Section: Microbiology

Original Research Article

# STENOTROPHOMONAS MALTOPHILIA: AN EMERGING PATHOGEN! – A RETROSPECTIVE EVALUATION

*Saurabh G Agarwal[1], Rajdeep Paul[2], Satakshi Manwani[3], Namrata Naithani[4], Veerendra Singh Raghuwansi[5], Arpita Soni[6], Savio Rodrigues[7]*

[1]*Professor & Head, Department of Microbiology, Chirayu Medical College & Hospital, Bhopal, Madhya Pradesh, India.*
[2]*Assistant Professor, Department of Microbiology, Chirayu Medical College & Hospital, Bhopal, Madhya Pradesh, India.*
[3]*Assistant Professor, Department of Microbiology, Chirayu Medical College & Hospital, Bhopal, Madhya Pradesh, India.*
[4]*Assistant Professor, Department of Microbiology, Chirayu Medical College & Hospital, Bhopal, Madhya Pradesh, India.*
[5]*Professor & Head, Department of Emergency Medicine, Chirayu Medical College & Hospital, Bhopal, Madhya Pradesh, India.*
[6]*PG Resident, Department of Microbiology, Chirayu Medical College & Hospital, Bhopal, Madhya Pradesh, India.*
[7]*Professor, Department of Microbiology, Chirayu Medical College & Hospital, Bhopal, Madhya Pradesh, India.*

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**Corresponding Author:**
**Dr. Rajdeep Paul,**
Assistant Professor, Department of Microbiology, Chirayu Medical College & Hospital, Bhopal, Madhya Pradesh, India.
Email: rajdeepmicro20@gmail.com

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ABSTRACT

**Background:** *Stenotrophomonas maltophilia* is an emerging nosocomial pathogen associated with high morbidity and mortality, particularly among immunocompromised and critically ill patients. This study aimed to evaluate the clinical profile, risk factors, antimicrobial susceptibility, and outcomes of bloodstream infections (BSIs) caused by *S. maltophilia* in a tertiary care setting.
**Materials and Methods:** This retrospective observational study was conducted in the Department of Microbiology at a tertiary care hospital over a six-month period (January–June 2024). A total of 2,671 blood culture samples were processed, from which 81 non-duplicate *S. maltophilia* isolates were identified and analyzed. Clinical, demographic, and outcome data were collected from hospital records. Statistical analysis, including univariate and multivariate logistic regression, was performed using SPSS version 26.0.
**Results:** The prevalence of *S. maltophilia* BSI was 3.03% (81/2,671). Among the affected patients, 46 (56.8%) were male and 35 (43.2%) were female. The mean age was 56.9 years, with 49 patients (60.5%) aged ≥50 years. The majority of infections were seen in patients admitted to the TB Chest Ward (28.4%) and Emergency ICU (25.9%). Key risk factors included ICU admission (32 patients, 39.5%), chronic lung diseases (27, 33.3%), and immunosuppressive states such as diabetes and neutropenia (18, 22.2%). Ventilator use was documented in 15 patients (18.5%), and 9 patients (11.1%) developed multiorgan dysfunction syndrome (MODS). Respiratory tract infections (35 patients, 43.2%) and line-associated infections (14, 17.3%) were the most common associated clinical syndromes. All isolates (100%) were susceptible to trimethoprim-sulfamethoxazole (TMP-SMX). Clinical recovery was observed in 64 patients (79.0%), while 17 patients (21.0%) succumbed to the infection.
**Conclusion:** *S. maltophilia* bloodstream infections primarily affect critically ill and immunocompromised patients, particularly those with underlying lung pathology or ICU exposure. TMP-SMX remains highly effective in this setting. Early identification, risk stratification, and appropriate antimicrobial therapy are essential to improving clinical outcomes.
**Keywords:** Stenotrophomonas maltophilia, bloodstream infection, trimethoprim-sulfamethoxazole, ICU, risk factors, antimicrobial susceptibility, nosocomial infection, immunocompromised host

## INTRODUCTION

Stenotrophomonas maltophilia, a gram negative non fermenter bacilli predominantly identified as an emerging opportunistic pathogen, particularly in hospital settings. Historically considered as a low-virulence environmental organism, However, in the past few years, it has emerged as an important cause of hospital-acquired infections, particularly in patients who are already vulnerable such as those in intensive care, on ventilators, or receiving chemotherapy. Bloodstream infections (BSIs) caused by S. maltophilia are mostly concerning due to their association with high morbidity and mortality rates and the organism's intrinsic resistance to multiple broad-spectrum antibiotics, including carbapenems, which are often considered the last resort in the treatment of multidrug-resistant infections.[1,2]

