence of S. maltophilia in clinical samples

Among the clinical samples, 12/126 samples (9.5%) tested positive for S. maltophilia. Positive growth was observed in sputum (5/33; 15.2%), blood (2/17; 11.8%), oral swab (3/34; 8.8%), and CSF (2/15; 13.3%). No growth has been observed in samples of urine (0/27; 0%) (Table 3). The statistical analysis (p=0.645) revealed no statistically significant difference in prevalence across various clinical sample types.

Table 3: S. maltophilia from various clinical samples.

Patient*	Sputum n (%)	Blood n (%)	Oral swab n (%)	Urine n (%)	CSF n (%)	Total (%)
ICU	4/22(18%)	2/10(20%)	2/12(16.6%)	0/15(0%)	1/5(20%)	9/59(15.2%)
MAW	1/11(9%)	0/12(0%)	1/22(4.5%)	0/12(0%)	1/10(10%)	3/67(4.4%)
Total (%)	5/33(15%)	2/17(11.7%)	3/34(8.8%)	0/27(0%)	2/15(13%)	12/126 (9.5%)

* ICU: intensive care unit, MAW: medical administration ward

Prevalence of S. maltophilia among different age groups

In an analysis of the age distribution among patients with infections, twelve of the 126 (9.5%) clinical specimens tested positive for S. maltophilia (Table 4). Infants (0-1 year) had the highest prevalence rate of 29.4% (10/34), followed by children (1–14 days) at 5.88% (1/17). Conversely, youth aged 15 to 19 years and adults aged 20 to 59 years showed no detectable cases (0%). The elderly (> 60 years) demonstrated a relatively low prevalence rate of 3.57% (1/28). In terms of clinical sample types, sputum samples yielded 5/33 (15%) positives, blood samples showed 2/17(11.7%) positives, oral swabs resulted in 3/34 (8.8%) positives, while cerebrospinal fluid (CSF) obtained specimens showed 2/15 (13%) positives. Urine samples have not yielded any positive cases 0/27 (0%).

Table 4: S. maltophilia from various clinical samples according to age groups.

Age group	Sputum *n* (%)	Blood *n* (%)	Oral swab *n* (%)	Urine *n* (%)	CSF *n* (%)	Total *n* (%)
Infant (0-1 Year)	4/7 (57%)	1/8(12.5%)	3/8(37.5%)	0/3(0%)	2/8(25%)	10/34(29%)
Children (1-14 Years)	0/2(0%)	1/8(12.5%)	0/3(0%)	0/3(0%)	0/1(0%)	1/17(5.8%)
Youth (15-19 Years)	0/0(0%)	0/0(0%)	0/3(0%)	0/3(0%)	0/0(0%)	0/6(0%)
adult (20-59 Years)	0/15(0%)	0/0(0%)	0/13(0%)	0/8(0%)	0/5(0%)	0/41(0%)
Elderly (> 60)	1/9(11%)	0/1(0%)	0/7(0%)	0/10(0%)	0/1(0%)	1/28(3.5%)
Total	5/33(15%)	2/17(11.7%)	3/34(8.8%)	0/27(0%)	2/15(13%)	12/126(9.5%)

Antibiotic susceptibility of S. maltophilia

The antibiotic susceptibility for all hospital environment and clinical S. maltophilia isolates (37 isolates) was screened as presented in Table 5. In general, CAZ displayed a complete resistance rate (100%), and TTC displayed a high resistance rate (94.6%). In contrast, SXT exhibited the lowest resistance (29%).

Table 5: Antimicrobial susceptibility of hospital environment and clinical S. maltophilia isolates.

Antibiotic groups	Antibiotics	Resistance *n* (%)			
		Hospital Environment isolates (*n* 25)	Clinical isolates (*n* 12)	All isolates (*n* 37)	*P value*
β -Lactam Combination	TTC	24 (96%)	11 (91.6%)	35 (94.6%)	0.585
Cephalosporin	CAZ	25 (100%)	12 (100%)	37 (100%)	0.585
Sulfonamide	SXT	9 (36%)	2 (16.6%)	11 (29%)	0.228
Tetracycline	MI	8 (32%)	11 (91.6%)	19 (51%)	0.001
Chloramphenicol	C	16 (64%)	10 (83.3%)	26 (70%)	0.228
Fluoroquinolones	LEV	16 (64%)	8 (66.6%)	24 (64.86)	0.873

Regarding multidrug-resistant (MDR) organisms in the hospital environment and clinical samples, all clinical isolates (12/12; 100%) tested positive for MDR. Conversely, the rate in hospital environmental samples was 88% (22/25). This indicates that there is no significant difference in the distribution of MDR between the two sample types, with a *p-value* of 0.736.

