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MICROBIOLOGICAL PROFILE OF SEVERE PNEUMONIA IN CHILDREN ADMITTED TO THE PEDIATRIC INTENSIVE CARE UNIT OF A TERTIARY CARE HOSPITAL: A RETROSPECTIVE DESCRIPTIVE STUDY

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ABSTRACT
Severe pneumonia is a leading reason for admission to pediatric intensive care units (PICUs), and local microbiological and susceptibility data are needed to guide empirical therapy. We describe the microbiological profile, recorded risk factors, antimicrobial susceptibility and outcomes of 26 children aged 1 month to 18 years with severe pneumonia admitted to the PICU of a tertiary care teaching hospital in Sangli, Maharashtra, India, between 1 July and 31 December 2024. Records were analyzed retrospectively. Categorical data are presented as counts and percentages with Wilson 95% confidence intervals, and risk factors were compared across severity groups using two-sided Fisher exact tests. Fifteen children (57.7%) were male and 11 (42.3%) were younger than one year, ratio of females were 11 out of 26, which is 42.3%. Gram-negative bacteria were recorded in 12 children (46.2%) and Gram-positive bacteria in three (11.5%); *Klebsiella pneumoniae* was the most frequent organism (8/26; 30.8%). Influenza virus was the most common viral detection (4/26; 15.4%). Prior antibiotic use was recorded in 13 children (50.0%), but no risk factor was significantly associated with severity (all $P > 0.05$). Amikacin (9/10; 90.0%) and gentamicin (10/12; 83.3%) showed the highest recorded sensitivity and ceftriaxone the lowest (5/10; 50.0%). Three children (11.5%) died, two of the four labelled as multidrug-resistant (MDR). Gram-negative organisms, particularly *K. pneumoniae*, predominated in this small single-centre series. The findings are descriptive and should not be generalized; larger prospective studies with standardized specimen collection are warranted.

KEYWORDS: Severe pneumonia; Pediatric intensive care; *Klebsiella pneumoniae*; Antimicrobial susceptibility; Multidrug resistance; Children

INTRODUCTION
Pneumonia remains one of the leading infectious causes of death in children younger than five years worldwide, with the greatest burden in low- and middle-income countries (Rudan et al., 2008; McAllister et al., 2019). Children with severe disease frequently require hospitalization and, when respiratory failure or hemodynamic instability develops, admission to a pediatric intensive care unit (PICU). Empirical antimicrobial therapy in this setting is chosen before microbiological results are available, so knowledge of the organisms and susceptibility patterns encountered locally is clinically relevant (Dhane et al., 2023; Pawar et al., 2023).

Assigning a single causative agent in childhood pneumonia is difficult. Upper airway specimens may reflect colonization, viral nucleic acid may persist or be detected alongside bacteria, and prior antibiotic exposure reduces culture yield (Zar et al., 2017; Murdoch et al., 2012). The Pneumonia Etiology Research for Child Health (PERCH) study illustrated that the etiology of hospitalized severe pneumonia varies by age and site and that viruses account for a large proportion of cases (PERCH Study Group, 2019). Indian studies have addressed risk factors for pneumonia and severe pneumonia in community and ward settings (Goyal et al., 2021; Save et al., 2026), and others have described nosocomial and ventilator-associated infections in PICUs (Deep et al., 2004; Bhattacharya et al., 2023). Data on children admitted to a PICU with severe pneumonia, excluding ventilator-associated pneumonia, are comparatively limited (Patil et al., 2023; Malla et al., 2023; Ghatage et al., 2026).

We therefore aimed to describe the microbiological profile of severe pneumonia among children admitted to the PICU of a tertiary care hospital. The specific objectives were to (1) describe the distribution of recorded bacterial and viral organisms; (2) describe demographic and clinical risk factors; (3) summarize reported antimicrobial susceptibility; (4) describe multidrug-resistant (MDR) classification and clinical outcomes; and (5) explore associations between selected risk factors and pneumonia severity.