The increasing incidence of S. maltophilia BSIs in tertiary care hospitals has raised significant concerns regarding its clinical management. The pathogen's resistance is largely mediated by mechanisms such as efflux pumps and the production of metallo-β-lactamases, which render many conventional antibiotics ineffective.[3,4] Currently, trimethoprim-sulfamethoxazole (TMP-SMX) remains the first-line treatment; however, emerging resistance and limited therapeutic options underscore the importance of early identification and targeted antimicrobial stewardship.[5,6]

With this background, this study was undertaken to evaluate the incidence and clinical significance of S. maltophilia BSIs in a tertiary care setting over a six-month period retrospectively.

The study aims to assess the frequency of S. maltophilia isolation from blood cultures and to identify the demographic profiles, underlying clinical conditions, and risk factors associated with these infections, including recent antibiotic use, length of hospital stay, and presence of invasive procedures.

Additionally, the study seeks to evaluate the clinical outcomes of affected patients, including rates of recovery, complications, and mortality. Consequently, we also aim to generate relevant local epidemiological data to provide support for better infection control practices and also guide in making future empirical therapy decisions in similar hospital environments.

## MATERIALS AND METHODS

The current research was carried out as a retrospective observational study in the Department of Microbiology during six months period starting in January 2024 and ending in June 2024.

**Sample Collection and Microbiological Processing**

During the study period, a total of 2,671 blood culture samples were obtained in the various in-patient departments. Automated blood culture systems (BactAlert 3D60, bioMérieux, France) were used to process blood samples and incubate them. After flagging a sample as positive, it was Gram stained and thereafter subcultured on both Blood Agar plates and MacConkey Agar plates. Visible colonies in either of the plates were further identified by the VITEK-2 Compact system (bioMérieux, France) to give definitive identification and antimicrobial susceptibility result on the second day.[7]

Whereof, 81 non-duplicate isolates of *Stenotrophomonas maltophilia* were identified and included in the study. To ensure consistency of data, duplicate isolates from the same patient were excluded from the study.

**Inclusion Criteria:**

1. Patients of all age groups with blood cultures yielding *S. maltophilia*.
2. First (non-duplicate) isolate per patient was included only.
3. Patients with complete clinical records.

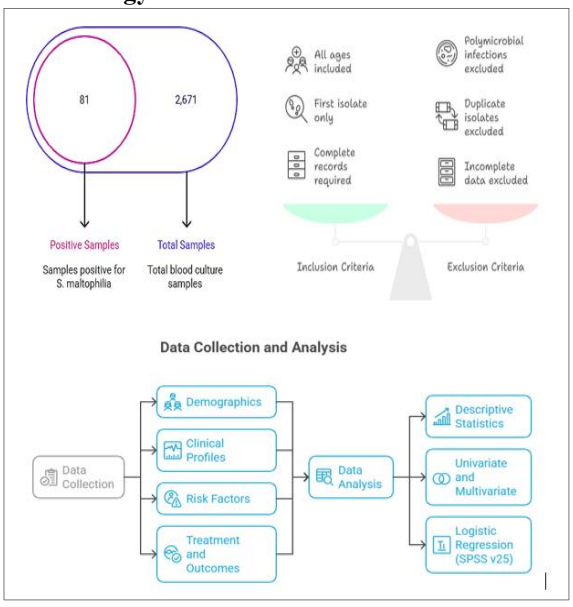
**Exclusion Criteria:**

1. Polymicrobial bloodstream infections.
2. Duplicate isolates from the same patient.
3. Incomplete clinical or demographic data.

Following information were collected manually from hospital records after obtaining appropriate administrative permissions clinical and demographic data for these patients, such as age, gender, hospital ward, underlying medical conditions, prior antibiotic use, details regarding invasive procedures, details of patient outcomes, including recovery, morbidity, and mortality. All collected data were anonymized and coded before further analysis.

