



## Original Research Article

# CLINICAL SPECTRUM AND ANTIMICROBIAL PROFILE OF *KLEBSIELLA OXYTOCA* INFECTIONS AT A TERTIARY CARE TEACHING HOSPITAL: A CROSS-SECTIONAL STUDY

Nivedita Priyadarshini I<sup>1</sup>, Anitha D<sup>2</sup>

<sup>1</sup>Postgraduate, Department of Microbiology, Sri Devaraj Urs Medical College/ Sri Devaraj Urs Academy of Higher Education and Research, Kolar, Karnataka, India.

<sup>2</sup>Professor, Department of Microbiology, Sri Devaraj Urs Medical College/ Sri Devaraj Urs Academy of Higher Education and Research, Kolar, Karnataka, India.

Received : 18/07/2026  
Received in revised form : 01/08/2026  
Accepted : 14/08/2026

## Corresponding Author:

**Dr. Anitha D,**  
Professor, Department of Microbiology,  
Sri Devaraj Urs Medical College/ Sri  
Devaraj Urs Academy of Higher  
Education and Research, Kolar,  
Karnataka, India.  
Email: anithadeva77@gmail.com

DOI: 10.70034/ijmedph.2026.3.523

Source of Support: Nil,  
Conflict of Interest: None declared

Int J Med Pub Health  
2026; 16 (3); 3351-3354

## ABSTRACT

**Background:** *Klebsiella oxytoca* is an important pathogen associated with a wide range of infections, including bloodstream infections, pneumonia, urinary tract infections, wound infections, and health care associated infections. The emergence of multidrug-resistant (MDR) strains has become a major therapeutic challenge worldwide. However, data regarding the clinical spectrum and antimicrobial susceptibility pattern of *K. oxytoca* in our hospital are limited. This study aimed to evaluate the clinical spectrum and antimicrobial susceptibility pattern of *K. oxytoca* isolates.

**Materials and Methods:** A cross-sectional study was conducted at a tertiary care teaching hospital from June 2022 to May 2026. Data on *K. oxytoca* isolates from various clinical specimens were retrieved from the microbiology laboratory repository. Demographic details, clinical spectrum, and antimicrobial susceptibility patterns were analyzed.

**Results:** A total of 61 *K. oxytoca* isolates were included. Most patients belonged to the 41–60-year age group (37.70%), followed by the 61–80-year age group (31.15%). Females constituted 60.66% of the study population. Pus was the most common specimen (49.18%), followed by urine (21.31%) and sputum (11.48%). Skin and soft-tissue infections and wound infections accounted for the majority of cases (50.82%). Multidrug resistance was observed in all isolates (100%). The highest sensitivity to chloramphenicol (77.27%), followed by amikacin (68.97%), meropenem (62.07%), and gentamicin (60.66%), whereas lower sensitivity was observed with ceftriaxone (32.20%) and ciprofloxacin (31.03%).

**Conclusion:** *Klebsiella oxytoca* is an important pathogen with a diverse clinical spectrum and a high burden of multidrug resistance. Continuous antimicrobial surveillance, infection-control measures, and institution-specific antibiotic stewardship programs are essential to guide empirical therapy.

**Keywords:** *Klebsiella oxytoca*; antimicrobial susceptibility; multidrug resistance; surgical-site infections; clinical spectrum.

## INTRODUCTION

*Klebsiella oxytoca* is a Gram negative, non-motile, encapsulated, lactose fermenting facultative anaerobic bacteria belonging to the genus *Klebsiella* within the family Enterobacteriaceae and is widely distributed in nature.<sup>[1,2]</sup> In humans, *Klebsiella*

