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Microbiological profile of an Emerging Global Opportunistic Pathogen*:* *Stenotrophomonas maltophilia*

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ABTRACT:

Stenotrophomonas maltophilia is a nonfermenting Gram-negative rod that is ubiquitous in nature. This pathogen is frequently responsible for nosocomial outbreaks, especially in intensive care units (ICU). *Stenotrophomonas maltophilia* infections are associated with a high mortality in case of pneumonia and septicemia. **Objective:** Study focused on detects prevalence and antibiotics sensitivity of *Stenotrophomonas maltophilia*. **Method: A study conducted at** Microbiology Department of Smt. B. K. Shah Medical Institute and Research Centre, Piparia from January 2023 to December 2023. Culture for all the samples was done on sheep blood agar and MacConkey agar followed by Incubation at 37°C for 18–24 hours in 5–10% CO_2. Bacterial isolates identified by standard laboratory procedure and antibiotic sensitivity was done by VITEK 2 compact system of bioMerieux. **Results:** 23 isolates of *S. maltophilia* were identified from various samples, with maximum number from sputum (n = 11, 47%) followed by blood (n = 6, 26.08%). Most of the patients (n = 13, 56.52%) were in the age group of 41–60 years. Predominant presenting symptoms were observed as respiratory tract infections 14 (60.87%). The isolates had high susceptibility to trimethoprim-sulfamethoxazole (TMP-SXT) (91.3%) and Minocycline (60.9%). **Conclusion:** It is very important to give pathogen specific antibiotics as per antibiotics sensitivity testing, because it has shown to decrease the patient stay in the hospital and also decrease the mortality rate. New treatment guidelines recommend combination of antibiotics to obtain synergic effect.

Keywords: *Stenotrophomonas maltophilia*, TMP-SXT, VITEK 2 compact system

INTRODUCTION:

Stenotrophomonas maltophilia is a nonfermenting Gram-negative rod that is ubiquitous in nature (predominantly occurring in aquatic environments and on plants) [1]. Biochemically, it is catalase positive and oxidase negative, and it produces acid from maltose (hence the name *"maltophilia"*).[2-3] Due to its charged cell wall surface and biofilm production, it may attach to and survive on abiotic surfaces in clinical settings (eg, central venous catheters, disinfectant and hand-washing solutions, solutions for hemodialysis, endoscopes, inspiration/expiration circuits of ventilators, nebulizers, tap water, and showerheads).[4-7] This pathogen is frequently responsible for nosocomial outbreaks, especially in intensive care units (ICUs).[8,9] Before the 1980s, there have been seldom reports of the isolation of this microorganism in the context of human infections; however, after the 1980s, the prevalence of nosocomial infections associated with *S maltophilia* has increased rapidly.[10-11] *Stenotrophomonas maltophilia* infections are associated with a high crude mortality of 25% to 75% in case of pneumonia and 20% to 60% in case of bacteremia. The mortality rate increases sharply if the patients receive inappropriate antimicrobial therapy (which mainly occurs empirically).[9-11] On the one hand, *S maltophilia* is a pathogen of low virulence and limited invasiveness; therefore, bypassing the natural defenses of the body is crucial for the development of any pathologies.[12] Advancements in medical interventions (complex surgeries, chemotherapy of advanced malignancies, immunosuppressive therapy for organ transplantation, or autoimmune disorders) have also resulted in the increase in the number of patients at risk.[10-12] Nonetheless, advancements in the identification methods in clinical microbiology laboratories (eg, polymerase chain reaction, mass spectrometry, and sequencing) have allowed for the more precise identification of this pathogen.[13-15] To complicate things even further, the prevalence of community-acquired *S maltophilia* infections (presumably due to the increase in the number of immunocompromised/debilitated patients in outpatient care settings) has also increased since the 2000s.[16]