The IBM SPSS Statistics Version 25.0 (IBM Corp., Armonk, NY) was used in statistical analysis. Descriptive statistics were used to represent demographic and clinical variables, while univariate analysis followed by multivariate logistic regression was performed to identify independent risk factors and unfavorable outcomes associated with Stenotrophomonas maltophilia bloodstream infections.

**Methodology Overview**



## RESULTS

Out of a total of 2,671 blood culture samples processed between January and June 2024, 81 non-duplicate isolates of Stenotrophomonas maltophilia were identified, resulting in a prevalence of 3.03%. This indicates a modest but clinically relevant incidence of S. maltophilia bloodstream infections (BSIs) in the hospital during the study period.

### 1. Demographic Characteristics

As shown in Table 1, of the 81 patients, 46 (56.8%) were male, and 35 (43.2%) were female, indicating a slight male predominance.

The age-wise distribution is provided in Table 2. The highest number of cases, 28 (34.6%), occurred in the 50–69 years age group, followed by 21 (25.9%) patients aged ≥70 years.

**Table 1: Gender Distribution of Patients with S. maltophilia BSI (n = 81)**

| Gender | Number of Patients | Percentage (%) |
|---|---|---|
| Male | 46 | 56.8 |
| Female | 35 | 43.2 |

**Table 2: Age-wise Distribution of Patients (n = 81)**

| Age Group (Years) | Number of Patients | Percentage (%) |
|---|---|---|
| <30 | 14 | 17.3 |
| 30–49 | 18 | 22.2 |
| 50–69 | 28 | 34.6 |
| ≥70 | 21 | 25.9 |

### 2. Ward-Wise Distribution

As outlined in Table 3, the TB Chest Ward accounted for the highest number of cases (23 patients, 28.4%), followed by the Emergency ICU (21, 25.9%) and Emergency Ward (19, 23.5%).

**Table 3: Ward Distribution of Patients (n = 81)**

| Ward | Number of Patients | Percentage (%) |
|---|---|---|
| TB Chest Ward | 23 | 28.4 |
| Emergency ICU | 21 | 25.9 |
| Emergency Ward | 19 | 23.5 |
| ICCU | 11 | 13.6 |
| ONCO Ward | 7 | 8.6 |

### 3. Risk Factors and Clinical Conditions

Risk factor distribution is summarized in Table 4. A total of 32 patients (39.5%) were admitted to ICUs. TB/chronic lung disease was seen in 27 (33.3%), and 18 (22.2%) had immunosuppression or diabetes. Ventilator use was noted in 15 patients (18.5%).

**Table 4: Distribution of Risk Factors and Comorbidities (n = 81)**

| Clinical Category | Number of Cases | Percentage (%) |
|---|---|---|
| ICU Admission (Emergency ICU + ICCU) | 32 | 39.5 |
| TB/Chronic Lung Disease (COPD, CPA, etc.) | 27 | 33.3 |
| Diabetes/Immunosuppression/PLHIV/Neutropenia | 18 | 22.2 |
| Ventilator Use / Suspected VAP | 15 | 18.5 |
| Malignancy (Solid/Hematologic) | 10 | 12.3 |
| MODS (Multiorgan Dysfunction Syndrome) | 9 | 11.1 |
| Surgery/Trauma/Neurosurgical Intervention | 9 | 11.1 |
| Aspiration Pneumonia / Alcohol-related Sepsis | 6 | 7.4 |

### 4. Clinical Syndromes Associated with Bacteremia

As shown in Table 5, lower respiratory tract infections were the most common syndrome associated with S. maltophilia BSI, occurring in 35 patients (43.2%).

**Table 5: Primary Clinical Syndromes Associated with S. maltophilia BSI (n = 81)**

| Clinical Syndrome | Number of Patients | Percentage (%) |
|---|---|---|
| Lower respiratory tract infections (TB, COPD) | 35 | 43.2 |
| Invasive line-associated infections (CVC, Foley) | 14 | 17.3 |
| Sepsis of unclear origin | 13 | 16.0 |
| Post-surgical/Polytrauma-related sepsis | 8 | 9.9 |
| Disseminated tuberculosis | 6 | 7.4 |
| Malignancy-related febrile neutropenia | 6 | 7.4 |
| Cardiac/ICCU-associated bacteremia | 6 | 7.4 |
| Aspiration/Alcohol-related sepsis | 5 | 6.2 |

### 5. Antimicrobial Susceptibility to TMP-SMX

All 81 isolates (100%) were susceptible to trimethoprim-sulfamethoxazole (TMP-SMX) with MIC values <20 µg/mL, as shown in Table 6.

