International Journal of Medical and Pharmaceutical Research

Online ISSN-2958-3683 | Print ISSN-2958-3675
Frequency: Bi-Monthly
Available online on: https://ijmpr.in/

Original Article

Bacteriological Profile and Antimicrobial Susceptibility Patterns of Stenotrophomonas maltophilia in Intensive Care Units: An Observational Cross-Sectional Study

Pushpendra Pathak[1], Ramanath Karicheri[2], Mohd. Areeb[3]

[1,3]Research Scholar, Department of Microbiology, Index Medical College Hospital and Research Centre, Indore, Madhya Pradesh, India (Malwanchal University)
[2]Professor, Department of Microbiology, Index Medical College Hospital and Research Centre, Indore, Madhya Pradesh, India (Malwanchal University)

OPEN ACCESS

Corresponding Author:

Pushpendra Pathak
Research Scholar, Department of Microbiology, Index Medical College Hospital and Research Centre, Indore, Madhya Pradesh, India (Malwanchal University)

Received: 04-05-2026
Accepted: 01-06-2026
Available online: 09-07-2026

ABSTRACT

Background: *Stenotrophomonas maltophilia* is an emerging opportunistic, non-fermenting Gram-negative bacillus increasingly associated with healthcare-associated infections in intensive care units (ICUs). Its clinical importance is related to intrinsic multidrug resistance and its association with critically ill patients, prolonged hospitalization, prior antibiotic exposure, respiratory infections, and invasive devices.

Objective: To study the bacteriological profile and antimicrobial susceptibility pattern of *S. maltophilia* isolated from ICU patients in a tertiary care hospital.

Materials and Methods: This observational cross-sectional laboratory-based study was conducted in the Department of Microbiology, Index Medical College Hospital & Research Centre, Malwanchal University, Indore, Madhya Pradesh, India, from 1 January 2024 to 1 December 2025. Clinical samples from ICU patients were processed using standard microbiological methods. Identification was performed by colony morphology, Gram staining, oxidase testing, biochemical reactions and/or automated identification systems such as VITEK 2. Antimicrobial susceptibility testing was performed by Kirby-Bauer disk diffusion on Mueller-Hinton agar and interpreted according to applicable CLSI guidelines. Data were analysed using Microsoft Excel and IBM SPSS version 29.

Results: Among 266 ICU patients, 22 *S. maltophilia* isolates were recovered, giving an isolation rate of 8.3%. The highest number of isolates was seen in patients aged 30-60 years, 13(59.1%), followed by those aged >60 years, 8 (36.4%). Males accounted for 14(63.6%) isolates and females for 8(36.4%). Respiratory ICU contributed the highest number of isolates 10(45.5%), followed by Surgical ICU 7(31.8%) and Medical ICU 5(22.7%). Endotracheal aspirate was the most common specimen 10 (45.5%), followed by blood (8, 36.4%). Susceptibility was highest to trimethoprim-sulfamethoxazole 18(81.8%), followed by minocycline 17(77.3%) and levofloxacin 14(63.6%). Ventilator use was significantly associated with infection/colonization ($p<0.05$), whereas gender was not significantly associated ($p>0.05$).

Conclusion: *S. maltophilia* is an emerging ICU-associated pathogen, particularly in respiratory specimens and patients exposed to invasive devices. Trimethoprim-sulfamethoxazole, minocycline and levofloxacin remain important therapeutic options, but therapy should be guided by antimicrobial susceptibility testing. Continuous surveillance is necessary to guide empirical therapy and infection-control strategies in ICU settings.

Keywords: *Stenotrophomonas maltophilia; intensive care unit; antimicrobial susceptibility; trimethoprim-sulfamethoxazole; minocycline; levofloxacin; multidrug resistance.*

INTRODUCTION

Stenotrophomonas maltophilia (Stenos, Greek: narrow; trophos, Greek: one who feeds; monas, Greek: a unit, monad; i.e., a unit feeding on few substrates; and malt, Old English: malt; philos, Greek: friend; i.e., a friend of malt). The type strain was isolated in 1958 from an oropharyngeal swab of a patient with oral carcinoma [1]. and named Pseudomonas maltophilia [2]. Subsequently, Swings et al, (1981) further proposed that P. maltophilia be reclassified in the genus Xanthomonas as X. maltophilia [3].