Regarding the source type of the isolates, the resistance rate was 100% toward CAZ in environmental (25 isolates) and clinical S. maltophilia (12 isolates). Also, the β-lactam combination antibiotic TTC exhibited a high rate of resistance in environmental and clinical isolates (96% and 91.6%, respectively). Also, environmental and clinical isolates showed less resistance toward LEV (64% and 66.6%, respectively). On the other hand, the SXT, exhibited a low resistance rate in both types of isolates (36% in environmental isolates and 16.6% in clinical isolates). Interestingly, a statistically significant difference in resistance patterns was observed between environmental and clinical isolates to MI. Environmental isolates exhibited relatively low resistance to MI (32%), whereas clinical isolates demonstrated significantly higher resistance (91.6%).

DISCUSSION

The present investigation highlights the presence of S. maltophilia in both environmental and clinical hospital settings in Duhok, emphasizing its importance as an emerging hospital-acquired pathogen.

The incidence of nosocomial infections caused by S. maltophilia is increasing, with 99.6% being healthcare-associated [18]. The current study revealed a contamination rate of 16.1% of the environmental samples testing positive for S. maltophilia. This finding was close to that reported in Italy by Cristina[19].

There were significant differences in the prevalence of S. maltophilia in different sources of the hospital environment. The development of biofilms in sinks and drains facilitates horizontal gene transfer. Conversely, clinical environments exert selective pressure that favor S. maltophilia strains with higher antibiotic resistance and greater ability to infect human hosts compared to other hospital sources.

The moist environments of sink drains likely facilitate the development of biofilm and persistence[19]. Also, sink drains could provide a potential risk for S. maltophilia through the contamination of health care equipment near sinks. ***Matheu et al.***[20] reported that all of the sink drain samples were positive for S. maltophilia in Salt Lake City of USA. In the current study, 4% of S. maltophilia were isolated from medical devices, which was in agreement with a study reported in Iran by Amoli[21]. In contrast, another study conducted in Iran reported that the prevalence rate of S. maltophilia was 0.6% among 170 devices[22]. The results of the current study revealed a significant contamination rate of sinks, containers, and devices in the ICU. Similar findings were found in a Brazilian hospital, where 67.9% were from the ICU and 32.1% were from non-ICU wards[23]. On the other hand, no S. maltophilia was found on surfaces, which could indicate how important moisture is for the survival of S. maltophilia. The contamination rate of containers (Luken trap or bronchoalveolar lavage trap) with S. maltophilia was 24%. The contamination rate of humidifier containers was 3%, isolated from leftover containers after prolonged periods in burn, a plastic surgery hospital in Duhok, as burn patients use considerably fewer ventilators than those in the ICU, where O_2 humidifiers are often used.

From the clinical perspective, 9.5% of the patients tested positive for S. maltophilia, which was higher than the WHO record (5.3%). Although different rates were observed in different regions (7.9% in Europe and 10.5% in the Western Pacific)[24], a similar result (8%) was recorded in Saudi Arabia[25]. Additionally, a slightly higher incidence rate (14%) was reported in Mosul, Iraq, by Fadhil and coworkers[26].

Sputum was the more common source (15.2%) of clinical isolates in the current study, which is consistent with the prevalence of S. maltophilia (13-20%) recorded in many previous studies conducted in Iran, Saudi Arabia, Qatar, Turkey, and Mexico[21, 27-30]. The ability of S. maltophilia to develop biofilms on plastic and respiratory support equipment can be responsible for its elevated prevalence[31].

Meta-analyses have confirmed a strong association between mechanical ventilation and S. maltophilia pneumonia in ICU patients[28, 32].

The current research found that 8.8% of oral swabs isolated S. maltophilia, with 6% exhibiting clinical signs and 2% showing no clinical signs. Studies showed that 29.1% of isolated bacteria signify colonization rather than invasive illness[29, 33].

Cerebrospinal fluid constituted 13.3% incidence in our investigation, and the incidence rate of CSF infection was higher than the rates reported in many studies conducted in other studies, which ranged from 2-4%[27, 34]. Mechanical ventilation and indwelling catheters increase the incidence of S. maltophilia infections[32]. The incidence rate of S. maltophilia from blood was 11.8%, which is roughly comparable to other research findings[14]. There were no S. maltophilia-positive isolates found in urine samples obtained from suspected patients who were undergoing urinary catheter procedures. This observation corresponds with existing data indicating that infections of the urinary tract caused by S. maltophilia are uncommon[21, 27].