MATERIAL AND METHODS

Study design and setting

This was a retrospective descriptive study conducted in the PICU of Bharati Vidyapeeth (Deemed to be University) Medical College and Hospital, Sangli, Maharashtra, India. The study period was 1 July to 31 December 2024. The report follows the STROBE recommendations for observational studies (von Elm et al., 2007).

Participants

Records of children aged 1 month to 18 years admitted to the PICU with severe pneumonia were screened, and a convenience sample was analyzed. Severe pneumonia was classified as severe or very severe. Children with ventilator-associated pneumonia and records in which cultures were considered to represent contamination or colonization were excluded. In total, 26 children were included.

Data collection and definitions

Data were abstracted on sex, age group (<1 year or ≥1 year), nutritional status (normal, moderate or severe malnutrition), recorded risk factors (age under 1 year, malnutrition, incomplete immunization, low birth weight, underlying comorbidity, prior antibiotic use, prematurity and recurrent hospitalization), organisms detected, antibiotic susceptibility results, MDR status and disposition (discharged or died). More than one organism could be recorded for a child. Normal throat flora was not counted as a pathogen. Specimens, culture methods, viral testing platform, susceptibility testing method and interpretive standard were described by the laboratory authors: specimen types, media, identification method, CLSI/EUCAST version, including viral panel) (Shinde et al., 2026; Wang et al., 2026; Survase et al., 2025; Walvekar et al., 2025; Konduskar et al., 2025).

Statistical analysis

Categorical variables are presented as frequencies and percentages; proportions of key outcomes are accompanied by Wilson 95% confidence intervals. Susceptibility percentages use the number of susceptible, intermediate and resistant results reported for each antibiotic as the denominator and are record-level results rather than unique-isolate antibiograms. Risk factors were compared between children with very severe and severe pneumonia, and mortality was compared by MDR status, using two-sided Fisher exact tests. All comparisons were exploratory and unadjusted, and no causal inference is drawn. $P < 0.05$ was considered statistically significant (Memon et al., 2026; Patil, 2026; Shingade et al., 2026; Patil and Mali, 2026; Patil, 2026; Patil, 2026; Patil et al., 2025; Patil et al., 2025; Diwate et al., 2025; Patil et al., 2025; Sharma et al., 2027).

Ethics

The study was approved by the Institutional Ethics Committee of Bharati Vidyapeeth (Deemed to be University) Medical College and Hospital, Sangli [approval date And number: 4th July 2026: BV(DU)MC&H/Sangli/IEC/661/26].

RESULTS

Participant characteristics

Twenty-six children were included, of whom nine (34.6%) were classified as very severe and 17 (65.4%) as severe pneumonia. Fifteen (57.7%) were male and 11 (42.3%) were younger than one year. Nineteen children (73.1%) had normal nutritional status, four (15.4%) moderate and three (11.5%) severe malnutrition (Table 1).

Table 1. Demographic characteristics of the 26 children

Characteristic	N	%
Male	15	57.7
Female	11	42.3
Age under 1 year	11	42.3
Age 1 year or older	15	57.7
Normal nutritional status	19	73.1
Moderate malnutrition	4	15.4
Severe malnutrition	3	11.5
Very severe pneumonia	9	34.6
Severe pneumonia	17	65.4

Percentages use all 26 children as the denominator.