*oxytoca* is a member of the normal gut microbial flora and has been detected in the stool of 8% to 10% of healthy adults by culture-based methods. It is also found on the skin and in the oropharynx.<sup>[2]</sup> It has emerged as an important pathogen responsible for a broad range of severe infections, such as bloodstream infections, pneumonia, urinary tract infections and

wound infections. It has also been implicated in hospital-associated infections and outbreaks. Despite its clinical relevance, *Klebsiella oxytoca* has remained relatively under-recognised and is often over shadowed by the other pathogenic species like, *Klebsiella pneumoniae*.<sup>[3]</sup> In healthcare facilities, *Klebsiella oxytoca* accounts for 13% to 24% of nosocomial bacteraemia. *Klebsiella oxytoca* may also be especially pathogenic due to the secretion of cytotoxin.<sup>[1]</sup> *Klebsiella oxytoca* can produce a biofilm and adhere to the host cells leading to persistence of the infection and antibiotic resistance. There are several adhesin genes associated with the biofilm formation and antibiotic resistance in *Klebsiella* species.<sup>[4]</sup> *Klebsiella oxytoca* is quite different from *Klebsiella pneumoniae* in many respects, such as antimicrobial resistance, virulence, and disease spectrum. Recent findings have significantly advanced the knowledge of this important pathogen. For example, genome-based taxonomic studies have shown that *Klebsiella oxytoca* is not a single species but in fact a complex comprising at least six species and is named as *Klebsiella oxytoca* complex; *Klebsiella grimontii*, *Klebsiella huaxiensis*, *Klebsiella michiganensis*, *Klebsiella oxytoca*, *Klebsiella pasteurii*, and *Klebsiella spallanzanii*.<sup>[2]</sup> In recent years, multidrug resistant (MDR) *Klebsiella oxytoca* has been increasingly isolated from healthcare settings, due to extensive use of broad spectrum antibiotics in hospitalized patients.<sup>[5]</sup> As there is no information on the rate of isolation, clinical profile and antimicrobial susceptibility pattern of *Klebsiella oxytoca* from various clinical samples in our hospital, we planned to conduct this study to generate data on the above said parameters. This helps us to know the spectrum of illness and antimicrobial susceptibility pattern of *Klebsiella oxytoca*. Further, the data will aid in formulation of local antibiotic policy to guide the clinicians for administering appropriate empirical antibiotic treatment.

## Objectives

- To evaluate the clinical spectrum of *Klebsiella oxytoca* isolates
- To determine the Antimicrobial Susceptibility Pattern of *Klebsiella oxytoca*

## MATERIALS AND METHODS

This is a cross-sectional laboratory-based study conducted at a Tertiary care teaching hospital. From June 2022 to May 2026, data on isolation of *Klebsiella oxytoca* from various samples (Blood, body fluids, pus, Endotracheal aspirate, urine, sputum, tissue and miscellaneous sample) in the hospital was collected from the repository at Microbiology laboratory, of the hospital. Details regarding age, gender, date of admission, diagnosis, type of sample, department, date of sample sent for culture, pathogen isolated and its antibiotic sensitivity pattern was collected from the repository, entered in excel and analysed.

### Inclusion criteria:

- All samples received in the microbiology lab from which *Klebsiella oxytoca* is isolated are included.

### Exclusion criteria:

- Duplicate isolates.
- Isolates for which no clinical information is available in the laboratory form.

## RESULTS

A total of 61 clinical specimens were included in the study. The demographic characteristics and department-wise distribution of patients are summarized in [Table 1]. The majority of patients belonged to the 41–60 years age group (37.70%), followed by the 61–80 years age group (31.15%). Female patients constituted 60.66% of the study population, while males accounted for 39.34%.

**Table 1: Demographic and Department-wise Distribution of Patients (n = 61)**

| Variable          | Category | Number (%) |
|-------------------|----------|------------|
| Age group (years) | <20      | 3 (4.92)   |
|                   | 21–40    | 13 (21.31) |
|                   | 41–60    | 23 (37.70) |
|                   | 61–80    | 19 (31.15) |
|                   | >80      | 3 (4.92)   |
| Gender            | Male     | 24 (39.34) |
|                   | Female   | 37 (60.66) |

The specimen-wise distribution is shown in [Table 2]. *Klebsiella oxytoca* was isolated mainly from pus samples, accounting for 49.18% of all samples, followed by urine (21.31%) and sputum

(11.48%). Blood samples constituted 6.56% of the total specimens, while miscellaneous specimens, body fluids, endotracheal aspirates, and tissue samples together accounted for 11.48%.