A higher frequency of S. maltophilia was found among newborns (29.4%), demonstrating enhanced susceptibility in the neonatal and pediatric groups. This aligns with many case studies of S. maltophilia-related pneumonia, as well as sepsis in NICU patients[33]. This is supported by previous studies indicating that infants and newborns in NICUs have an elevated risk owing to their immature immune systems, extended hospital stays, and recurrent exposure to invasive interventions[33, 35]. Hafiz and others[28] revealed that the S. maltophilia isolate was found in 16.5% of adults aged 19–44 years, 24% of adults aged 45–64 years, and 25% of adults aged 65–84 years. The elderly had a lower but still significant prevalence (3.57%), which reflects being more susceptible to hospital-acquired illnesses as well as a weak immune system.

Antibiotic susceptibility testing revealed alarm resistance patterns globally[36, 37]. In the current study, environmental and clinical isolates were almost universally resistant to ticarcillin-clavulanic acid and ceftazidime, reflecting widespread β-lactamase production by S. maltophilia[38].

Clinical isolates showed resistance to SXT, the first-line medication, at a rate of 16.67%, which was greater than the global resistant average of about 9.2%[29]. The rate of resistance to SXT in samples isolated from the environment was higher than in clinical samples same result was reported by [14]. This may result from prolonged exposure to disinfectants and antibiotic residues in medical settings, which provide selective pressure. The development of biofilms in sinks and drains facilitates horizontal gene transfer. Conversely, clinical environments may prefer fewer resistant variants that are more adept at infecting human hosts. Levofloxacin represents an alternative to TMP-SMX. 73.2% of isolates from Qatar exhibited susceptibility to levofloxacin[29], whereas global resistance estimates stand at 19.29%, hence constraining its value; yet, several investigations remain to support its application in combination therapies[29]. This heightened resistance may stem from selection pressure due to extended antibiotic usage in ICU environments[32]. Chloramphenicol has shown limited efficacy overall, with resistance rates ranging from 64% to 83%. The restricted application in modern medicine probably results in diminished selective pressure while simultaneously constraining its therapeutic efficacy. Our data confirm the concept that environmental reservoirs play a substantial role in nosocomial transmission[39]. The higher resistance rates in clinical samples compared to those from the environment likely show that patients were exposed to more antibiotics, which matches earlier studies[39].

Multidrug-resistant bacterial infections have emerged as a critical global public health issue[40, 41]. Multidrug-resistant S. maltophilia was present in all clinical samples and most hospital environmental samples, with no significant differences between the two sources. The MDR rate in the clinical S. maltophilia was higher than what other studies have found in Egypt (62.9%)[42], Iraq (91%)[43], and Australia (83.3%)[44]. Likewise, the environmental MDR rate (88%) was higher than that was recorded in Egypt (64.3%)[42]. The elevated MDR incidence in the current study may indicate extensive or inappropriate antibiotic utilization in local healthcare facilities, inadequate infection control measures, and environmental contamination within the hospital.

The results showed no statistically significant differences in resistance patterns between environmental and clinical isolates. However, the resistance rate to minocycline was significantly higher in clinical isolates (91.6%) compared to environmental isolates (32%), with a statistically significant difference in resistance rate in both isolates. This result might reflect regional overuse or prior antibiotic exposure among patients.

This disparity might reflect regional overuse or prior antibiotic exposure among patients. The levofloxacin resistance rate in our sample was 64.6% for both environmental and clinical samples. The clinical isolates demonstrated slightly higher resistance rates, a problematic outcome because of the limitation of therapeutic options. The ways that S. maltophilia resists treatment include making metallo-β-lactamases (L1, L2) that break down many types of β-lactam antibiotics and having efflux pumps. The formation of biofilms, horizontal gene transfer and environmental adaptability may promote the development of resistance.

The study had certain limitations. For example, the absence of isolates from youth and adult groups might indicate limited exposure to invasive procedures and an inadequate sample size from the adults.

