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Research Article
doi: 10.61705/8jcbn261
Ace J. Addict., 7 (1): 64-69 | 2026

Bacterial Profile of Respiratory Isolates in a Tertiary Care Teaching Hospital in Central India: A Retrospective Laboratory-Based Study

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OPEN ACCESS

Key Words
respiratory specimens; bacterial isolates; organism distribution; retrospective study; tertiary care hospital; Central India

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Received: 15 Oct 2026
Accepted: 25 Oct 2026
Published: 4 Nov 2026

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ABSTRACT

Background: Respiratory specimens submitted for bacterial culture may yield a diverse range of organisms, and the distribution of recovered isolates varies with patient population, specimen type, clinical setting, and local epidemiology. Interpretation requires attention to specimen quality and the possibility of airway colonization, particularly in patients with artificial airways [1–3].

Objective: To describe the distribution of clinically significant bacterial isolates recovered from respiratory specimens in a tertiary care teaching hospital in Central India.

Methods: This retrospective laboratory-based observational study reviewed respiratory culture records from the Department of Microbiology, Sri Aurobindo Medical College and Postgraduate Institute, Indore, Madhya Pradesh, India. The source manuscript specifies January–December 2025; this period and the final eligible denominator must be verified against the laboratory export. Identification was based on standard microbiological procedureas and an automated identification system where used. Organism frequencies were summarized descriptively. Antimicrobial susceptibility results were not analysed in this version.

Results: The source records report 746 respiratory isolates. The most frequently listed organisms were Pseudomonas aeruginosa (128), Acinetobacter baumannii complex (122), Escherichia coli (104), Klebsiella pneumoniae (103), and Klebsiella pneumoniae subsp. pneumoniae (95). Pseudomonas putida (25) and Enterobacter cloacae complex (24) were also listed. Candida albicans (34) appeared in the source table but is a fungus and should be excluded from the bacterial denominator or reported separately. The two Klebsiella categories may overlap and require reconciliation. Exact specimen-wise counts and the complete list of remaining organisms were not supplied.

Conclusion: A retrospective review of respiratory culture records can describe organisms recovered in routine diagnostic practice. Before prevalence estimates are reported, the dataset should be checked for the correct denominator, duplicate records, taxonomic overlap, non-bacterial isolates, and missing organism and specimen counts. This analysis describes bacterial distribution only and does not assess antimicrobial resistance or support empirical antibiotic recommendations.

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INTRODUCTION

Respiratory tract infections are an important cause of morbidity and hospital admission, and their microbiological evaluation can be challenging because the respiratory tract is not uniformly sterile. The organisms recovered from a specimen depend on the clinical syndrome, the anatomical site sampled, the patient's underlying conditions, recent antimicrobial exposure, duration of hospitalization, use of invasive airway devices, and the local epidemiological setting. Consequently, the spectrum of organisms reported by a tertiary-care diagnostic laboratory may differ from that observed in community-based populations or in hospitals with different case mixes [1–3].

In hospitalized patients, especially those requiring intensive care or airway instrumentation, Gram-negative bacilli may be recovered frequently from respiratory specimens. Organisms such as Pseudomonas aeruginosa, Acinetobacter baumannii complex, Klebsiella species, and Escherichia coli are clinically important because they can cause serious lower respiratory tract infections in susceptible patients. However, the recovery of a species from a respiratory sample should not automatically be interpreted as proof of causation. Its significance must be assessed in relation to the presenting illness, radiological and clinical findings, specimen quality, microscopy, and the possibility of airway colonization [1,2,4–6].

Specimen quality and collection procedures are therefore central to respiratory microbiology. Expectorated sputum may be contaminated by oropharyngeal flora, while endotracheal and tracheal aspirates can contain organisms that colonize the airway without causing invasive infection. Bronchoalveolar lavage and other lower respiratory samples may provide different diagnostic information, but their interpretation also depends on the clinical context and the methods used for collection and processing. Appropriate specimen selection, transport, culture, organism identification, and communication between the clinical and laboratory teams help improve the usefulness of culture results [1–3].

Local laboratory data can support an understanding of the organisms encountered in routine practice and can provide a baseline for quality improvement, diagnostic stewardship, and future surveillance. Such data are most informative when the study population, specimen types, study period, inclusion criteria, duplicate-isolate policy, and denominator are clearly defined. Organism categories must also be mutually exclusive and taxonomically consistent. These considerations are particularly important when results are summarized as frequencies or percentages, because an uncertain denominator or overlapping labels can distort the apparent distribution.

The present study was planned as a retrospective description of bacterial isolates reported from respiratory specimens in a tertiary-care teaching hospital in Indore, Madhya Pradesh, Central India. The focus is the distribution of organisms listed in the supplied laboratory records rather than antimicrobial susceptibility or resistance trends. Since the available source material contains unresolved issues in the total denominator, the separation of two Klebsiella pneumoniae labels, and the inclusion of Candida albicans alongside bacterial entries, the findings are presented cautiously and these data-quality issues are identified explicitly. The study is intended to describe local laboratory recovery patterns and to highlight the checks needed before reliable prevalence estimates can be reported.