**Table 2: Specimen-wise Distribution (n = 61)**

| Specimen | Number (%) |
|----------|------------|
| Pus      | 30 (49.18) |
| Urine    | 13 (21.31) |
| Sputum   | 7 (11.48)  |
| Blood    | 4 (6.56)   |

|                       |          |
|-----------------------|----------|
| Miscellaneous         | 3 (4.92) |
| Fluid                 | 2 (3.28) |
| Endotracheal aspirate | 1 (1.64) |
| Tissue                | 1 (1.64) |

The disease- and condition-wise distribution of cases is presented in [Table 3]. Skin and soft-tissue infections and wound infections constituted the largest proportion of cases, accounting for 50.82% (31/61), followed by urinary tract infections (21.31%) and respiratory infections (13.11%).

Bloodstream and systemic infections accounted for 11.48% of the cases, while intra-abdominal infections constituted 3.28% of the total cases. Skin and soft-tissue infections/wound infections were the predominant clinical presentation associated with *Klebsiella oxytoca* infection in the present study.

**Table 3: Disease/Condition-wise Distribution (n = 61)**

| Disease category                                 | Number (%)  |
|--------------------------------------------------|-------------|
| Skin and soft-tissue infections/Wound infections | 31 (50.82)  |
| Urinary tract infections                         | 13 (21.31)  |
| Respiratory infections                           | 8 (13.11)   |
| Bloodstream/Systemic infections                  | 7 (11.48)   |
| Intra-abdominal infections                       | 2 (3.28)    |
| Total                                            | 61 (100.00) |

The antimicrobial susceptibility profile is summarized in [Table 4]. Multidrug resistance was found in all 61 (100%) isolates studied. With regard to the sensitivity among these isolates, chloramphenicol demonstrated the highest sensitivity (77.27%), followed by amikacin (68.97%), meropenem (62.07%), gentamicin (60.66%), and co-

trimoxazole (59.32%). Moderate susceptibility was observed with ertapenem (58.93%), imipenem (58.62%), doxycycline (58.49%), and cefepime (52.94%). Lower sensitivity rates were observed for ceftriaxone (32.20%), ciprofloxacin (31.03%), ceftazidime (36.07%), and amoxicillin-clavulanic acid (37.93%).

**Table 4: Antibiotic Susceptibility Pattern**

| Antibiotic                  | Sensitivity (%) |
|-----------------------------|-----------------|
| Chloramphenicol             | 77.27           |
| Amikacin                    | 68.97           |
| Meropenem                   | 62.07           |
| Gentamicin                  | 60.66           |
| Co-trimoxazole              | 59.32           |
| Ertapenem                   | 58.93           |
| Imipenem                    | 58.62           |
| Doxycycline                 | 58.49           |
| Cefepime                    | 52.94           |
| Levofloxacin                | 44.19           |
| Cefotaxime                  | 38.64           |
| Piperacillin-tazobactam     | 38.33           |
| Amoxicillin-clavulanic acid | 37.93           |
| Ceftazidime                 | 36.07           |
| Ceftriaxone                 | 32.20           |
| Ciprofloxacin               | 31.03           |

## DISCUSSION

In the present study, 61 isolates of *Klebsiella oxytoca* recovered from various clinical specimens were analyzed to determine their clinical spectrum and antimicrobial susceptibility pattern. The majority of patients belonged to the 41–60-year age group (37.7%), followed by the 61–80-year age group (31.1%). Similar findings have been reported in previous studies, where *Klebsiella* infections were found predominantly among middle-aged and elderly individuals because of the higher prevalence of comorbidities, prolonged hospitalization, and increased exposure to invasive procedures.<sup>[1,6,9]</sup> Female patients constituted 60.66% of the study population, in contrast to several studies that reported a male predominance among *Klebsiella*

infections.<sup>[1,7]</sup> This difference may be attributed to the higher number of urinary tract infections and specimens received from surgical and obstetric units during the study period.