The main clinical manifestations of *S maltophilia* infections include nosocomial lower respiratory tract infections (LRTIs; namely, tracheobronchitis/pneumonia, usually associated with mechanical ventilation) and bacteremia. Nevertheless, other manifestations, for example, wound/soft tissue infections (ie, ecthyma gangrenosum), cellulitis, mastoiditis, meningitis, peritonitis, bone and joint infections, urinary tract infections, conjunctivitis, and otitis media have also been described. [9-11] These infections usually occur in severely debilitated, immunosuppressed individuals, in addition to patients with a chronic illness or a developmental abnormality affecting a specific organ system.[17-19] *Stenotrophomonas maltophilia* represents the fourth most common pathogen among nonfermenting gram-negative bacteria (following *Pseudomonas aeruginosa*, *Acinetobacter* spp, and *Burkholderia cepacia complex*), with a reported incidence of 7.1 to 37.7 cases/10 000 discharges (regarding nosocomial infections)[20].

Stenotrophomonas maltophilia may colonize the respiratory tract and persist in the sputum of these patients for a long period of time; therefore, it may be difficult to ascertain the clinical significance of a positive culture result from the microbiology laboratory.[21-22] However, previously verified colonization is one of the main risk factors for manifestation of *S maltophilia* LRTI; thus, culture positivity for this microorganism does pertain clinically useful information.[21-22] While some reports suggest that *S maltophilia* LRTIs are characterized by the lack of acute inflammatory

response, Di Bonaventura et al found an pronounced inflammatory response (increased expression of IL-8 and TNF-α) in murine airway epithelial cells and macrophages, which may contribute to airway inflammation *in vivo*.[23-24] Histologically, *S maltophilia* LRTIs are frequently characterized by focal lung necrosis and lung hemorrhage, while pleural effusions and cavitations are rarely observed.[20] As many *S maltophilia* infections are polymicrobial, clinicians should be extremely cautious when interpreting radiological findings (especially in patients with cancer), as several copathogens (eg, *Pseudomonas* spp, *Acinetobacter* spp, *Nocardia* spp, *Staphylococcus aureus*, and opportunistic fungi) may be present simultaneously.[11-12] In severely immunosuppressed patients, fatal hemorrhagic pneumonia may occur, which is the fulminant course of the infection.[10-12] In addition, *S maltophilia* is a well-known colonizer and pathogen in patients with cystic fibrosis (CF); it has been described that the colonization/infection rate (especially in 10^5-10^6 CFU) correlates well with disease progression and loss of lung function.[25-26] Air-borne transmission of this microorganism from the cough (aerosol) of patients with CF have also been described.[25-26]

Due to the proclivity of this microorganism to become multidrug resistant (MDR) and extensively drug resistant (XDR), it has been listed by the World Health Organization as one of the most concerning multidrug resistant organisms worldwide.[27] Apart from SMX/TMP and fluoroquinolones, other drugs that may be considered for therapy (and several case reports are available in successfully curing patients) are the tetracyclines (doxycycline, minocycline, and tigecycline), ticarcillin/clavulanate, ceftazidime, colistin, and chloramphenicol.

Despite the abundance of global surveillance studies published, there are only few reports assessing the microbiological and clinical significance of *S maltophilia* in LRTIs, as the majority of studies have focused on the isolation of MDR *Pseudomonas* spp and *Acinetobacter* spp. The aim of this study was to assess the prevalence of *S maltophilia* in respiratory tract specimens at a tertiary-care hospital in Hungary retrospectively, during a 10-year study period (2008-2017).

MATERIAL & METHOD: This study was done from January 2023 to December 2023, at the Clinical Microbiology Laboratory, Dhiraj Hospital, Piparia, Vadodara (Gujarat). All the patient's samples whose cultures grew *S. maltophilia* during the study period were included in the study.

Culture for all the samples was done on sheep blood agar and MacConkey agar followed by Incubation at 37°C for 18–24 hours in 5–10% CO_2.