Stenotrophomonas maltophilia is a Gram-negative, aerobic, non-fermenting bacillus belonging to the family Xanthomonadaceae. Initially, it was classified under the genera Pseudomonas and Xanthomonas, but later reassigned to the genus Stenotrophomonas in the early 1990s based on genotypic and phenotypic characteristics [4,5].

Morphologically, S. maltophilia appears as straight or slightly curved rods measuring approximately 0.4–0.7 μm in width and 0.7–1.8 μm in length. Microscopically, the cells occur singly or in short chains and exhibit motility due to polar flagella [5].

Stenotrophomonas maltophilia is a ubiquitous environmental bacterium found in water, soil, animals and plant rhizospheres, and it can colonise damp surfaces in residential and healthcare settings [5]. During the past decade, it has been increasingly recognised as an important Gram-negative multidrug-resistant (MDR) pathogen [6].

As an opportunistic pathogen, *S. maltophilia* is frequently associated with healthcare-associated infections in weakened and immunocompromised individuals. Community-acquired infections have also been reported, although they are less common [7]. In hospital settings, *S. maltophilia* is clinically significant as a cause of catheter-related bacteraemia, pneumonia, soft-tissue infection, meningitis, prosthetic valve endocarditis and ocular infection, particularly among critical-care and oncology patients [8].

Although *S. maltophilia* is not considered highly virulent, its clinical importance is related to underlying malignancy, indwelling devices, chronic respiratory disease, immunosuppression, prior antibiotic exposure, prolonged hospitalization and ICU stay [5]. Virulence-associated properties such as adhesion, biofilm formation, hydrophobicity, motility and extracellular enzyme production may contribute to colonization and infection [9,10]. Biofilm formation on abiotic and biotic surfaces may protect the organism from host immune responses and antimicrobial penetration, facilitating persistence on ventilator circuits and central venous catheters [11,12].

S. maltophilia has significant intrinsic and acquired resistance to multiple antimicrobial classes, limiting treatment options [13-16]. It commonly shows resistance to expanded-spectrum penicillins, third-generation cephalosporins, carbapenems, aminoglycosides and several quinolones. Trimethoprim-sulfamethoxazole has traditionally been considered the preferred agent, but resistance and treatment limitations are increasingly recognised [5,8]. Recent guidance has highlighted trimethoprim-sulfamethoxazole, levofloxacin, minocycline and cefiderocol as important agents, while CLSI breakpoint changes have revised the interpretation of susceptibility for this organism [17,18].

The present study aims to determine the bacteriological profile and antimicrobial susceptibility patterns of *Stenotrophomonas maltophilia* isolated from patients admitted to intensive care units in a tertiary care hospital. The study also aims to assess the distribution of isolates across clinical specimens and ICU settings, and to evaluate the resistance patterns of S. maltophilia to commonly used antimicrobial agents to support appropriate antimicrobial therapy and infection control practices.

Considering the increasing recognition of *Stenotrophomonas maltophilia* as an important opportunistic nosocomial pathogen in critically ill patients, continuous surveillance of its occurrence and antimicrobial susceptibility pattern is essential. ICU patients are particularly vulnerable due to prolonged hospitalization, mechanical ventilation, invasive devices, prior exposure to broad-spectrum antibiotics, and underlying comorbid conditions. Since *S. maltophilia* possesses intrinsic resistance to multiple antimicrobial classes and has limited therapeutic options, local data on its distribution and susceptibility profile are required for guiding effective treatment strategies. Therefore, the present observational cross-sectional study was undertaken to evaluate the bacteriological profile and antimicrobial susceptibility patterns of *S. maltophilia* isolated from intensive care unit patients at a tertiary care hospital.

MATERIALS AND METHODS

Study design and setting

This observational cross-sectional laboratory-based study was conducted in the Department of Microbiology, Index Medical College Hospital & Research Centre, Malwanchal University, Indore, Madhya Pradesh, India, from 1 January 2024 to 1 December 2025. The study included clinical samples from patients admitted to Medical ICU, Surgical ICU, Respiratory ICU and Paediatric ICU.

