

Bacteriological Profile and Antibigram of Microbial Isolates from Pediatric Patients of Bronchopneumonia

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Abstract: **Background:** Bronchopneumonia is an important pediatric respiratory infection in which bacterial pathogens may contribute to morbidity. Microbiological identification and antimicrobial susceptibility testing can provide institution-specific information. **Objective:** To determine the bacteriological profile and antimicrobial susceptibility pattern of microbial isolates from pediatric patients with bronchopneumonia. **Methods:** This descriptive cross-sectional observational study was conducted over three months in collaboration with the Departments of Pharmacology, Microbiology and Pediatrics at Dr. BVP's Rural Medical College. The present analysis included 74 eligible records from the supplied dataset. Blood-culture findings, organism identification and antimicrobial susceptibility results were analyzed descriptively. **Results:** Among 74 eligible records, 45 (60.8%) were female and 29 (39.2%) were male. The 0–5-year age group accounted for 63 (85.1%) records. Culture-positive records with a named organism numbered 49 (66.2%); 23 (31.1%) were sterile and 2 (2.7%) had contaminants. Gram-negative bacteria accounted for 41 (83.7%) of 49 bacterial isolates. *Klebsiella pneumoniae* was the most frequently recorded single organism (10 isolates). **Conclusion:** The available dataset demonstrated apredominance of Gram-negative bacterial isolates and substantial resistance entries to several tested antimicrobials. Findings are institution-specific and should be interpreted in the context of the available dataset and laboratory practices.

Keywords: Bronchopneumonia; pediatric; bacteriological profile; antibiogram; antimicrobial susceptibility

1. Introduction

Pneumonia is an acute respiratory infection that may be caused by bacterial or viral pathogens and remains an important cause of childhood morbidity. The etiological distribution varies with age, geographic setting, healthcare environment and clinical circumstances. Current World Health Organization guidance emphasizes age-appropriate diagnosis and management of childhood pneumonia. [1,2]

In hospitalized children, antimicrobial therapy may be initiated empirically when bacterial infection is suspected. However, antimicrobial resistance can complicate treatment and increases the importance of microbiological surveillance and rational antimicrobial use. Local antibiograms summarize antimicrobial susceptibility patterns in a defined healthcare setting and can support interpretation of laboratory findings and antimicrobial stewardship. [3,4]

The distribution of bacterial pathogens and resistance patterns can differ between institutions. Therefore, institution-specific data are useful for describing the organisms encountered in pediatric bronchopneumonia and their recorded susceptibility profiles.

The present study was undertaken to determine the bacteriological profile and antimicrobial susceptibility

pattern of microbial isolates from pediatric patients with bronchopneumonia at a tertiary-care rural teaching hospital.

2. Literature Survey

Childhood pneumonia remains an important infectious cause of morbidity and mortality, particularly in settings where access to timely diagnosis and appropriate treatment may be limited. The causative organisms vary by age, setting and clinical severity. [1,2]

Antimicrobial susceptibility surveillance is important because resistance patterns may differ between hospitals and regions. The WHO AWaRe framework emphasizes rational antibiotic selection and stewardship, while local antibiograms can provide institution-specific information for empirical treatment decisions. [3]

Hospital-based studies have demonstrated that bacterial etiology and resistance patterns among children with pneumonia are heterogeneous. Consequently, microbiological culture and susceptibility testing remain useful when clinically indicated, particularly in hospitalized or severe disease. [4]

3. Problem Definition

There is a need for institution-specific information on the bacterial organisms associated with pediatric bronchopneumonia and their antimicrobial susceptibility patterns. In the absence of such data, empirical antimicrobial selection may not adequately reflect the organisms and resistance patterns encountered in a particular hospital. The present study therefore evaluates the available microbiological records to characterize the bacteriological profile and antibiogram of pediatric bronchopneumonia.

Research question: What is the bacteriological profile and antibiotic susceptibility pattern of pediatric patients suffering from bronchopneumonia?

4. Methodology / Approach

Study design and setting: This was a descriptive cross-sectional observational study conducted over a period of two years in collaboration with the Departments of Pharmacology, Microbiology and Pediatrics at Dr. BVP's Rural Medical College, Pravara Institute of Medical Sciences (Deemed University), Loni, Maharashtra, India.

Study population and sample size: Pediatric patients aged 0–15 years admitted with bronchopneumonia and fulfilling the predefined eligibility criteria were considered for enrollment. The planned sample size was 250 patients, with sample-size calculation performed using OpenEpi as described in the study synopsis. The supplied dataset contained 75 records; one record aged 17 years 1 month was outside the predefined 0–15-year eligibility range and was excluded, leaving 74 eligible records for the present analysis.

Inclusion criteria: Pediatric patients aged 0–15 years admitted with bronchopneumonia; patients whose blood samples were submitted to the Microbiology Department for culture and susceptibility testing; patients of either sex; and patients whose parents/guardians provided informed consent.