The Department of Surgery contributed the highest number of isolates (49.18%), and pus was the most common specimen (49.18%), followed by urine (21.31%) and sputum (11.48%). Similar observations were reported by Sarma et al., who found pus and urine to be the predominant clinical specimens yielding *Klebsiella* isolates.<sup>[1]</sup> *Klebsiella oxytoca* has increasingly been recognized as an important nosocomial pathogen responsible for surgical-site infections, wound infections, and device-associated infections.<sup>[2,10]</sup>

Skin and soft-tissue infections and surgical site infections constituted the largest proportion of cases (50.82%), followed by urinary tract infections

(21.31%) and respiratory infections (13.11%). Although *K. oxytoca* is traditionally associated with urinary tract infections and pneumonia, but our study showed more of skin and soft tissue infections and healthcare-associated infections.<sup>[2,3]</sup> Genome-based studies have further demonstrated that *K. oxytoca* comprises a complex of closely related species with varying virulence and resistance characteristics.<sup>[2]</sup> Biofilm formation and the presence of adhesin genes play a crucial role in the persistence and pathogenicity of *K. oxytoca*. Shrief et al. demonstrated that biofilm-associated genes enhance bacterial adherence and contribute to antimicrobial resistance, particularly in urinary isolates.<sup>[4]</sup> Biofilm-producing strains exhibit significantly higher resistance to multiple classes of antibiotics, thereby complicating treatment outcomes.<sup>[13]</sup> Multidrug resistance (MDR) was observed in all *Klebsiella oxytoca* isolates (100%) in the present study, indicating an alarming increase in resistant strains in our healthcare setting. Similar findings have been reported by Sabzivand et al. and Yang et al., who demonstrated the increasing prevalence of MDR *K. oxytoca* harboring extended-spectrum  $\beta$ -lactamase and carbapenemase genes.<sup>[2,5]</sup> Decré et al. also reported outbreaks caused by multidrug-resistant *K. oxytoca* in hospital settings.<sup>[9]</sup> The high prevalence of MDR *Klebsiella oxytoca* in our study may be attributed to prolonged hospitalization, extensive use of broad-spectrum antibiotics, and biofilm formation by the organism.<sup>[4,13]</sup> In the present study, chloramphenicol (77.27%) and amikacin (68.97%) showed the highest sensitivity, followed by meropenem (62.07%) and gentamicin (60.66%). However, the moderate susceptibility to carbapenems is concerning, as carbapenem-resistant *K. oxytoca* strains are increasingly being reported worldwide.<sup>[2,12]</sup> The low susceptibility to third-generation cephalosporins and fluoroquinolones observed in the present study is comparable to findings from previous studies, which have attributed this resistance to the widespread dissemination of extended-spectrum  $\beta$ -lactamase (ESBL)-producing strains.<sup>[5,11]</sup> The present study has certain limitations. Being a retrospective laboratory-based study conducted at a single tertiary-care center, the findings may not be generalizable to other healthcare settings. Furthermore, molecular characterization of resistance genes and virulence determinants was not performed. Future multicentric studies incorporating molecular techniques are required to better understand the epidemiology and resistance mechanisms of *K. oxytoca*.

## CONCLUSION

In conclusion, the present study highlights the diverse clinical manifestations and evolving antimicrobial resistance profile of *Klebsiella oxytoca*. The predominance of surgical-site infections and the increasing resistance to commonly used antibiotics emphasize the need for continuous surveillance and formulation of local antibiotic policies to optimize empirical treatment and improve patient outcomes.