Inclusion and exclusion criteria

All ICU patients from whom *S. maltophilia* was isolated from clinically relevant samples during the study period were included. To avoid duplication, only the first isolate from each patient was considered. Samples were included only when relevant clinical and microbiological data were available. Repeat isolates from the same patient, isolates from non-ICU patients, and contaminated or clinically insignificant mixed-growth specimens were excluded.

Sample collection and processing

Clinical specimens, including blood, endotracheal aspirate, sputum, bronchoalveolar lavage, urine, pus/wound swab, catheter tip and body fluids, were collected using aseptic precautions and transported promptly to the microbiology laboratory. Blood samples were inoculated into blood-culture bottles and incubated using an automated blood culture system, where available. Other specimens were inoculated on blood agar, MacConkey agar and other appropriate media and incubated aerobically at 37°C for 18-24 hours. Preliminary identification was based on colony morphology, Gram staining, oxidase test, motility and biochemical reactions. Final identification was performed by conventional biochemical tests and/or automated identification systems such as VITEK 2, depending on availability.

Antimicrobial susceptibility testing

Antimicrobial susceptibility testing was performed by the Kirby-Bauer disk diffusion method on Mueller-Hinton agar. Results were interpreted according to the applicable CLSI recommendations during the study period. The antimicrobial agents analysed for *S. maltophilia* were trimethoprim-sulfamethoxazole, levofloxacin and minocycline.

Statistical analysis

Data were entered in Microsoft Excel and analysed using IBM SPSS Statistics version 29. Categorical variables were expressed as frequencies and percentages. Associations between categorical variables were assessed using the chi-square test or Fisher's exact test, as appropriate. A p-value of <0.05 was considered statistically significant.

Ethical approval

The study was approved by the Institutional Ethics Committee of Malwanchal University (IEC: MU/Research/EC/Ph.D/2023/347). Patient confidentiality was maintained throughout the study.

RESULTS

A total of 22 *S. maltophilia* isolates were obtained from 266 ICU patients during the study period, giving an isolation rate of 8.3%. The majority of isolates were recovered from patients aged 30-60 years, 13(59.1%), followed by patients aged >60 years, 8(36.4%). Only one isolate (4.5%) was recovered from a patient aged <30 years. The mean age was 56.8 ± 15.4 years. Male patients accounted for 14 isolates (63.6%) and female patients for 8 isolates (36.4%). ICU-wise distribution showed that the highest number of isolates came from the Respiratory ICU, 10 (45.5%), followed by Surgical ICU 7(31.8%) and Medical ICU 5(22.7%). No isolate was recovered from the Paediatric ICU. Sample-wise, endotracheal aspirate was the most common specimen 10(45.5%), followed by blood, 8 (36.4%). Pus/wound swab contributed 2 isolates (9.1%), while urine and sputum/BAL contributed 1 isolate each (4.5%). In antimicrobial susceptibility testing, trimethoprim-sulfamethoxazole showed the highest susceptibility,18(81.8%), followed by minocycline 17 (77.3%) and levofloxacin 14(63.6%). Statistical analysis showed that ventilator use was significantly associated with infection/colonization with *S. maltophilia* ($p<0.05$), whereas gender was not significantly associated ($p>0.05$).

Table 1. Age-wise distribution of patients with S. maltophilia infection/colonization

Age group	Number of ICU patients (N=266)	S. maltophilia isolates (n=22)
<30 years	35 (13.2%)	1 (4.5%)
30-60 years	139 (52.3%)	13 (59.1%)
>60 years	92 (34.6%)	8 (36.4%)
Mean age	56.8 ± 15.4 years	

Table 2. Gender-wise distribution of patients with S. maltophilia infection/colonization

Gender	Number of ICU patients (n=266)	S. maltophilia isolates (n=22)
Male	182 (68.4%)	14 (63.6%)
Female	84 (31.6%)	8 (36.4%)
Total	266 (100%)	22 (100%)

Table 3. Distribution of S. maltophilia isolates according to ICU type

ICU type	Number of isolates	Percentage
Medical ICU	5	22.7%
Surgical ICU	7	31.8%
Respiratory ICU	10	45.5%
Paediatric ICU	0	0.0%
Total	22	100%