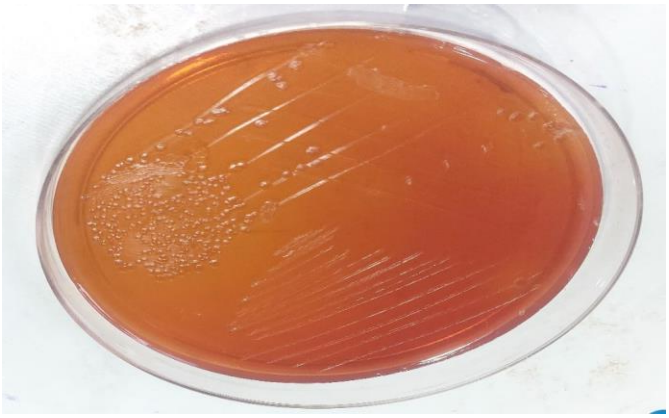

Figure 1*: S. maltophilia* on MacConkey agar

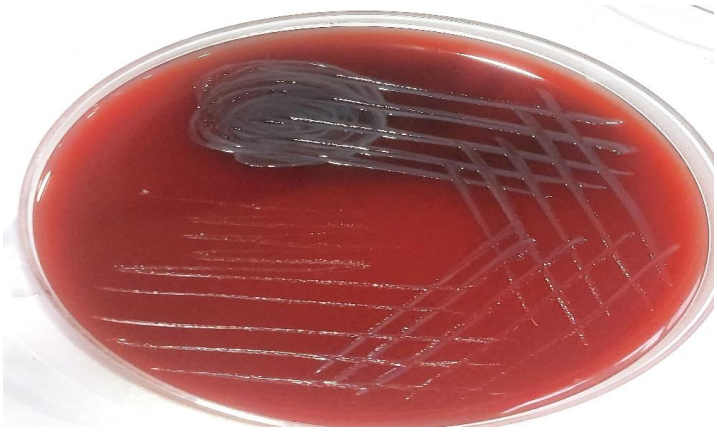

***Figure 2: S. maltophilia* on Sheep blood agar**

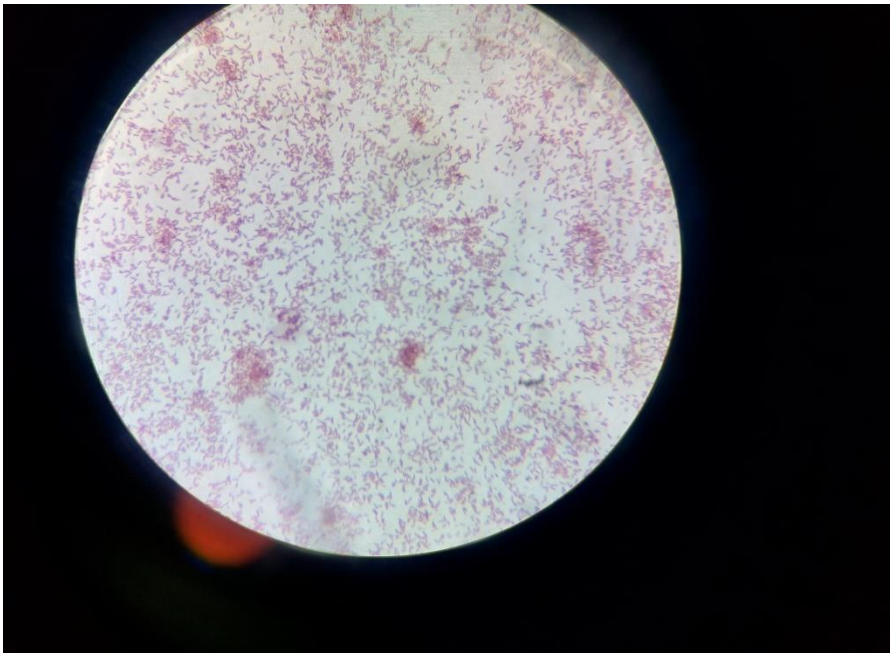

Figure 3 Gram stain picture of *S. maltophilia* in 100x lens

Final identification and antibiotic susceptibility test was made by bioMerieux's automated VITEK 2 compact system as per manufacturer's instructions. For gram negative organism VITEK® 2 GN card was used and antimicrobial sensitivity done by ready-to-use, flexible VITEK® 2 AST N406 card. Antimicrobial susceptibility testing was performed according to Clinical Laboratory Standards Institute (CLSI) guidelines 2022 and reporting following antibiotics Trimethoprim-sulfamethoxazole (TMP-SXT), levofloxacin, Minocycline, Chloramphenicol, & Ceftazidime by bioMerieux's automated VITEK 2 compact system.

RESULT & DISCUSSION: In the study period, 23 isolates of *S. maltophilia* were identified from various samples, with maximum number from sputum (n = 11, 47%) followed by blood (n = 6, 26.08%), endotracheal aspirate (n = 2, 8.69%), wound swab (n = 2, 8.69%), one (4.35%) from BAL and one (4.35%) from the urine. Male to female ratio of study cases was 14:09. Most of the patients (n = 13, 56.52%) were in the age group of 41–60 years. Predominant presenting symptoms

were observed as respiratory tract infections 14 (60.87%). The detailed clinico-demographic profile of the study population is shown in Table no 01.

TABLE: 01

Sr. No.	**Parameter**	Culture Positive Cases (n=23)
1.	Gender	
	Male	14 (60.87%)
	Female	9 (39.13%)
2.	Age Group	
	20-40	2 (8.69%)
	41-60	13 (56.52%)
	>60	8 (34.78%)
3.	Sample wise distribution of *S. maltophilia*	
	Sputum	11 (47%)
	Blood	6 (26.08%)
	Endotracheal aspirate	2 (8.69%)
	Pus & Wound swab	2 (8.69%)
	BAL	1 (4.35%)
	Urine	1 (4.35%)