Study limitation:

While this study provides important findings, several limitations should be considered. The limited geographical region and size of the sample could limit the generalizability of the results. A relatively short sampling period may not reflect seasonal variation in S. maltophilia prevalence. The lack of advanced molecular typing, including whole-genome sequencing with clinical outcome information, impairs the correlation of genotypic characteristics with disease severity. The study additionally examined resistance to a specific range of antibiotics and excluded environmental control factors, such as disinfection protocols and antibiotic usage from natural sources. Recognizing these limitations in further research will be crucial for a more thorough comprehension of S. maltophilia in hospital environments.

CONCLUSION

S. maltophilia represents an important emerging pathogen among environmental and clinical specimens. The elevated levels of multidrug resistance, in addition to the existence of several virulence-associated genes, reflect the complexity of treating S. maltophilia infections in clinical settings. The increased susceptibility to trimethoprim/sulfamethoxazole indicates it is the most effective treatment option, although rising resistance signals possible future constraints. The results underscore the necessity for regular antimicrobial susceptibility assessments, efficient infection control protocols, and ongoing surveillance of environmental reservoirs for avoiding nosocomial transmission. The environment could serve as a reservoir for antibiotic resistance genes, which can move between human and environmental bacteria. This exchange may drive independent resistance evolution, with the risk of novel antibiotic resistance genes spreading to human pathogens. To combat this, surveillance of both clinical and environmental isolates is crucial, along with stricter regulations to reduce antibiotic pollution and slow resistance development in nature. Additional research emphasizing the molecular mechanisms underlying resistance with biofilm formation is essential to enhance and understand the pathogenicity of S. maltophilia in order to formulate more successful treatment strategies.

CONFLICT OF INTERESTS

There are no conflicts of interest.

ETHICS APPROVAL AND CONSENT TO PARTICIPATE

This study and methodology received approval from the Research Ethics Committee of the Ministry of Health, Duhok Directorate General of Health, Kurdistan Region, Iraq approved this study with No. 30102024-9-42, under the supervision of Prof. Mahde Assafi.

FUNDING

Self-funding by authors.

AVAILABILITY OF DATA AND MATERIALS

The editorial board can obtain the data upon request.

AUTHOR CONTRIBUTIONS

AHMED ZA and ASSAFI MS carried out the work. AHMED ZA performed the protocol. AHMED ZA was responsible for collecting the scientific data. AHMED ZA wrote the initial draft of the manuscript. All authors did a revision of the manuscript. All authors read and approved the final version to be published

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عزل وتوصيف بكتريا ستينوتروفوموناس ملتوفيلا من بيئات المستشفى والعينات السريرية في مدينة دهوك، اقيلم كردستان، العراق

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المقدمة: تمثل بكتريا Stenotrophomonas maltophilia ممرضا انتهازيا متعدد المقاومة للمضادات، وانها ترتبط بشكل متكرر في اصابات العدوى المصاحبة للرعاية الصحية, خاصة لدى الاشخاص ضعيفي المناعة.

الهدف: هدفت هذا الدراسة الى تقييم مدى انتشار بكتريا S. maltophilia وحساسيتها للمضادات الحيوية المعزولة من عينات بيئية وسريرية في مستشفيات مدينة دهوك، العراق.

الطريقة: تم جمع ١٥٥ عينة من بيئة المستفيات و ١٢٦ عينة سريرية بين الاشهر نوفمبر ٢٠٢٤ وفبراير ٢٠٢٥. تم تحديد العزلات من خلال الخصائص الزرعية، الاختبارات الكيميائية الحيوية، والتشخيص الجزيئي عن طريق تفاعل البلمرة المتسلسل.

النتائج: تم تحديد ٢٥ (١٦,١٪)عزلة بيئية وكذلك ١٢ (٩,٥٪) عزلة سريرية بانها S. maltophilia.

كانت مصادر العزل الرئيسية هي مصارف الاحواض كذلك عينات البلغم. اضهر الرضع اعلى نسبة في معدلات العدوى. بينت اختبارات الحساسية للمضادات الحيوية معدلات مقاومة عالية. حيث سجل السفتازيديم نسبة مقاومة ١٠٠٪ والتكارسيلين-حامض الكلافولنك مقاومة تفوق ٩٠٪. الترايميثوبريم/ سلفاميثوكسازول سجل اعلى معدل للحساسية.

الخلاصة: توكد هذه النتائج على ضرورة تطبيق بروتوكولات صارمة لمكافحة العدوى، والتاكيد على اهمية المراقبة المستمرة والمضاد المستخدم للعلاج للمواجهة الفعالة لعدوى بكتريا S. maltophilia في بيئات الرعاية الصحية.