Microbiological findings

Gram-negative bacteria were recorded in 12 of 26 children (46.2%; 95% CI 28.8–64.5) and Gram-positive bacteria in three (11.5%; 95% CI 4.0–29.0). *Klebsiella pneumoniae* was the most frequent organism (8/26; 30.8%; 95% CI 16.5–50.0), followed by *Acinetobacter baumannii* (2/26; 7.7%); *Burkholderia cepacia*, *Enterobacter cloacae* and *Sphingomonas paucimobilis* were each found in one child (3.8%). Coagulase-negative staphylococci were

recorded in two children (7.7%) and *Staphylococcus aureus* in one (3.8%). Because five Gram-negative isolates were listed among 12 children with Gram-negative findings, at least one child had more than one organism recorded. Influenza virus was the most frequent viral detection (4/26; 15.4%; 95% CI 6.1–33.5), followed by respiratory syncytial virus and rhinovirus (two children each; 7.7%), and parainfluenza virus and human metapneumovirus (one child each; 3.8%). Normal throat flora was recorded in nine children (34.6%) and was excluded (Table 2; Figures 1 and 2).

Table 2. Organisms recorded among the 26 children

Organism	n	%
Gram-negative bacteria (children with any Gram-negative finding: 12; 46.2%)		
Klebsiella pneumoniae	8	30.8
Acinetobacter baumannii	2	7.7
Burkholderia cepacia	1	3.8
Enterobacter cloacae	1	3.8
Sphingomonas paucimobilis	1	3.8
Gram-positive bacteria (children with any Gram-positive finding: 3; 11.5%)		
Coagulase-negative staphylococci	2	7.7
Staphylococcus aureus	1	3.8
Viruses		
Influenza virus	4	15.4
Respiratory syncytial virus	2	7.7
Rhinovirus	2	7.7
Parainfluenza virus	1	3.8
Human metapneumovirus	1	3.8

Mixed detections were possible; counts are therefore not mutually exclusive. Normal throat flora (9 children; 34.6%) is excluded.

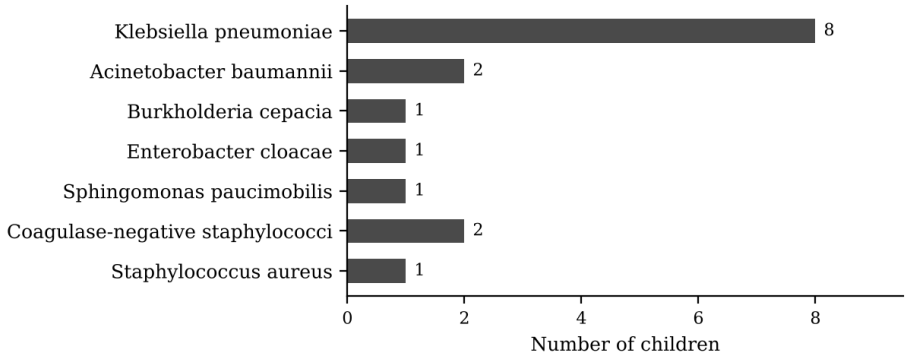

Figure 1. Bacterial organisms recorded among the 26 children. Multiple detections may occur in the same child.

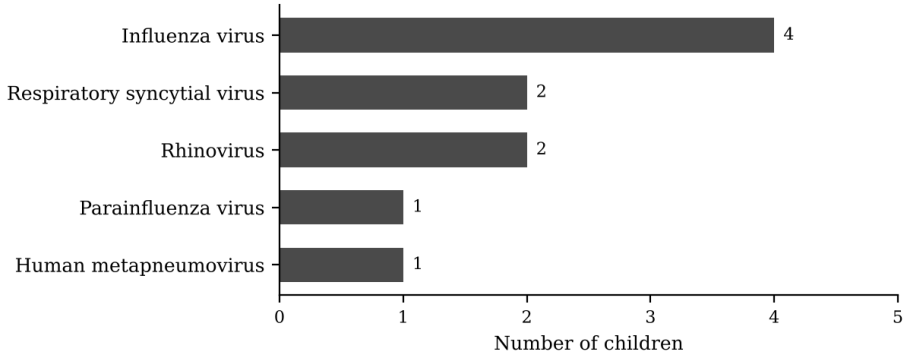

Figure 2. Viral detections among the 26 children. Multiple detections may occur in the same child.