The isolates had high susceptibility to trimethoprim-sulfamethoxazole (TMP-SXT) (91.3%) and Minocycline (60.9%) and least susceptible to Ceftazidime (34.8%). The drug susceptibility among fluoroquinolones was comparable with levofloxacin having slightly higher sensitivity than ciprofloxacin. Amongst isolates 30.4% and 34.8% were resistant to both Fluoroquinolones (Ciprofloxacin and Levofloxacin respectively) tested. Antibiogram of isolates is depicted in Table no 02.

TABLE: 02

Antibiotics	**Sensitive**	**Resistance**
Trimethoprim- sulfamethoxazole (TMP-SXT)	21 (91.3%)	02 (8.7%)
Levofloxacin	8 (34.8%)	15 (65.2%)
Ciprofloxacin	7 (30.4%)	16 (69.6%)
Minocycline	14 (60.9%)	9 (39.1%)
Chloramphenicol	11 (47.8%)	12 (52.2%)
Ceftazidime	8 (34.8%)	15 (65.2%)

DISCUSSION:

In the present study, the predominance of by *S. maltophilia* infection in males is probably due to the behavioural and socioeconomic factors in India, where males in larger proportion to females

are involved with outdoor activities and females often don't present in the early course of the illness.

Present study reports that maximum infected cases almost 56.52% with by *S. maltophilia* were between the age group of 41–60 years and about 08 (34.78%) patients were in age group of 61–80 years. This can be attributed to a weekend immune system response observed in older age group which rendered them more susceptible to infections by *S. maltophilia*.

Present study shows that respiratory tract is the most common system involved (60.87%) followed by blood stream infection (26.08%) and pus & wound swab infection (8.69%). Pulmonary diseases like chronic obstructive pulmonary diseases, bronchiectasis and acute respiratory distress syndrome have been found to be the most frequent comorbidities in *S. maltophilia* infection..

Our study reports maximum susceptibility of *S. maltophilia* to co-trimoxazole (91.3%), followed by Minocycline (60.9%) and Chloramphenicol (47.8%). Likewise, the management of the cases infected by *S. maltophilia* vary in different study.