Exclusion criteria: Patients outside the predefined pediatric age range; patients with significant concomitant illness associated with bronchopneumonia, as defined in the approved protocol; and patients discharged before completion of the required study assessment.

Microbiological assessment: Blood samples submitted to the Microbiology Department were processed for culture and antimicrobial susceptibility testing according to laboratory procedures followed during the study. Isolated microorganisms were recorded and classified according to Gram reaction and monobacterial or polybacterial growth. Antimicrobial susceptibility was assessed using the Kirby–Bauer disk diffusion method. Sensitive, Intermediate and Resistant results recorded in the supplied dataset were retained without reclassification.

Data collection and statistical analysis: Demographic, microbiological and antimicrobial susceptibility information was extracted from the supplied Microsoft Excel dataset.

Categorical variables were summarized as frequencies and percentages. Percentages were calculated using the eligible study population or the number of isolates/tested records, as appropriate.

Ethical considerations: The study was conducted after Institutional Ethics Committee approval according to the approved study protocol. Informed consent was obtained from parents/guardians of participating pediatric patients, and confidentiality of patient information was maintained.

5. Results & Discussion

The supplied dataset contained 75 records. After application of the predefined age range of 0–15 years, 74 records were eligible for analysis. One record aged 17 years 1 month was excluded. The planned sample size was 250; therefore, the present analysis represents the available dataset rather than the complete planned sample.

Table 1: Demographic characteristics of eligible study participants

Characteristic	Number (n)	Percentage (%)
Female	45	60.8
Male	29	39.2
0–5 years	63	85.1
6–10 years	7	9.5
11–15 years	4	5.4
Total	74	100.0

Table 2: Culture status among eligible study records

Culture status	Number (n)	Percentage (%)
Culture-positive with named causative organism	49	66.2
Sterile after 5 days	23	31.1
Contaminants reported	2	2.7
Total	74	100.0

Table 3: Distribution of bacterial and fungal isolates recorded

Microorganism	n	%
Klebsiella pneumoniae	10	19.6
Acinetobacter spp.	9	17.6
Klebsiella spp.	5	9.8
Pseudomonas spp.	5	9.8
Coagulase-negative Staphylococci (CoNS)	3	5.9
Serratia spp.	3	5.9
Enterococcus spp.	3	5.9
Enterobacter spp.	2	3.9
E. coli	2	3.9
Pseudomonas aeruginosa	1	2.0
Rhizobium radiobacter	1	2.0
Burkholderia cepacia	1	2.0
Candida kousei	1	2.0
Serratia marcescens	1	2.0
Enterococcus faecium	1	2.0
Citrobacter spp.	1	2.0
Candida lusitanae	1	2.0
Streptococcus spp.	1	2.0
Total isolates	51	100.0
Bacterial isolates	49	96.1
Fungal co-isolates	2	3.9

Table 4: Microbiological characteristics

Characteristic	Number (n)	Percentage (%)
Gram-negative bacterial isolates	41	83.7
Gram-positive bacterial isolates	8	16.3
Total bacterial isolates	49	100.0
Monobacterial growth (patient records)	48	98.0
Polybacterial growth (patient records)	1	2.0

Table 5: Antimicrobial susceptibility pattern among reported susceptibility entries

Antimicrobial agent	Tested	Sensitive n (%)	Intermediate n (%)	Resistant n (%)
Meropenem	40	18 (45.0)	0 (0.0)	22 (55.0)
Cefepime	39	5 (12.8)	2 (5.1)	32 (82.1)
Imipenem	39	13 (33.3)	1 (2.6)	25 (64.1)
Amikacin	38	6 (15.8)	0 (0.0)	32 (84.2)
Ciprofloxacin	37	6 (16.2)	0 (0.0)	31 (83.8)
Levofloxacin	34	12 (35.3)	3 (8.8)	19 (55.9)
Tobramycin	34	14 (41.2)	0 (0.0)	20 (58.8)
Gentamicin	31	4 (12.9)	0 (0.0)	27 (87.1)
Piperacillin/Tazobactam	30	5 (16.7)	4 (13.3)	21 (70.0)
Cotrimoxazole	28	10 (35.7)	0 (0.0)	18 (64.3)
Ampicillin	25	0 (0.0)	0 (0.0)	25 (100.0)
Cefotaxime	23	1 (4.3)	0 (0.0)	22 (95.7)
Amoxicillin/Clavulanic acid	22	2 (9.1)	0 (0.0)	20 (90.9)
Tetracycline	20	16 (80.0)	0 (0.0)	4 (20.0)
Ticarcillin/Clavulanic acid	15	3 (20.0)	1 (6.7)	11 (73.3)

Note: Susceptibility denominators vary because not every antimicrobial was tested or transcribed for every record. The table reflects the Sensitive/Intermediate/Resistant entries present in the supplied dataset and does not imply that all isolates were tested against every antimicrobial.