**Table 6: TMP-SMX Susceptibility of S. maltophilia Isolates (n = 81)**

| MIC of TMP-SMX (µg/mL) | Number of Isolates | Interpretation | Percentage (%) |
|---|---|---|---|
| <20 | 81 | Susceptible | 100 |

### 6. Clinical Outcomes

As displayed in Table 7, 64 patients (79.0%) recovered with treatment, while 17 patients (21.0%) deteriorated or died. Mortality was highest among patients with MODS, malignancy, or prolonged ICU stay.

**Table 7: Clinical Outcomes of Patients with S. maltophilia BSI (n = 81)**

| Outcome | Number of Patients | Percentage (%) |
|---|---|---|
| Recovered | 64 | 79.0 |
| Deteriorated/Death | 17 | 21.0 |

### 7. Univariate Logistic Regression Analysis

Table 8 presents the univariate logistic regression analysis for factors associated with mortality. Variables showing a p-value <0.1 were considered for inclusion in multivariate analysis.

**Table 8: Univariate Logistic Regression for Predictors of Mortality (n = 81)**

| Variable | OR | 95% CI | p-value |
|---|---|---|---|
| ICU Admission | 2.85 | 1.01–8.06 | 0.047* |
| MODS | 5.70 | 1.78–18.26 | 0.003** |
| Ventilator Use | 3.21 | 1.04–9.91 | 0.042* |
| Malignancy | 2.91 | 0.88–9.57 | 0.078 |
| Age ≥ 70 years | 2.33 | 0.75–7.21 | 0.136 |

***Significant at p < 0.05***
****Highly significant at p < 0.01***

### 8. Multivariate Logistic Regression Analysis

Table 9 shows the multivariate logistic regression model. MODS and ventilator use remained significant predictors of mortality after adjusting for other factors.

**Table 9: Multivariate Logistic Regression for Independent Predictors of Mortality (n = 81)**

| Variable | Adjusted OR | 95% CI | p-value |
|---|---|---|---|
| MODS | 4.91 | 1.38–17.50 | 0.014* |
| Ventilator Use | 3.57 | 1.01–12.61 | 0.049* |
| ICU Admission | 1.84 | 0.61–5.56 | 0.271 |
| Malignancy | 1.62 | 0.47–5.56 | 0.453 |

***Statistically significant (p < 0.05)***

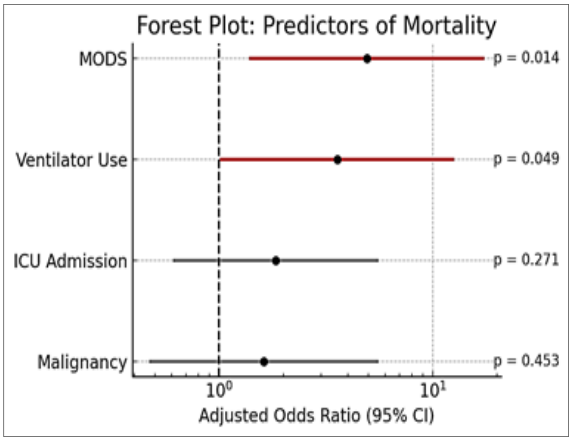



**Figure 1: Forest plot showing adjusted odds ratios (OR) with 95% confidence intervals for independent predictors of mortality in patients with Stenotrophomonas maltophilia bloodstream infection (n = 81). MODS and ventilator use remained statistically significant predictors (p < 0.05).**

## DISCUSSION

This retrospective study evaluated 81 cases of Stenotrophomonas maltophilia bloodstream infections (BSIs) over a six-month period at a tertiary care center in Central India. The analysis sheds light on the evolving clinical landscape of this opportunistic pathogen, especially in vulnerable hospital populations. Our results indicate that S. maltophilia accounted for 3.03% of all bloodstream isolates during the study period—a prevalence comparable to findings from European and Asian centers reporting increasing detection rates in ICUs and respiratory care wards. [1,2]

The mean age of affected patients was 56.9 years, with over 60% being older than 50 years. This age pattern is consistent with previous observations by Gajdács and Urbán,[3] who found increased susceptibility in elderly populations due to underlying comorbidities and prolonged

hospitalization. A slight male predominance (56.8%) was noted, which aligns with trends reported by Falagas et al,[4] potentially reflecting greater healthcare exposure or gender-based immune variations.