CONCLUSION:

Treatment with nonspecific antibiotics may have pre-disposed the patients to get infected by this pathogen. It is very important to give pathogen specific antibiotics as per antibiotics sensitivity testing, because it has shown to decrease the patient stay in the hospital and also decrease the mortality rate. New treatment guidelines recommend combination of antibiotics to obtain synergic effect. Few studies have shown the synergic effect with Trimethoprim-Sulfamethoxazole and Tigecycline, and between Amikacin and Tigecycline. It is also observed that when TMP-SMX is combined with either ceftazidime, ciprofloxacin or tobramycin, it produces higher bactericidal efficacy against *S. maltophilia* clinical isolates.

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REFERENCES:

1. Adegoke AA, Stenström TA, Okoh AI. Stenotrophomonas maltophilia as an emerging ubiquitous pathogen: looking beyond contemporary antibiotic therapy. Front Microbiol. 2017;8:2276. [PMC free article] [PubMed] [Google Scholar]
2. Carmody LA, Spilker T, LiPuma JJ. Reassessment of Stenotrophomonas maltophilia phenotype. J Clin Microbiol. 2011;49(3):1101–1103. [PMC free article] [PubMed] [Google Scholar]
3. Singhal L, Kaur P, Gautam V. Stenotrophomonas maltophilia: from trivial to grievous. Indian J Med Microbiol. 2017;35(4):469–479. [PubMed] [Google Scholar]
4. Brooke JS. Stenotrophomonas maltophilia: an emerging global opportunistic pathogen. Clin Microbiol Rev. 2012;25(1):2–41. [PMC free article] [PubMed] [Google Scholar]
5. Cervia JS, Ortolano GA, Canonica FP. Hospital tap water as a source of Stenotrophomonas maltophilia infection. Clin Infect Dis. 2008;46(9):1485–1487. [PubMed] [Google Scholar]
6. Looney WJ. Role of Stenotrophomonas maltophilia in hospital-acquired infection. Br. J. Biomed Sci. 2005;62(3):145–154. [PubMed] [Google Scholar]
7. Brooke JS. New strategies against Stenotrophomonas maltophilia: a serious worldwide intrinsically drug-resistant opportunistic pathogen. Expert Rev Anti Infect Ther. 2014;12(1):1–4. [PubMed] [Google Scholar]
8. Gulcan H, Kuzucu C, Durmaz R. Nosocomial Stenotrophomonas maltophilia cross-infection: three cases in newborns. Am J Infect Control. 2004;32(6):365–368. [PubMed] [Google Scholar]
9. Rajkumari N, Mathur P, Gupta AK, Sharma K, Misra M.C. Epidemiology and outcomes of Stenotrophomonas maltophilia and Burkholderia cepacia infections among trauma patients of India: a five year experience. J Infect Prev. 2015;16(3):103–110. [PMC free article] [PubMed] [Google Scholar]
10. Denton M, Kerr KG. Microbiological and clinical aspects of infection associated with Stenotrophomonas maltophilia. Clin. Microbiol. Rev. 1998;11(1):57–80. [PMC free article] [PubMed] [Google Scholar]
11. Gilardi GL. Pseudomonas maltophilia infections in man. Am J Clin Pathol. 1969;51(1):58–61. [PubMed] [Google Scholar]
12. Wang Y, He T, Shen Z, Wu C. Antimicrobial resistance in Stenotrophomonas spp. Microbiol Spectr. 2018;6(1):1–14. [PubMed] [Google Scholar]
13. Schaumann R, Knoop N, Genzel GH. et al. Discrimination of enterobacteriaceae and non-fermenting gram negative bacilli by MALDI-TOF mass spectrometry. Open Microbiol J. 2013;7:118–122. [PMC free article] [PubMed] [Google Scholar]
14. Steensels D, Verhaegen J, Lagrou K. Matrix-assisted laser desorption ionization-time of flight mass spectrometry for the identification of bacteria and yeasts in a clinical microbiological laboratory: a review. Acta Clin Belg. 2011;66(4):267–273. [PubMed] [Google Scholar]
15. Gautam V, Sharma M, Singhal L. et al. MALDI-TOF mass spectrometry: An emerging tool for unequivocal identification of non-fermenting Gram-negative bacilli. Indian J Med Res. 2017;145(5):665–672. [PMC free article] [PubMed] [Google Scholar]
16. Falagas M.E, Kastoris AC, Vouloumanou EK, Dimopoulos G. Community-acquired stenotrophomonas maltophilia infections: a systematic review. Eur J Clin Microbiol Infect Dis. 2009;28(7):719–730. [PubMed] [Google Scholar]