Risk factors and severity

Prior antibiotic use was recorded in 13 children (50.0%; 95% CI 32.1–67.9), underlying comorbidity in eight (30.8%), low birth weight in five (19.2%), and prematurity and recurrent hospitalization in four each (15.4%). Malnutrition was recorded as a risk factor in nine children (34.6%), whereas the nutritional-status classification identified seven (26.9%) as malnourished. No child had incomplete immunization (Table 3; Figure 3). None of the exploratory comparisons between very severe and severe pneumonia reached statistical significance; prior antibiotic use (P = 0.097) and recurrent hospitalization (P = 0.104) showed numerical differences only (Table 4).

Table 3. Recorded risk factors

Risk factor	Present, n (%)	Absent, n (%)
Age under 1 year	11 (42.3)	15 (57.7)
Malnutrition (risk field)	9 (34.6)	17 (65.4)
Incomplete immunization	0 (0.0)	26 (100.0)
Low birth weight	5 (19.2)	21 (80.8)
Underlying comorbidity	8 (30.8)	18 (69.2)
Prior antibiotic use	13 (50.0)	13 (50.0)
Prematurity	4 (15.4)	22 (84.6)
Recurrent hospitalization	4 (15.4)	22 (84.6)

Multiple risk factors could occur in the same child.

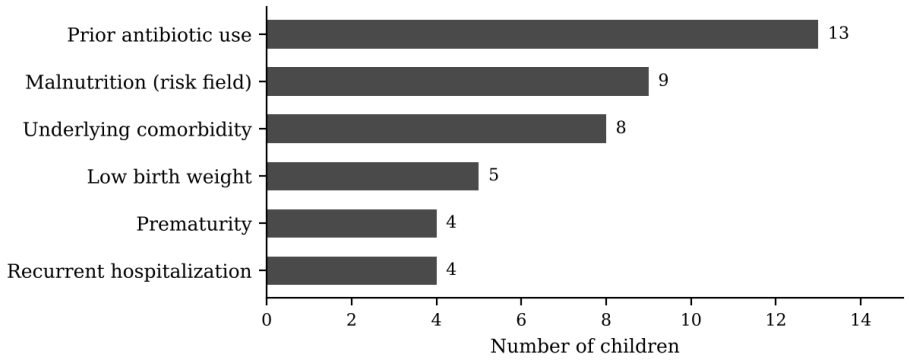

Figure 3. Recorded risk factors among the 26 children. Multiple risk factors may occur in the same child.

Table 4. Risk factors by pneumonia severity

Risk factor	Very severe (n = 9), n (%)	Severe (n = 17), n (%)	Fisher P
Age under 1 year	3 (33.3)	8 (47.1)	0.683
Malnutrition (risk field)	4 (44.4)	5 (29.4)	0.667
Incomplete immunization	0 (0.0)	0 (0.0)	1.000
Low birth weight	1 (11.1)	4 (23.5)	0.628
Underlying comorbidity	3 (33.3)	5 (29.4)	1.000
Prior antibiotic use	7 (77.8)	6 (35.3)	0.097
Prematurity	1 (11.1)	3 (17.6)	1.000
Recurrent hospitalization	3 (33.3)	1 (5.9)	0.104

Two-sided Fisher exact tests; exploratory and unadjusted.

Antibiotic susceptibility

Susceptibility results were reported for 14 antibiotics, with denominators ranging from one to 13 tests per drug (Table 5). Colistin was reported sensitive in all 10 tests. Among the other commonly tested agents, amikacin was sensitive in 9/10 (90.0%), gentamicin in 10/12 (83.3%), piperacillin-tazobactam in 8/10 (80.0%), imipenem in 8/10 (80.0%), meropenem in 9/12 (75.0%) and cefepime in 8/11 (72.7%). Sensitivity to ceftriaxone was 5/10

(50.0%) and to ciprofloxacin 8/13 (61.5%). Ceftazidime (0/3), levofloxacin (1/4) and minocycline (1/1) were tested in very few instances (Figure 4).