## REFERENCES

1. Sarma M, Kumar R, Das B, Sinha S, Salini G, Jagrati, et al. Isolation, identification and antibiotic sensitivity pattern of *Klebsiella* species isolated from various clinical specimens in a medical college and hospital. *Int J Curr Microbiol App Sci*. 2019;8(12):2546–57.
2. Yang J, Long H, Hu Y, Feng Y, McNally A, Zong Z. *Klebsiella oxytoca* complex: update on taxonomy, antimicrobial resistance, and virulence. *Clin Microbiol Rev*. 2022;35:e00006-21.
3. Qin S, Yu Z, Shen Y, et al. Global emergence, evolution and international dissemination of the ST145 *Klebsiella oxytoca* lineage. *NPJ Antimicrob Resist*. 2026;4(28):1–9.
4. Shrief R, Hassan R, Zaki M, Rizk M. Molecular study of *Klebsiella oxytoca* associated with urinary tract infection in children. *Open Microbiol J*. 2022;16:e187428582201070.
5. Sabzivand N, Nazari S, Shirvani F, Azimi L, Salmanzadeh Ahrabi S, Mohammadi Estiri M. Epidemiology and antimicrobial resistance of toxin-producing *Klebsiella oxytoca* clinical isolates from children admitted to the oncology chemotherapy center in Mofid Children's Hospital in Tehran, Iran: a cross-sectional study. *Health Sci Rep*. 2024;7:e2275.
6. Podschun R, Ullmann U. *Klebsiella* spp. as nosocomial pathogens: epidemiology, taxonomy, typing methods and pathogenicity factors. *Clin Microbiol Rev*. 1998;11(4):589–603.
7. Magill SS, Edwards JR, Bamberg W, Beldavs ZG, Dumyati G, Kainer MA, et al. Multistate point-prevalence survey of healthcare-associated infections. *N Engl J Med*. 2014;370(13):1198–208.
8. Leitner E, Zarfel G, Luxner J, Herzog K, Pekard-Amenitsch S, Hoenigl M, et al. Contaminated hand-washing sinks as the source of a clonal outbreak of *Klebsiella oxytoca* on a haematology ward. *J Hosp Infect*. 2015;90(1):35–40.
9. Decré D, Burghoffer B, Gautier V, Petit JC, Arlet G. Outbreak of multidrug-resistant *Klebsiella oxytoca* involving strains with extended-spectrum  $\beta$ -lactamases and strains with extended-spectrum activity of the chromosomal  $\beta$ -lactamase. *J Antimicrob Chemother*. 2004;54(5):881–8.
10. Singh L. *Klebsiella oxytoca*: an emerging pathogen? *Med J Armed Forces India*. 2016;72(Suppl 1):S59–61.
11. Fevre C, Passet V, Weill FX, Grimont PA, Brisse S. Variants of the *Klebsiella pneumoniae* OKP chromosomal beta-lactamase are divided into two main groups, OKP-A and OKP-B. *Antimicrob Agents Chemother*. 2005 Dec;49(12):5149–52.
12. Hoenigl M, Valentin T, Zarfel G, Wuerstl B, Leitner E, Salzer HJ, et al. Nosocomial outbreak of carbapenemase-producing *Klebsiella oxytoca* in Austria. *Antimicrob Agents Chemother*. 2012;56(4):2158–61.
13. Vuotto C, Longo F, Balice MP, Donelli G, Varaldo PE. Antibiotic resistance related to biofilm formation in *Klebsiella pneumoniae*. *Pathogens*. 2014;3(3):743–58.
14. David S, Reuter S, Harris SR, Glasner C, Feltwell T, Argimon S, et al. Epidemic of carbapenem-resistant *Klebsiella pneumoniae* in Europe is driven by nosocomial spread. *Nat Microbiol*. 2019;4(11):1919–29.
15. Martin RM, Bachman MA. Colonization, infection, and the accessory genome of *Klebsiella pneumoniae*. *Front Cell Infect Microbiol*. 2018;8:4.