17. Falagas ME, Kastoris AC, Vouloumanou EK, Rafailidis PI, Kapaskelis AM, Dimopoulos G. Attributable mortality of Stenotrophomonas maltophilia infections: a systematic review of the literature. Future Microbiol. 2009;4(9):1103–1109. [PubMed] [Google Scholar]
18. del Toro MD, Rodríguez-Bano J, Herrero M. et al. Clinical epidemiology of Stenotrophomonas maltophilia colonization and infection: a multicenter study. Medicine (Baltimore). 2002;81(3):228–239. [PubMed] [Google Scholar]
19. Al-Anazi KA, Al-Jasser AM. Infections caused by Stenotrophomonas maltophilia in recipients of hematopoietic stem cell transplantation. Front Oncol. 2014;4:232. [PMC free article] [PubMed] [Google Scholar]
20. Gales A.C, Jones RN, Forward KR, Liñares J, Sader HS, Verhoef J. Emerging importance of multidrug-resistant Acinetobacter species and Stenotrophomonas maltophilia as pathogens in seriously ill patients: geographic patterns, epidemiological features, and trends in the SENTRY antimicrobial surveillance program (1997-1999). Clin Infect Dis. 2001;32(suppl 2):S104–113. [PubMed] [Google Scholar]
21. Millar FA, Simmonds NJ, Hodson ME. Trends in pathogens colonising the respiratory tract of adult patients with cystic fibrosis, 1985-2005. J Cyst Fibros. 2009;8(6):386–391. [PubMed] [Google Scholar]
22. Bostanghadiri N, Ghalavand Z, Fallah F. Characterization of phenotypic and genotypic diversity of Stenotrophomonas maltophilia strains isolated from selected hospitals in Iran. Front Microbiol. 2019;10:1191. [PMC free article] [PubMed] [Google Scholar]
23. Di Bonaventura G, Pompilio A, Zappacosta R. et al. Role of excessive inflammatory response to Stenotrophomonas maltophilia lung infection in DBA/2 mice and implications for cystic fibrosis. Infect Immun. 2010;78(6):2466–2476. [PMC free article] [PubMed] [Google Scholar]
24. Pompilio A, Ciavardelli D, Crocetta V. et al. Stenotrophomonas maltophilia virulence and specific variations in trace elements during acute lung infection: implications in cystic fibrosis. PLoS One. 2014;9(2):e88769. [PMC free article] [PubMed] [Google Scholar]
25. Berdah L, Taytard J, Leyronnas S, Clement A, Boelle PY, Corvol H. Stenotrophomonas maltophilia: a marker of lung disease severity. Pediatr Pulmonol. 2018;53(4):426–430. [PMC free article] [PubMed] [Google Scholar]
26. Barsky EE, Williams KA, Priebe GP, Sawicki GS. Incident Stenotrophomonas maltophilia infection and lung function decline in cystic fibrosis. Pediatr. Pulmonol. 2017;52(10):1276–1282. [PubMed] [Google Scholar]
27. Gajdács M. The concept of an ideal antibiotic: implications for drug design. Molecules. 2019;24(5):E892. [PMC free article] [PubMed] [Google Scholar]