Table 5. Antibiotic susceptibility among reported tests

Antibiotic	Sensitive, n (%)	Intermediate, n (%)	Resistant, n (%)	Tested, n
Meropenem	9 (75.0)	0	3 (25.0)	12
Amikacin	9 (90.0)	0	1 (10.0)	10
Gentamicin	10 (83.3)	0	2 (16.7)	12
Ciprofloxacin	8 (61.5)	1 (7.7)	4 (30.8)	13
Ceftriaxone	5 (50.0)	0	5 (50.0)	10
Piperacillin-tazobactam	8 (80.0)	0	2 (20.0)	10
Cefepime	8 (72.7)	0	3 (27.3)	11
Imipenem	8 (80.0)	1 (10.0)	1 (10.0)	10
Colistin	10 (100.0)	0	0	10
Cotrimoxazole	10 (76.9)	0	3 (23.1)	13
Cefoperazone/sulbactam	8 (72.7)	1 (9.1)	2 (18.2)	11
Ceftazidime	0	0	3 (100.0)	3
Levofloxacin	1 (25.0)	0	3 (75.0)	4
Minocycline	1 (100.0)	0	0	1

Denominators are the number of reported susceptible, intermediate and resistant results per antibiotic; blanks and not-applicable entries are excluded. These are record-level results across organisms and specimens and do not constitute an organism-specific antibiogram.

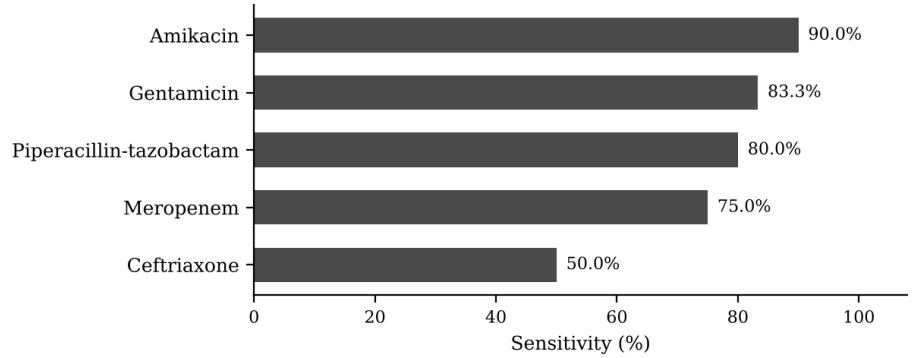

Figure 4. Sensitivity of selected antibiotics. Percentages use drug-specific tested denominators (Table 5).

MDR status and clinical outcome

Twenty-three children (88.5%; 95% CI 71.0–96.0) improved and were discharged, and three (11.5%; 95% CI 4.0–29.0) died. Four children were labelled MDR, 16 non-MDR, and MDR status was unclassified in six. Two of the four MDR children died (50.0%), compared with one of 16 non-MDR children (6.3%); all six children with unclassified status survived (Table 6). The difference between MDR and non-MDR children was not statistically significant (Fisher exact P = 0.088). By organism, deaths were recorded among children with *K. pneumoniae* (2/8), *A. baumannii* (1/2) and coagulase-negative staphylococci (1/2); no deaths occurred among children with viral detections (Table 7). Because organism-level rows overlap in children with mixed detections, they cannot be summed to obtain patient-level mortality.

Table 6. Outcome by MDR status

Outcome	MDR yes (n = 4)	MDR no (n = 16)	MDR unclassified (n = 6)	Total (n = 26)
Improved/discharged	2	15	6	23 (88.5%)

Outcome	MDR yes (n = 4)	MDR no (n = 16)	MDR unclassified (n = 6)	Total (n = 26)
Death	2	1	0	3 (11.5%)

Table 7. Recorded organisms and clinical outcome

Organism	Children, n	Discharged, n	Died, n
Klebsiella pneumoniae	8	6	2
Acinetobacter baumannii	2	1	1
Staphylococcus aureus	1	1	0
Burkholderia cepacia	1	1	0
Enterobacter cloacae	1	1	0
Sphingomonas paucimobilis	1	1	0
Coagulase-negative staphylococci	2	1	1
Influenza virus	4	4	0
Respiratory syncytial virus	2	2	0
Rhinovirus	2	2	0
Parainfluenza virus	1	1	0
Human metapneumovirus	1	1	0

Mixed detections may appear in more than one row; organism-level outcome counts should not be added to obtain patient-level mortality.

