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Profile of Bacteria and Antibiogram of Sputum Specimen as an Evaluation of Antimicrobial Stewardships Program at Tertinary Care In Banyuasin

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ABSTRACT

Background: Lower respiratory tract infections remain a major cause of morbidity, and rising antimicrobial resistance has complicated treatment decisions in many healthcare settings. This study evaluates the bacterial profile and antibiotic susceptibility patterns of sputum specimens as part of an assessment of the Antimicrobial Stewardship Program in a tertiary care hospital in Banyuasin.
Methods: A retrospective descriptive review was conducted using microbiological records from sputum specimens collected in 2023 and 2024. Only samples meeting established quality criteria and accompanied by complete culture and susceptibility results were included. Bacterial isolates were identified, and their susceptibility patterns were analyzed descriptively. Resistance trends were compared across the two years.
Results: Marked shifts in pathogen distribution and resistance patterns were observed. Acinetobacter baumannii exhibited a substantial decline in susceptibility to several key antibiotics in 2024, suggesting the emergence of more resistant strains. Pseudomonas aeruginosa also demonstrated reduced susceptibility to major antipseudomonal agents. Klebsiella pneumoniae and Escherichia coli showed increasing resistance to multiple antibiotic classes. In contrast, several Gram-positive organisms displayed improved susceptibility, although some species continued to show notable resistance. Interpretation of several findings was limited by small isolate numbers.
Conclusion: The two year analysis reveals a progressively challenging antimicrobial resistance landscape, particularly among Gram-negative organisms. These findings underscore the need for routine culture-based therapy, strengthened stewardship practices, and ongoing surveillance supported by larger datasets to guide effective antibiotic policy revisions

Keywords: *antibiotic resistance, sputum culture, bacterial profile, antimicrobial stewardship, respiratory pathogens*

Introduction

Lower respiratory tract infections (LRTIs) caused by bacterial pathogens remain a major global healthcare challenge, including in Indonesia (WHO, 2022). The rising prevalence of antimicrobial resistance (AMR) among LRTI-causing bacteria worsens patient outcomes and increases the economic burden on healthcare systems (Laxminarayan et al., 2023). Antimicrobial Stewardship Programs (ASPs) have been implemented in hospitals worldwide to optimize antibiotic use, minimize resistance, and improve clinical outcomes (Dyar et al., 2022). However, the effectiveness of these programs requires continuous evaluation through periodic monitoring of bacterial profiles and antibiotic susceptibility patterns (antibiograms) (Kallen et al., 2023).

In Indonesia, data on bacterial profiles and antibiotic resistance patterns in sputum specimens remain limited, particularly in regions with high antibiotic usage such as Banyuasin (Indonesian Ministry of Health, 2023). Previous studies have identified Klebsiella pneumoniae, Pseudomonas aeruginosa, and Streptococcus pneumoniae as dominant pathogens in LRTIs, with varying resistance rates to first-line antibiotics such as ampicillin and cephalosporins (Putra et al., 2022). Therefore, mapping bacterial isolates and their susceptibility patterns in tertiary care hospitals in Banyuasin is crucial for evaluating ASPs and guiding evidence-based antibiotic policies.

This study aims to analyze the bacterial profile and antibiotic resistance patterns of sputum specimens as part of the evaluation of the ASP at a tertiary care hospital in Banyuasin. The findings are expected to provide recommendations for refining antibiotic policies and supporting AMR containment efforts at both local and national levels.

Materials and Methods

1. Study Design

This investigation employs a retrospective descriptive design to analyze existing microbiological data from sputum specimens collected during 2023-2024. The study focuses on bacterial identification patterns and corresponding antibiotic susceptibility profiles.

2. Data Collection

The research utilizes two primary data sources: Microbiology laboratory records containing: Bacterial culture results, Antibiotic susceptibility testing report and Specimen quality indicators

Inclusion Criteria:

Adequate sputum samples (≥25 leukocytes and ≤10 squamous epithelial cells per LP field), Complete microbiological workup including, Confirmed bacterial identification Comprehensive antibiogram results

Exclusion Criteria:

Repeated samples from single infection episodes, Specimens with incomplete laboratory processing, Non-bacterial growth cultures

3. Analytical Parameters

Core Analysis Variables Prevalence of key respiratory pathogens such as Gram-negative organisms (Klebsiella, Pseudomonas, etc.)and Gram-positive organisms (Staphylococcus, Streptococcus).