Aim and Objective

To describe the frequency distribution of clinically significant bacterial isolates recovered from respiratory specimens received in the Department of Microbiology during the study period.

Materials and Methods

Study design and setting

This was a retrospective laboratory-based observational study conducted in the Department of Microbiology, Sri Aurobindo Medical College and Postgraduate Institute, Indore, Madhya Pradesh, India. The laboratory provides diagnostic services to inpatient and outpatient departments, including intensive care units, emergency services, medical and surgical wards, and specialty departments.

Study period

The source manuscript specifies January 2025 to December 2025. The study period must be confirmed against the date range used for the final laboratory data extraction before submission.

Study population and specimens

Eligible records were those of respiratory specimens yielding growth considered clinically significant under the laboratory criteria applied during the study period. Specimen types listed in the source material included sputum, endotracheal aspirates,

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bronchoalveolar lavage, tracheal aspirates, pleural fluid, and other lower respiratory tract specimens. Specimen acceptance and interpretation should follow documented laboratory procedures and clinical context [1,3].

Inclusion and exclusion criteria

The source protocol lists clinically significant respiratory isolates as eligible. Duplicate isolates from the same patient during the same episode, contaminated specimens, records with incomplete laboratory information, and isolates considered to represent colonization were listed as exclusions. The operational definitions and deduplication rule used in the original study should be inserted exactly as applied; they should not be reconstructed retrospectively.

Specimen processing and organism identification

The source manuscript describes specimen processing using standard microbiological procedures. Specimen quality was assessed where applicable. Specimens were inoculated onto appropriate media, including blood agar and MacConkey agar, with chocolate agar used when indicated, and incubated aerobically at 35–37°C for approximately 18–24 hours. Identification was based on colony morphology, Gram staining, biochemical characteristics, and the VITEK 2 Compact system where applicable. The final version should retain only procedures that were actually used during the study period.

Data collection and statistical analysis

Laboratory records were reviewed for specimen type and organism identification, with patient identifiers removed before analysis. Organism frequencies and percentages were intended to be summarized descriptively. The denominator should be explicitly defined as the number of eligible bacterial isolates after removing duplicate records and non-bacterial isolates. If multiple organisms were recovered from one specimen, the counting approach should be stated. Candida albicans should be excluded from the bacterial denominator or reported separately as a fungal isolate. The supplied text does not contain sufficient verified counts to calculate or reproduce complete prevalence percentages.

Ethical considerations

Insert the verified Institutional Ethics Committee name, approval number, and approval date. State that informed consent was waived only if this was formally approved and documented. Ethics approval and institutional permission must be confirmed before submission.

Results

The source manuscript reports 746 clinically significant respiratory isolates. The organism counts supplied in the source text are reproduced below for verification. Because the full organism list, final bacterial denominator, and taxonomic categories have not been reconciled in the supplied material, these counts should be treated as source-record counts rather than final prevalence estimates.

Organism as recorded in source	Number	Reporting note
Pseudomonas aeruginosa	128	Confirm final denominator
Acinetobacter baumannii complex	122	Confirm final denominator
Escherichia coli	104	Confirm final denominator
Klebsiella pneumoniae	103	Check possible overlap with next category
Klebsiella pneumoniae subsp. pneumoniae	95	Check possible overlap with previous category
Candida albicans	34	Fungal isolate; exclude from bacterial denominator or report separately
Pseudomonas putida	25	Confirm final denominator
Enterobacter cloacae complex	24	Confirm final denominator
Other organisms	Not specified	Insert complete organism list and exact counts

The organisms most frequently listed in the supplied records were Pseudomonas aeruginosa and Acinetobacter baumannii complex, followed by Escherichia coli and two separately listed Klebsiella categories. These two Klebsiella entries require review to determine whether they represent mutually exclusive categories or overlapping reporting labels.

The source manuscript states that sputum was the most common specimen, followed by endotracheal aspirates and bronchoalveolar lavage. Exact specimen-wise frequencies and percentages were

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not provided in the supplied text and should be inserted from the verified dataset.

No antimicrobial susceptibility results are reported in this manuscript. Consequently, antimicrobial resistance, multidrug-resistant phenotypes, carbapenem resistance, colistin activity, and empirical antibiotic selection are outside the scope of these results.

Discussion

This retrospective laboratory review describes the organisms listed in respiratory culture records from a tertiary-care teaching hospital in Central India. In the supplied records, Pseudomonas aeruginosa and Acinetobacter baumannii complex were among the most frequently listed organisms, followed by Escherichia coli and two separately reported Klebsiella categories. This pattern indicates that non-fermenting Gram-negative bacilli and Enterobacterales featured prominently in the available laboratory list. Nevertheless, the source dataset has not yet been reconciled sufficiently to support definitive prevalence estimates, and the order of organisms should be understood as a description of the supplied counts rather than a validated estimate of disease burden.