DISCUSSION

In this retrospective series of 26 children with severe pneumonia admitted to a PICU, Gram-negative bacteria were recorded about four times as often as Gram-positive bacteria, with *K. pneumoniae* the leading organism and influenza the leading viral detection. Overall mortality was 11.5%. Given the small sample, single-centre design and the possibility of mixed or colonizing isolates, we interpret the findings as a descriptive local snapshot rather than as estimates applicable to other settings.

Demographic characteristics

Eleven of 26 children (42.3%) were infants and 57.7% were male. A multicentre Indian prospective cohort of 7026 children aged 2–59 months with acute respiratory infection found that younger age, and on univariate analysis male sex, were associated with pneumonia, with younger age remaining significant in multivariable analysis (Goyal et al., 2021; Talsandekar et al., 2026; Lokapure and Patil, 2026; Patil and Girija, 2026; Phalake et al., 2026; Shinde et al., 2026; Wang et al., 2026). That study evaluated the risk of developing pneumonia rather than the age distribution of PICU admissions, and our data cannot show that infancy or male sex independently predicts severity. In the PERCH study, etiology likewise varied by age, underlining the need for age-specific interpretation (PERCH Study Group, 2019).

Bacterial profile

Gram-negative findings predominated (46.2% versus 11.5%), led by *K. pneumoniae* (30.8%). This is directionally consistent with Indian PICU reports in which *Klebsiella* was the commonest nosocomial isolate (33.3%; Deep et al., 2004) and was among the leading organisms in ventilator-associated pneumonia (21.6%; Bhattacharya et al., 2023), where Gram-negative bacteria were also the most frequent group. Those cohorts, however, comprised hospital-acquired or ventilator-associated infection, whereas ventilator-associated pneumonia was excluded here; the percentages are therefore not interchangeable, and the comparison is contextual. *S. aureus* accounted for 18.9% of isolates in the ventilator-associated pneumonia series (Bhattacharya et al., 2023) but for one child (3.8%) in ours, a difference that may reflect ventilator exposure, specimen selection and small numbers. The significance of the two coagulase-negative staphylococcal detections is uncertain without information on specimen source and repeat cultures, since these organisms commonly represent contamination or colonization. The low number of Gram-positive findings should not be read as evidence of a low Gram-positive pneumonia burden in the wider pediatric population.

Viral detections

Influenza (15.4%), RSV (7.7%) and rhinovirus (7.7%) were the commonest viral detections. The PERCH study estimated that viruses accounted for the majority of severe pneumonia in hospitalized children, with RSV contributing the largest fraction (PERCH Study Group, 2019), but it used an integrated case-control analysis that attributes etiology probabilistically; our detection frequencies are not comparable. We did not identify an Indian

PICU cohort with directly comparable influenza-specific denominators and therefore make no quantitative comparison. Detection of viral nucleic acid does not by itself establish causation, particularly when more than one organism is present (Murdoch et al., 2012), and detection frequencies depend on testing availability, season, age and the assay panel used.