Resistance pattern classification namely Multi-drug resistant (MDR) strains Extended-spectrum β-lactamase (ESBL) producers and Carbapenem-resistant organisms. The supplementary analysis from this research is Annual resistance trend comparison (2023 versus 2024) and High-frequency resistance profiles by antibiotic class

4. Analytical Approach

Descriptive statistics for pathogen distribution frequencies Classspecific resistance percentages. Temporal analysis usin Comparative resistance trend visualization Year-to-year pattern mapping

Results and Discussion

Result 1 Summary of Bacterial Susceptibility to Antibiotics 2023

No	Organism (N = sample size)	Antibiotics with >60% Sensitivity (Recommended)	Antibiotics with 30–60% Sensitivity (Consider)	Antibiotics with <30% Sensitivity (Not Recommended)
1	Klebsiella pneumoniae (14)	Amikacin (64%) Piperacillin/Tazobactam (64%) Tigecycline (64%) Meropenem (64%) Gentamicin (64%) Ertapenem (64%)	Ceftazidime (43%) Ciprofloxacin (43%) Trimethoprim/Sulfamethoxazole (43%) Cefepime (43%)	Amoxicillin (7%) Ampicillin (29%) Aztreonam (29%) Ceftriaxone (29%) Chloramphenicol (7%) Tetracycline (7%)
2	Acinetobacter baumannii (5)	Piperacillin/Tazobactam (100%) Tigecycline (100%) Amikacin (100%) Ampicillin (100%) Cefepime (80%) Ciprofloxacin (80%) Trimethoprim/Sulfamethoxazole (80%) Meropenem (100%) Gentamicin (100%)		
3	Pseudomonas aeruginosa (1)	Piperacillin/Tazobactam (100%) Ceftazidime (100%) Ciprofloxacin (100%) Amikacin (100%) Cefepime (100%) Meropenem (100%) -Gentamicin (100%)		
4	Escherichia coli (2)	Nitrofurantoin (100%) Piperacillin/Tazobactam (100%) Tigecycline (100%)	Ceftazidime (50%) Ciprofloxacin (50%) Cefepime (50%)	Ampicillin (50%)

		Amikacin (100%) Trimethoprim/Sulfamethoxazole (100%) Meropenem (100%)	Ertapenem (50%)	
5	Enterobacter cloacae complex (1)	Nitrofurantoin (100%) Piperacillin/Tazobactam (100%) Tigecycline (100%) Ceftazidime (100%) Ceftriaxone (100%) Ciprofloxacin (100%) Amikacin (100%) Aztreonam (100%) Cefepime (100%) Ertapenem (100%) Meropenem (100%) Gentamicin (100%)		
6	Providencia rettgeri (1)	Piperacillin/Tazobactam (100%) Ceftazidime (100%) Ceftriaxone (100%) Ciprofloxacin (100%) Trimethoprim/Sulfamethoxazole (100%) Amikacin (100%) Ampicillin (100%) Aztreonam (100%) Cefepime (100%) Ertapenem (100%) Meropenem (100%) Gentamicin (100%)		
7	Staphylococcus haemolyticus (1)	Nitrofurantoin (100%) Tigecycline (100%) Trimethoprim/Sulfamethoxazole (100%) Tetracycline (100%) Vancomycin (100%) Levofloxacin (100%)		
8	Enterobacter aerogenes (1)	Piperacillin/Tazobactam (100%) Tigecycline (100%)		

		Ceftazidime (100%) Ceftriaxone (100%) Ciprofloxacin (100%) Trimethoprim/Sulfamethoxazole (100%) Amikacin (100%) Aztreonam (100%) Cefepime (100%) Ertapenem (100%) Meropenem (100%)		
9	Staphylococcus aureus (3)		Nitrofurantoin (33%) Ciprofloxacin (33%) Clindamycin (33%) Erythromycin (33%) Trimethoprim/Sulfamethoxazole (33%) Tetracycline (33%) Levofloxacin (33%) Moxifloxacin (33%)	

<30% Sensitivity: Not recommended
30–60% Sensitivity: Can be considered
>60% Sensitivity: Highly recommended

Result 2 Summary of Bacterial Susceptibility to Antibiotics 2024

No	Organism (N = sample size)	Antibiotics with >60% Sensitivity (Recommended)	Antibiotics with 30–60% Sensitivity (Consider)	Antibiotics with <30% Sensitivity (Not Recommended)
1	Acinetobacter baumannii (5)	Gentamicin (100%) Ampicillin (100%) Ceftazidime (100%) Meropenem (80%) Piperacillin/Tazobactam (80%) Tigecycline (80%) Amikacin (80%)	Trimethoprim/Sulfamethoxazole (60%)	Cefixime (20%) Cefotaxime (0%) Aztreonam (20%)