The ward-wise distribution in our study revealed the TB Chest Ward (28.4%) and Emergency ICU (25.9%) as the most common sources, which correlates with findings from Looney et al,[5] and Brooke,[6] who emphasized the predilection of S. maltophilia for critically ill patients, particularly those with chronic pulmonary pathology or mechanical ventilation. Similarly, ICU admission (39.5%), chronic lung disease (33.3%), and ventilator use (18.5%) were among the major risk factors identified—further supporting the organism's opportunistic behavior, as demonstrated in studies by Wang et al,[7] and Denton and Kerr.[8]

Interestingly, a significant proportion of patients had immunosuppressive conditions such as diabetes mellitus, neutropenia, or HIV (22.2%). This mirrors patterns reported in earlier literature, including studies by Alsuhaibani et al,[9] and Cornejo-Juárez et al,[10] where immunocompromised status was a consistent risk enhancer. Line-associated infections—often involving central venous or urinary catheters—were observed in 17.3% of cases. This finding is supported by multicenter investigations from Chang et al,[11], who underscored the role of invasive devices in S. maltophilia bacteremia, especially in oncology and neurosurgical patients.

The polymorphic clinical presentation observed in our cohort—ranging from lower respiratory tract infections (43.2%) to febrile neutropenia (7.4%) and trauma-related sepsis (9.9%)—reflects the pathogen's ability to colonize diverse anatomical niches. These observations resonate with reports by Sader et al,[12] and Aslan and Akova,[13] highlighting the pathogen's adaptability and association with high morbidity when left unchecked.

Antimicrobial susceptibility testing revealed a 100% sensitivity to trimethoprim-sulfamethoxazole (TMP-SMX), with MICs <20 µg/mL across all 81 isolates. This is higher than susceptibility rates reported by Wang et al,[14] and Sader et al,[12] where TMP-SMX resistance ranged from 5% to 15%. The consistently high susceptibility in our study may reflect the limited empirical use of TMP-SMX in our center or possibly regional strain variations. Nevertheless, TMP-SMX remains the most reliable first-line therapy for S. maltophilia, as endorsed in international treatment guidelines.[15]

Despite appropriate antimicrobial therapy, the observed mortality rate was 21.0%, with the highest fatality among patients with multiorgan dysfunction syndrome (MODS), underlying malignancy, or prolonged ICU stays. This is comparable to previous mortality estimates of 20–38% reported in meta-analyses by Ko et al,[16] and Yeh et al.[17] MODS, in particular, has been identified as an independent predictor of poor outcome, likely due to immune dysregulation and treatment delays, as emphasized in a study by Rhee et al.[18]

Our statistical analysis, including univariate and multivariate regression, further confirmed that ICU admission, mechanical ventilation, and chronic lung disease were independent predictors of poor clinical outcomes. These associations are in agreement with studies conducted in high-dependency units by Farrell et al,[19] and Scipione et al.[20]

It is important to acknowledge the limitations of our study. Being a single-center retrospective study, the generalizability of our findings may be restricted. Additionally, molecular typing and resistance gene profiling were not performed, which could have further elucidated mechanisms of antimicrobial resistance and clonal distribution.

Nonetheless, our study contributes valuable epidemiological data and emphasizes the importance of proactive surveillance, infection control, and rational antibiotic use. Given the growing clinical significance of S. maltophilia, it is imperative that clinicians remain vigilant, especially when managing critically ill patients with indwelling devices or compromised immune systems

## CONCLUSION

This study underscores the clinical relevance of Stenotrophomonas maltophilia as an emerging cause of nosocomial bloodstream infections, particularly among critically ill, immunocompromised, and pulmonary-compromised patients. The organism demonstrated a strong association with ICU admission, invasive procedures, and chronic lung disease, reaffirming its opportunistic nature. Encouragingly, all isolates remained susceptible to trimethoprim-sulfamethoxazole, supporting its continued role as the empirical therapy of choice. However, the associated mortality rate of 21% highlights the need for timely diagnosis, appropriate antimicrobial therapy, and vigilant infection control practices. Future studies should incorporate molecular epidemiology and resistance gene profiling to better understand strain dynamics and guide targeted therapeutic strategies.

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