Risk factors and severity

Prior antibiotic use was the most frequently recorded risk factor (50.0%). Indian studies have implicated undernutrition and young age as risk factors for pneumonia (Goyal et al., 2021), and a prospective study from Mumbai in children aged 2 months to 5 years reported that poor nutrition, incomplete immunization, delayed care-seeking and prior antibiotic use were associated with severe pneumonia (Save et al., 2026). In our cohort none of the eight comparisons was statistically significant, although prior antibiotic use (77.8% versus 35.3%; P = 0.097) and recurrent hospitalization (33.3% versus 5.9%; P = 0.104) showed numerical differences. With nine children in the very severe group, the analysis had little power to detect moderate associations, and the findings should not be taken as evidence of absence of association. The difference between the nutritional-status classification and the malnutrition risk field also needs reconciliation, and causality cannot be determined from these data.

Antimicrobial susceptibility and MDR

Amikacin (90.0%) and gentamicin (83.3%) had the highest recorded sensitivity among commonly tested agents, and ceftriaxone the lowest (50.0%). The finding for amikacin parallels the maximum amikacin sensitivity reported among PICU nosocomial isolates in Mumbai (Deep et al., 2004), although that study concerned a different infection type and era. Because our figures pool tests across organisms and specimens, with denominators of 10–13 per agent, they should not be used as an organism-specific antibiogram. Colistin sensitivity (10/10) likewise requires verification of species, testing method and interpretive criteria before it informs treatment. Two of four MDR-labelled children died, compared with one of 16 non-MDR children; this was not statistically significant and rests on very few events, six children had no MDR classification, and we did not find a comparable MDR-stratified mortality estimate from Indian PICU studies against which to compare it. It suggests, at most, a hypothesis for larger studies.

Clinical outcome

Mortality in this series (11.5%) is numerically close to the 11.8% case fatality reported among 127 hospitalized Indian children aged 2 months to 5 years with pneumonia, in whom malnutrition, associated illness and disease severity were linked to death (Agrawal et al., 1995). Differences in era, age range, case definitions and PICU selection preclude direct comparison, and the estimate is imprecise (95% CI 4.0–29.0%) because only three deaths occurred. Organism-level mortality cannot be attributed causally: children with mixed detections contribute to more than one row of Table 7, and baseline severity and ventilation status were not analysed.

LIMITATIONS

The study has several limitations. The sample was small and drawn from a single centre by convenience sampling, and the retrospective design limits completeness of records. Specimen types, timing of sampling relative to antibiotic exposure and the clinical significance of individual isolates were not available for all children, and mixed detections prevented strict patient-level organism categories. Susceptibility denominators varied by drug and did not represent unique isolates. MDR status was unclassified in six children. No adjusted analyses were possible, and all comparisons were exploratory. These limitations preclude causal inference and generalization beyond the study setting.

CONCLUSION

Among 26 children with severe pneumonia admitted to a tertiary PICU, Gram-negative bacterial findings were more frequent than Gram-positive findings, *K. pneumoniae* was the most commonly recorded organism and influenza the leading viral detection. Amikacin and gentamicin showed the highest recorded sensitivity, and mortality was 11.5%. These descriptive data support continued local microbiological surveillance and antimicrobial stewardship, but confirmation in larger prospective studies with standardized specimens, case definitions and susceptibility reporting is required.

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CONFLICTS OF INTEREST

The authors declare no conflict of interest.

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NA

AUTHOR CONTRIBUTIONS

Dr. Abhijit Sanjay Bhimanpalli: Conceptualization, study design, data collection, data analysis, manuscript drafting, and final approval.

Dr. Suhas G. Kumbhar: Conceptualization, study supervision, data interpretation, manuscript revision, and final approval.

- Dr. Shilpa Shah: Microbiological data analysis, laboratory interpretation, manuscript revision, and final approval.
- Dr. Sadananda Hosamani: Data collection, data analysis, literature review, manuscript revision, and final approval.

All authors have read and approved the final version of the manuscript.

DATA AVAILABILITY STATEMENT

The data supporting the findings of this study are available from the corresponding author upon reasonable request. Due to patient confidentiality and institutional ethical restrictions, the raw data are not publicly available. Researchers with a legitimate interest may contact the corresponding author for access, subject to institutional approval.

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