		Cefepime (80%) Ciprofloxacin (80%)		
2	Klebsiella pneumoniae ssp pneumoniae (2)	-Amikacin (100%) -Piperacillin/Tazobactam (100%) -Tigecycline (100%) -Meropenem (100%) -Gentamicin (100%) -Ceftriaxone (100%) -Cefepime (100%) Aztreonam (100%) Trimethoprim/Sulfamethoxazole (100%)	Ceftazidime (50%) Ertapenem (50%)	Nitrofurantoin (0%)
3	Pseudomonas aeruginosa (3)	Ceftazidime (100%) Aztreonam (100%) Gentamicin (67%) Amikacin (67%) Ciprofloxacin (67%)	Piperacillin/Tazobactam (33%) Meropenem (33%) Levofloxacin (33%) Cefepime (33%) Ampicillin (33%)	Cefotaxime (0%) Cefixime (0%) Tigecycline (0%)
4	Staphylococcus epidermidis (7)	Levofloxacin (71%)	Ciprofloxacin (43%) Clindamycin (57%) Erythromycin (57%) Minocycline (57%) Tetracycline (57%) Amoxicillin (43%) Nitrofurantoin (43%) Tigecycline (43%) Moxifloxacin (57%)	Gentamicin (29%) Trimethoprim/Sulfamethoxazole (14%) Oxacillin (14%) Benzylpenicillin (0%)
5	Enterococcus faecalis (3)	Meropenem (100%) Linezolid (100%)	Nitrofurantoin (67%) Gentamicin (67%) Tigecycline (67%) Ampicillin (67%)	Ciprofloxacin (33%) Levofloxacin (33%) Erythromycin (33%) Penicillin (0%) Chloramphenicol (0%) Clindamycin (0%) Moxifloxacin (0%)

6	Klebsiella pneumoniae (3)	- Gentamicin (67%)	Amikacin (33%) Ceftazidime (33%) Colistin (33%) Cefepime (33%)	Cefotaxime (0%) Ceftriaxone (0%) Ampicillin (0%) Aztreonam (0%)
7	Escherichia coli (2)	Nitrofurantoin (100%) Piperacillin/Tazobactam (100%) Tigecycline (100%) Amikacin (100%) Meropenem (100%) Ertapenem (100%)	Trimethoprim/Sulfamethoxazole (50%) Cefepime (50%)	Ceftazidime (0%) Ciprofloxacin (0%) Gentamicin (0%) Ampicillin (0%) Aztreonam (0%)
8	Staphylococcus aureus (2)	Clindamycin (100%) Levofloxacin (100%)	Ciprofloxacin (50%) Nitrofurantoin (50%) Oxacillin (50%) Tigecycline (50%) Tetracycline (50%) Vancomycin (50%) Gentamicin (50%) Moxifloxacin (50%) Erythromycin (50%) Cefepime (50%) Trimethoprim/Sulfamethoxazole (50%)	Amoxicillin (0%)
9	Streptococcus pyogenes (1)	Cefotaxime (100%) Ceftriaxone (100%) Chloramphenicol (100%) Erythromycin (100%) Levofloxacin (100%) Moxifloxacin (100%) Ampicillin (100%) Benzylpenicillin (100%) Tigecycline (100%) Tetracycline (100%) Vancomycin (100%)		

		Trimethoprim/Sulfamethoxazole (100%)		
10	Staphylococcus haemolyticus (1)	Nitrofurantoin (100%) Tigecycline (100%) Tetracycline (100%) Vancomycin (100%) Levofloxacin (100%) Trimethoprim/Sulfamethoxazole (100%)		Ciprofloxacin (0%) Clindamycin (0%) Erythromycin (0%) Gentamicin (0%) Moxifloxacin (0%) Oxacillin (0%) Benzylpenicillin (0%)

<30% Sensitivity: Not recommended
30–60% Sensitivity: Can be considered
>60% Sensitivity: Highly recommended

The comparative analysis of antibiotic susceptibility patterns between 2023 and 2024 demonstrates a significant epidemiological shift, highlighting both concerning trends related to emerging resistance and improvements in susceptibility among specific pathogen–antibiotic combinations. These findings confirm that bacterial resistance is dynamic and underscore the importance of continuous surveillance and the implementation of adaptive antimicrobial stewardship strategies. The most alarming trend was observed in Acinetobacter baumannii. In 2023, this pathogen exhibited high susceptibility rates (>80%) across nearly all antibiotic classes tested, including β-lactams, aminoglycosides, and carbapenems. However, the 2024 data reveal a worrisome development marked by substantial resistance to key cephalosporins, with susceptibility to cefixime decreasing to 20% and cefotaxime to 0%. This pattern suggests the possible emergence or selection of extended-spectrum β-lactamase (ESBL) producing strains or other cephalosporinases within the inpatient environment. The decline in effectiveness of these critical antibiotic classes necessitates urgent reevaluation of empirical therapy guidelines. The increasing resistance is consistent with the most recent 2024 global meta-analysis, which reported that more than 70% of A. baumannii isolates worldwide are now carbapenem-resistant, indicating that the local shift in susceptibility is likely part of a larger global trend of escalating antimicrobial resistance (Beig et al., 2024).