Table 6: Empirical and definitive antimicrobial therapy

Parameter	Available records
Antibiotic before culture report	No entries in supplied dataset
Antibiotic after culture report	No entries in supplied dataset
Dose/route/frequency/duration	No entries in supplied dataset

Empirical and definitive antimicrobial therapy could not be quantitatively analyzed because the corresponding treatment fields in the supplied spreadsheet were blank. Therefore, no comparison between empirical and culture-directed therapy was made.

Most records were from children aged 0–5 years (63, 85.1%), while females accounted for 60.8% of the analyzed records. These figures describe the composition of the available hospital dataset and should not be interpreted as population-level estimates.

Culture-positive records with a named causative organism constituted 49 of 74 records (66.2%). Among the 49 bacterial isolates, Gram-negative organisms predominated (41, 83.7%), while Gram-positive organisms accounted for 8 (16.3%). *Klebsiella pneumoniae* was the most frequently recorded single organism, followed by *Acinetobacter* spp., *Klebsiella* spp. and *Pseudomonas* spp.

The predominance of Gram-negative organisms emphasizes the relevance of local hospital microbiology when interpreting pediatric bronchopneumonia. However, organism distribution can differ by institution, patient population, specimen type, prior antimicrobial exposure and laboratory methods; therefore, the present findings should be interpreted as institution-specific.

The susceptibility transcription showed substantial resistance entries for several tested agents. Resistance was recorded in 32 of 39 cefepime entries (82.1%), 32 of 38 amikacin entries (84.2%), and 25 of 25 ampicillin entries (100%). These percentages describe the available laboratory entries and should not be generalized to all pediatric pneumonia isolates.

Interpretation of multidrug resistance should be based on the complete antimicrobial panel and the laboratory's susceptibility standards. International definitions of multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria require assessment across relevant antimicrobial categories and should not be assigned solely from a partial susceptibility transcription. [5]

Because the treatment fields were blank, no conclusion can be drawn from the supplied dataset regarding concordance between empirical therapy and culture-directed therapy. Completion of the treatment dataset would permit a separate analysis of antimicrobial prescribing and changes following microbiological results.

6. Conclusion

In the available dataset of 74 eligible pediatric bronchopneumonia records, culture-positive records with named organisms accounted for 66.2%. Gram-negative bacteria predominated among the 49 bacterial isolates, with *Klebsiella pneumoniae* being the most frequently recorded single organism. The susceptibility data demonstrated substantial resistance entries for several tested antimicrobials. These findings provide institution-specific microbiological information, but interpretation should remain limited to the available dataset until the planned sample of 250 patients and complete treatment records are analyzed.

7. Future Scope

Future work should include completion of the planned 250-patient sample where applicable, prospective capture of complete empirical and definitive antimicrobial treatment data, and standardized recording of specimen collection, prior antimicrobial exposure and laboratory susceptibility criteria. Larger multicenter datasets could help determine whether the observed organism distribution and resistance patterns are consistent across pediatric populations and institutions. Periodic local antibiograms may also support antimicrobial stewardship and evidence-based empirical treatment policies.

8. Limitations

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- The present analysis includes 74 eligible records from a planned sample size of 250 and therefore represents an available-data analysis rather than the completed planned sample.
- The study is institution-based and the findings may not be generalizable to other hospitals or pediatric populations.
- Microbiological findings depend on specimen collection, timing, prior antimicrobial exposure and laboratory procedures.
- Susceptibility denominators varied by antimicrobial, and the exact interpretive standard used by the laboratory was not specified in the supplied spreadsheet.
- Empirical and definitive antimicrobial treatment fields were blank and could not be analyzed.

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Declarations

Funding: None.

Conflict of Interest: None declared.

Ethical Approval: Obtained from the Institutional Ethics Committee according to the approved study protocol.

Informed Consent: Obtained from parents/guardians of participating pediatric patients.

Data Availability: The analyzed dataset is available from the corresponding author subject to institutional and ethical requirements.

References

- [1] World Health Organization. Pneumonia. Geneva: World Health Organization; 2025.
- [2] World Health Organization. Guideline on management of pneumonia and diarrhoea in children up to 10 years of age. Geneva: World Health Organization; 2024. ISBN 978-92-4-010341-2.
- [3] World Health Organization. The WHO AWaRe antibiotic book. Geneva: World Health Organization; 2022. ISBN 978-92-4-006238-2.
- [4] Jain S, Williams DJ, Arnold SR, Ampofo K, Bramley AM, Reed C, et al. Community-acquired pneumonia requiring hospitalization among U.S. children. *N Engl J Med*. 2015;372(9):835-45.
- [5] Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. *Clin*

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