The prominence of Pseudomonas and Acinetobacter in respiratory microbiology is plausible in tertiary-care settings, particularly among patients with severe illness, prolonged hospitalization, or invasive airway devices. Published work on respiratory non-fermenters illustrates the importance of these organisms in selected hospital and intensive-care populations [4–6]. However, comparisons between studies require caution: the patient mix, ICU representation, specimen types, culture criteria, identification platforms, prior antibiotic exposure, and rules for counting repeat isolates can differ substantially. The present dataset does not include enough verified clinical and demographic detail to determine whether the observed distribution is driven by a particular ward, patient group, or respiratory syndrome.

A central consideration is that culture positivity and clinical infection are not synonymous. Endotracheal and tracheal aspirates may recover organisms colonizing the airway, while sputum can be affected by contamination with upper-airway flora. A laboratory result should therefore be interpreted alongside specimen quality, direct microscopy where available, clinical features, imaging, and the reason the sample was collected. Diagnostic guidance emphasizes the appropriate selection and handling of specimens and interpretation in the clinical context [1–3]. Because the supplied dataset does not provide patient-level clinical criteria or a verified operational definition for distinguishing infection from colonization, the current analysis should be interpreted as a review of laboratory-reported isolates, not as a direct measure of the incidence of bacterial respiratory infection.

The dataset also requires several corrections before the reported frequencies can be considered reliable. First, the source text gives a total of 746 isolates but does not provide a complete organism-by-organism table or explain how the total was assembled. Second, Klebsiella pneumoniae and Klebsiella pneumoniae subsp. pneumoniae appear as separate categories; these labels may overlap and must be checked against the original laboratory information system. Third, Candida albicans is a fungal organism and should not be included in the bacterial denominator. Fourth, the category “Other organisms” needs to be replaced with a complete list and counts, or defined transparently if a grouping is retained. Finally, the study period, deduplication rule, and treatment of specimens yielding more than one organism should be verified and reported consistently.

These issues are not merely editorial. An incorrect denominator, overlapping taxonomic categories, or a mixed bacterial-fungal count can alter the apparent proportions and may make comparisons with published studies misleading. A final results table should report the number of eligible bacterial isolates, the count and percentage for each mutually exclusive organism category, and the specimen-wise distribution where available. If the study counts isolates rather than patients or specimens, that unit of analysis should be stated explicitly. Any exclusions and duplicate-removal procedures should also be described so that readers can understand how the final analytic dataset was derived.

The current manuscript intentionally does not report antimicrobial susceptibility testing or resistance phenotypes. Although antimicrobial resistance is an important concern in hospital microbiology and is monitored through national and international surveillance initiatives [7,10–18], those sources cannot be used to infer the susceptibility profile of isolates in this dataset. In the absence of verified isolate-level susceptibility results and documented interpretive standards, no conclusions can be drawn here about multidrug resistance, carbapenem resistance, or appropriate empirical treatment. Keeping the manuscript focused on organism distribution avoids making claims that are not supported by the supplied data.

The study’s main strength is its use of routine diagnostic laboratory records from a tertiary-care

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teaching hospital, providing a potentially useful local snapshot across several respiratory specimen types. Its principal limitations are the retrospective single-centre design, incomplete organism and specimen-level information in the supplied material, lack of detailed clinical characteristics and outcomes, and unresolved classification and denominator issues. The available data also do not permit robust separation of colonization from infection or assessment of changes over time. Once the laboratory extract has been reconciled and the methods and ethics documentation verified, the descriptive findings may serve as a baseline for a more complete local analysis. Until then, the results should be treated as preliminary and should not be generalized beyond the records reviewed.

Strengths and Limitations

Strengths: The study draws on routine diagnostic laboratory data from a tertiary care teaching hospital and includes several lower respiratory specimen types.

Limitations: The retrospective single-centre design limits generalizability. The supplied manuscript does not contain the complete organism list, exact specimen-wise counts, or detailed patient characteristics and outcomes. The total denominator, the separate Klebsiella categories, and the handling of Candida albicans require verification. Antimicrobial susceptibility results were not analysed.

Conclusion

A retrospective review of respiratory culture records can describe the bacterial isolates recovered in a tertiary care teaching hospital. In the supplied records, Pseudomonas aeruginosa and Acinetobacter baumannii complex were among the most frequently listed organisms. Reliable reporting requires verification of the study period, complete organism list, bacterial denominator, specimen-wise distribution, taxonomic categories, deduplication approach, and ethics documentation. This manuscript is limited to bacterial distribution and does not draw conclusions about antimicrobial susceptibility or resistance.

Declarations

Acknowledgements: To be completed according to the actual contributions of laboratory staff and other personnel.

Funding: State the actual funding status.

Conflicts of interest: Each author should declare any relevant conflict of interest.

Author contributions: Assign contributions according to work actually performed by each author.

Data availability: State the institutionally approved data-sharing arrangement.

Ethics approval: Insert the verified committee name, approval number, and date. Describe any consent waiver only as documented in the approval.

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