Table 4. Sample-wise distribution of confirmed S. maltophilia isolates

Sample type	Number of isolates	Percentage
Endotracheal aspirate	10	45.5%
Blood	8	36.4%
Urine	1	4.5%
Pus/wound swab	2	9.1%
Sputum/BAL	1	4.5%
Total	22	100%

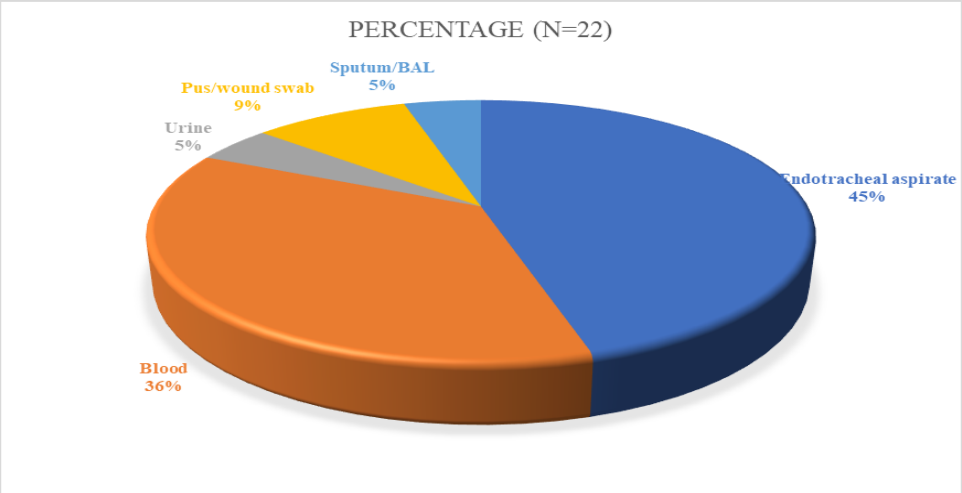

Figure 1.Sample-wise distribution of *Stenotrophomonas maltophilia* isolates.

Table 5. Antimicrobial susceptibility pattern of S. maltophilia isolates

Antibiotic	Susceptible n (%)	Intermediate n (%)	Resistant n (%)
Levofloxacin	14 (63.6%)	0	8 (36.4%)
Trimethoprim-sulfamethoxazole	18 (81.8%)	0	4 (18.2%)
Minocycline	17 (77.3%)	0	5 (22.7%)

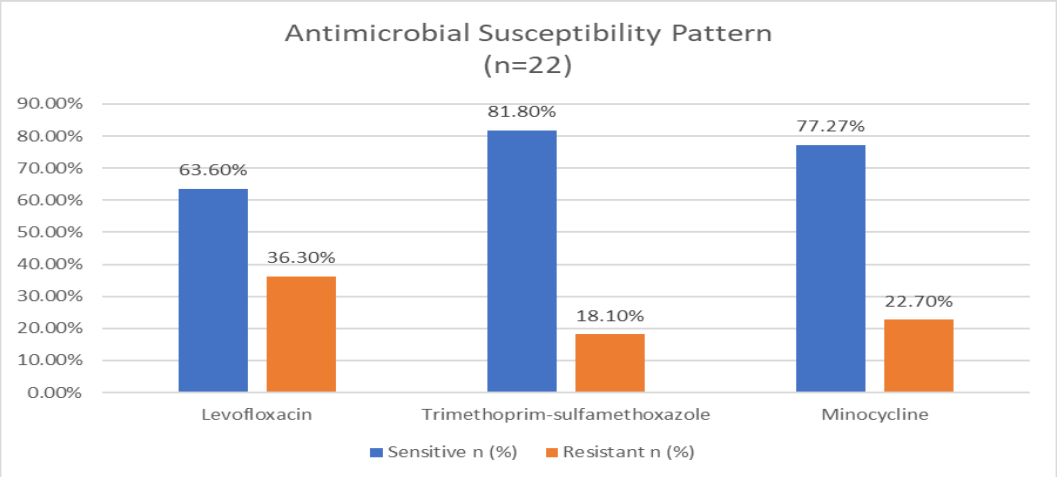

Figure 2. Antimicrobial susceptibility pattern of *Stenotrophomonas maltophilia* isolates.

Table 6. Statistical analysis

Parameter	p-value	Significance
Ventilator use vs infection/colonization	<0.05	Significant
Gender vs infection/colonization	>0.05	Not significant

DISCUSSION

Stenotrophomonas maltophilia is increasingly recognized as an important opportunistic, non-fermenting Gram-negative bacillus in hospital and intensive care settings. Although it is not considered a highly virulent organism, its ability to survive in moist hospital environments, colonize respiratory equipment, form biofilm and resist multiple antimicrobial classes makes it clinically significant among critically ill and immunocompromised patients. Brooke reported that *S. maltophilia* has emerged globally as an opportunistic pathogen, particularly among patients exposed to prolonged hospitalization, invasive devices and broad-spectrum antibiotics [5]. Similarly, Abbott et al. described changing disease patterns of *S. maltophilia* and highlighted its growing importance in nosocomial infections [16].

In the present study, *S. maltophilia* was isolated from 22 ICU patients. The majority of isolates were recovered from patients in the 30-60 years age group, followed by patients aged >60 years. This finding suggests that middle-aged and elderly patients admitted to ICUs may be more vulnerable to colonization or infection, possibly due to comorbidities, prolonged ICU stay, invasive procedures and previous antimicrobial exposure. Muder et al. similarly noted that *S. maltophilia* infections are commonly associated with hospitalized and critically ill patients, especially those with severe underlying illness [8].

Male predominance was observed in the present study, with 14 of 22 isolates recovered from male patients. However, gender was not statistically significant in our analysis. This indicates that the occurrence of *S. maltophilia* infection/colonization may be more strongly associated with ICU-related risk factors such as ventilator use, catheterization and antibiotic exposure rather than gender alone. Falagas et al. also emphasized that host-related and healthcare-associated risk factors play a major role in the development of *S. maltophilia* infections [7].

In our study, the highest number of isolates was obtained from the Respiratory ICU, followed by Surgical ICU and Medical ICU. This supports the role of *S. maltophilia* as an important pathogen in critically ill patients with respiratory involvement. Respiratory ICU patients commonly require mechanical ventilation, endotracheal intubation, oxygen therapy and prolonged antibiotic treatment, all of which increase the risk of colonization and infection. Di Bonaventura et al. demonstrated that *S. maltophilia* can adhere to respiratory epithelial cells and contribute to inflammatory lung infection [9]. De Oliveira-Garcia et al. also reported that fimbrial structures and adherence mechanisms help *S. maltophilia* attach to epithelial and abiotic surfaces, contributing to persistence in hospital environments [10].

Sample-wise distribution showed that endotracheal aspirate was the most common specimen, accounting for 45.5% of isolates, followed by blood culture at 36.4%. This indicates that *S. maltophilia* in ICU settings is mainly associated with respiratory tract infection/colonization and ventilator-associated events. Isolation from blood samples also highlights its role as a cause of bloodstream infections, especially in patients with central venous catheters and other invasive devices. Muder et al. reported that *S. maltophilia* is associated with pneumonia, catheter-related bacteraemia, soft-tissue infection, meningitis and endocarditis in hospitalised patients [8]. Biofilm formation on indwelling medical devices may further contribute to persistence and bloodstream invasion. Elvers et al. and De Vidipo et al. demonstrated biofilm-forming ability and epithelial interaction of *S. maltophilia*, which may explain its association with ventilator circuits, catheters and ICU-related infections [11,12].

Antimicrobial susceptibility testing showed that trimethoprim-sulfamethoxazole had the highest susceptibility rate, with 18 of 22 isolates susceptible. Minocycline also showed good activity, followed by levofloxacin. These findings support the continued role of trimethoprim-sulfamethoxazole as an important therapeutic option for *S. maltophilia*. However, resistance to trimethoprim-sulfamethoxazole was observed in 18.2% of isolates, which is clinically important because therapeutic options are limited. Hu et al. reported increasing resistance determinants against trimethoprim-sulfamethoxazole among clinical *S. maltophilia* isolates, supporting the need for continuous antimicrobial surveillance [14]. Sanchez et al. also emphasized that intrinsic and acquired resistance mechanisms make *S. maltophilia* difficult to treat [15].

Levofloxacin susceptibility was observed in 63.6% of isolates, while resistance was seen in 36.4%. Although levofloxacin may be considered as an alternative agent, the comparatively higher resistance in the present study indicates that it should be used only after susceptibility confirmation. Minocycline showed 77.3% susceptibility and may be considered a useful alternative, particularly when trimethoprim-sulfamethoxazole resistance or intolerance is present. Bakthavatchalam et al. reported that CLSI revised the minocycline susceptibility breakpoints for *S. maltophilia* in 2024, which can affect interpretation of susceptibility rates when compared with older breakpoints [19]. Recent IDSA guidance and PK/PD-based

studies also support susceptibility-guided treatment using active agents such as trimethoprim-sulfamethoxazole, minocycline, levofloxacin and cefiderocol in appropriate clinical settings [18,20].

The resistance pattern of *S. maltophilia* is mainly due to intrinsic mechanisms such as multidrug efflux pumps, reduced outer-membrane permeability, aminoglycoside-modifying enzymes and beta-lactamases. The organism is intrinsically resistant to many beta-lactams, including carbapenems, which may explain its emergence in patients previously exposed to broad-spectrum antibiotics. Abbott et al. suggested that increased use of carbapenems and other broad-spectrum antibiotics may contribute to the rising isolation of *S. maltophilia* in hospitals [16]. CLSI has also updated breakpoints for this organism, including removal of ceftazidime breakpoints and revision of minocycline breakpoints, reflecting changing understanding of its treatment relevance [17].

A statistically significant association was found between ventilator use and infection/colonisation in the present study. This finding is important because ventilator-associated colonisation and biofilm formation are major contributors to ICU-acquired respiratory infections, particularly among critically ill patients requiring mechanical ventilation and prolonged ICU care [24]. The predominance of endotracheal aspirate isolates further supports this observation. Carbonell et al. reported that *S. maltophilia* is an important pathogen in critically ill ICU patients and is frequently associated with respiratory infections, invasive devices, prior broad-spectrum antibiotic exposure and prolonged ICU stay [21]. Puech et al. observed that ventilator-associated pneumonia caused by *S. maltophilia* is clinically important and that appropriate antimicrobial therapy was associated with better outcomes [22]. Cristina et al. described an ICU outbreak of *S. maltophilia* and emphasized the role of environmental surveillance and infection-control measures in preventing transmission [23]. Therefore, strict infection-control practices, proper disinfection of respiratory equipment, antimicrobial stewardship and early removal of invasive devices whenever possible are essential to reduce the burden of *S. maltophilia* in ICU settings [21-24].

This study shows a high prevalence of LRTIs and multidrug-resistant Gram-negative organisms. Empirical antibiotic policies should consider local resistance patterns, with emphasis on rational antibiotic use to mitigate AMR [25].

Overall, the present study highlights the emergence of *S. maltophilia* as an important ICU-associated pathogen, particularly in respiratory specimens and bloodstream infections. The organism showed the highest susceptibility to trimethoprim-sulfamethoxazole, followed by minocycline and levofloxacin. However, resistance even to preferred therapeutic agents emphasizes the need for routine susceptibility testing, continuous surveillance, antimicrobial stewardship and strict infection-control measures.

Limitations

This study has certain limitations. It was a single-centre study with a small number of *S. maltophilia* isolates. Differentiation between colonization and true infection was based on available clinical and microbiological documentation and may not be absolute in all cases. Molecular characterization of resistance mechanisms and MIC-based testing were not performed. Exact risk-factor denominators and exact p-values should be added in future analyses to strengthen statistical interpretation.

CONCLUSION

Stenotrophomonas maltophilia is an emerging opportunistic pathogen in intensive care units, especially among critically ill patients with respiratory involvement and invasive devices. Its intrinsic multidrug resistance limits therapeutic options and makes accurate identification essential. Trimethoprim-sulfamethoxazole, minocycline and levofloxacin remain important therapeutic options; however, treatment should be guided by antimicrobial susceptibility testing. Continuous surveillance of antimicrobial susceptibility patterns, strict infection-control practices and antimicrobial stewardship are necessary to guide empirical therapy and reduce ICU-associated transmission.

Declarations

Ethical approval: Approved by the Institutional Ethics Committee of Malwanchal University (IEC: MU/Research/EC/Ph.D/2023/347).

Funding: To be declared by the authors, as per journal requirement.

Conflicts of interest: To be declared by the authors, as per journal requirement.

Data availability: The data supporting the findings of this study are available from the corresponding author on reasonable request, subject to institutional policies.

REFERENCES

1. Hugh, R., & Leifson, E. (1963). A description of the type strain of *Pseudomonas maltophilia*. *International Bulletin of Bacteriological Nomenclature and Taxonomy, 13*, 133–138.
2. Hugh, R., &Ryschenkow, E. (1961). *Pseudomonas maltophilia*, an *Alcaligenes*-like species. *Journal of General Microbiology, 26*, 123–132.
3. Swings, J., De Vos, P., Van den Mooter, M., & De Ley, J. (1983). Transfer of *Pseudomonas maltophilia* Hugh 1981 to the genus *Xanthomonas* as *Xanthomonas maltophilia* (Hugh 1981) comb. nov.*International Journal of Systematic Bacteriology, 33*, 409–413.
4. Ryan, R. P., Monchy, S., Cardinale, M., Taghavi, S., Crossman, L., Avison, M. B., Berg, G., van der Lelie, D., & Dow, J. M. (2009). The versatility and adaptation of *Stenotrophomonas maltophilia*. *Nature Reviews Microbiology, 7*(7), 514–525.
5. Brooke, J. S. (2012). *Stenotrophomonas maltophilia: An emerging global opportunistic pathogen*. **Clinical Microbiology Reviews, 25**(1), 2–41.https://doi.org/10.1128/CMR.00019-11.
6. Brooke, J. S. (2014). New strategies against *Stenotrophomonas maltophilia*: A serious worldwide intrinsically drug-resistant opportunistic pathogen.*Expert Review of Anti-infective Therapy, 12*(1), 1–4. https://doi.org/10.1586/14787210.2014.866515.
7. Falagas, M. E., Kastoris, A. C., Vouloumanou, E. K., & Dimopoulos, G. (2009). Community-acquired *Stenotrophomonas maltophilia* infections: Asystematic review. *European Journal of Clinical Microbiology & Infectious Diseases, 28*(7), 719–730. https://doi.org/10.1007/s10096-009-0709-5.
8. Muder, R. R. (2007). Optimizing therapy for Stenotrophomonas maltophilia. Seminars in Respiratory and Critical Care Medicine, 28(6), 672–677.https://doi.org/10.1055/s-2007-996414.
9. Di Bonaventura, G., Pompilio, A., Zappacosta, R., Petrucci, F., Fiscarelli, E., Rossi, C., et al. (2010). Excessive inflammatory response of DBA/2micetoStenotrophomonas maltophilia lung infection: Implications in cystic fibrosis. *Infection and Immunity, 78*(6), 2466–2476.https://doi.org/10.1128/IAI.01391-09.
10. De Oliveira-Garcia, D., Dall'Agnol, M., Rosales, M., Azzuz, A. C., Alcantara, N., Martinez, M. B., et al. (2003). Fimbriae and adherence ofStenotrophomonas maltophilia to epithelial cells and to abiotic surfaces. *Cellular Microbiology, 5*(9), 625–636. https://doi.org/10.1046/j.1462-5822.2003.00306.x.
11. Elvers, K. T., Leeming, K., & Lappin-Scott, H. M. (2001). Binary culture biofilm formation by *Stenotrophomonas maltophilia* and *Fusariumoxysporum*. *Journal of Industrial Microbiology & Biotechnology, 26*(3), 178–183. https://doi.org/10.1038/sj.jim.7000100.
12. De Vidipo, L. A., De Marques, E. A., Puchelle, E., & Plotkowski, M. C. (2001). *Stenotrophomonas maltophilia* interaction with human epithelialrespiratory cells *in vitro*. *Microbiology and Immunology, 45*(8), 563–569.https://doi.org/10.1111/j.1348-0421.2001.tb01287.x
13. Rutter, W. C., Burgess, D. R., & Burgess, D. S. (2016). Increasing incidence of multidrug resistance among cystic fibrosis respiratory bacterial isolates. *Microbial Drug Resistance, 22*(7), 573–581. https://doi.org/10.1089/mdr.2015.0338.
14. Hu, L. F., Chen, G. S., Kong, Q. X., Gao, L. P., Chen, X., Ye, Y., et al. (2016). Increase in the prevalence of resistance determinants to trimethoprim/sulfamethoxazole in clinical *Stenotrophomonas maltophilia* isolates in China. *PLoS ONE, 11*(6), e0157693.https://doi.org/10.1371/journal.pone.01576.
15. Sánchez, M. B. (2015). Antibiotic resistance in the opportunistic pathogen *Stenotrophomonas maltophilia*. *Frontiers in Microbiology, 6*, 658.https://doi.org/10.3389/fmicb.2015.00658.
16. Abbott, I. J., Slavin, M. A., Turnidge, J. D., Thursky, K. A., & Worth, L. J. (2011). *Stenotrophomonas maltophilia*: Emerging disease patterns and challenges for treatment. *Expert Review of Anti-infective Therapy, 9*(4), 471–488. https://doi.org/10.1586/eri.11.24.
17. Clinical and Laboratory Standards Institute. (2024). *Performance standards for antimicrobial susceptibility testing* (34th ed., CLSI supplement M100).Clinical and Laboratory Standards Institute.
18. Tamma, P. D., Heil, E. L., Justo, J. A., Mathers, A. J., Satlin, M. J., & Bonomo, R. A. (2024). *Infectious Diseases Society of America 2024 guidance on the treatment of antimicrobial-resistant Gram-negative infections*. *Clinical Infectious Diseases*. Advance online publication. https://doi.org/10.1093/cid/ciae403.
19. Bakthavatchalam, Y. D., Soman, R., Veeraraghavan, B., et al. (2024). Understanding the rationale and clinical impact of the revised CLSI 2024 minocycline susceptibility breakpoints against *Stenotrophomonas maltophilia*. *European Journal of Clinical Microbiology & Infectious Diseases, 43*,2453–2457. https://doi.org/10.1007/s10096-024-04930-0.
20. Barrasa, H., Morán, M. A., Fernández-Ciriza, L., Isla, A., Solinís, M. Á., Canut-Blasco, A., et al. (2024). Optimizing antibiotic therapy for *Stenotrophomonas maltophilia* infections in critically ill patients: A pharmacokinetic/pharmacodynamic approach. *Antibiotics, 13*(6), 553https://doi.org/10.3390/antibiotics13060553.
21. Carbonell, N., Motos, A., Torres, A., & Ceccato, A. (2024). *Stenotrophomonas maltophilia*: The landscape in critically ill patients. *Antibiotics, 13*(7),577. https://doi.org/10.3390/antibiotics13070577.

22. Puech, B., Canoui, E., Timsit, J.-F., et al. (2021). Effect of antibiotic therapy on the prognosis of ventilator-associated pneumonia caused by *Stenotrophomonas maltophilia*. *Annals of Intensive Care, 11*, 160. https://doi.org/10.1186/s13613-021-00948-2.
23. Cristina, M. L., Spagnolo, A. M., Ottria, G., et al. (2024). *Stenotrophomonas maltophilia* outbreak in an intensive care unit. *Microorganisms, 12*(5),998. https://doi.org/10.3390/microorganisms12050998.
24. Dimopoulos, G., Velegraki, M., Falagas, M. E., et al. (2023). *Upraising Stenotrophomonas maltophilia in critically ill patients*. *Microorganisms, 11*(3), 781.https://doi.org/10.3390/microorganisms11030781.
25. Afaq N et al. A Study of Bacteriological Profile and its Antibiogram in Respiratory Tract Infections Among the Patients Attending Tertiary Care Teaching Hospital,Greater Noida. International Journal of Environmental SciencesISSN: 2229-7359Vol. 11 No. 23s, 2025