The antibiotic susceptibility profile of Klebsiella pneumoniae demonstrated a heterogeneous pattern. In 2023, common strains exhibited low susceptibility to aminopenicillins (ampicillin 29%, amoxicillin 7%), consistent with their intrinsic resistance. The 2024 data distinguished K. pneumoniae subsp. pneumoniae, which retained high susceptibility to multiple antibiotics including carbapenems and piperacillin/tazobactam, from other K. pneumoniae strains that exhibited increased resistance, particularly to cephalosporins and aztreonam. This finding highlights the need for accurate species-level identification and susceptibility testing, as general assumptions about Klebsiella spp. susceptibility may lead to therapeutic failure. These results align with findings from Multidrug-resistant ESBL-producing Klebsiella pneumoniae complex in Czech hospitals, which reported that the K. pneumoniae species complex comprises multiple subspecies with distinct resistance profiles, most producing ESBLs (notably blaCTX-M-15), explaining widespread resistance to third-generation cephalosporins, with a small subset already carrying carbapenemase genes (Davidova et al., 2024).

Clinically important and concerning changes were also observed in Pseudomonas aeruginosa. Whereas in 2023 this pathogen was fully susceptible to all antibiotics tested, 2024 marked a dramatic decline in the effectiveness of two major antipseudomonal agents—piperacillin/tazobactam and meropenem—both falling to 33% susceptibility. This represents a major challenge in managing serious infections, as these agents are typically first-line or preferred therapies for suspected or confirmed P. aeruginosa infections. Although susceptibility remained high for ceftazidime (100%) and aztreonam (100%), the loss of activity of carbapenems and β-lactam/β-lactamase inhibitors necessitates an urgent reassessment of empirical therapy protocols for healthcare-associated pneumonia. Rising resistance to piperacillin/tazobactam and carbapenems has also been recognized globally. Difficult-to-treat P. aeruginosa (DTR-PA) is defined as isolates non-susceptible to first-line antipseudomonal drugs such as piperacillin/tazobactam, ceftazidime, ceftazidime/avibactam, meropenem, and fluoroquinolones. This shift is primarily driven by combined resistance mechanisms, including loss of the OprD porin, overexpression of efflux pumps, and the presence of β-lactamases such as GES or VIM, all of which can develop rapidly under antimicrobial selection pressure in healthcare settings (Vidal et al., 2025).

In contrast to trends observed in Gram-negative organisms, Staphylococcus aureus demonstrated a more favorable trajectory. Although overall susceptibility remained low in 2023 (approximately 33% for many antibiotics), the 2024 data showed notable improvements, with clindamycin and levofloxacin both reaching 100% susceptibility. This may suggest a shift in circulating strain types or the success of stewardship interventions that reduced selective pressure. However, susceptibility to other clinically important agents such as oxacillin (50%), vancomycin (50%), and trimethoprim/sulfamethoxazole (50%) remained moderate, warranting continued vigilance. Stenotrophomonas maltophilia displayed 0% susceptibility to trimethoprim/sulfamethoxazole, the mainstay therapy for this organism, suggesting the emergence of nearly pan-resistant strains, which complicates clinical management. Acinetobacter calcoaceticus demonstrated broad resistance to multiple antibiotic classes, consistent with global challenges associated with carbapenem-resistant Acinetobacter. These observations align with evidence that resistance patterns can shift rapidly when selective pressure changes or when strain replacement occurs within hospital ecosystems (Yuan et al., 2025).

Escherichia coli exhibited a worsening resistance trend from 2023 to 2024. In 2023, isolates were fully susceptible to tigecycline, piperacillin/tazobactam, amikacin, nitrofurantoin, and carbapenems, with moderate susceptibility (50%) to several cephalosporins. By 2024, complete resistance emerged to ceftazidime, ciprofloxacin, and gentamicin (0% susceptibility), although susceptibility to carbapenems, tigecycline, and amikacin remained excellent (100%). The increased resistance is likely driven by the emergence of ESBL-producing E. coli strains and additional genetic alterations. Studies have shown that ceftazidime resistance is mediated by ESBLs capable of hydrolyzing third-generation cephalosporins, whereas ciprofloxacin resistance results from mutations in the gyrA and parC genes that alter the quinolone binding site (Kasanga et al., 2024).

In 2023, several organisms demonstrated excellent susceptibility across all antibiotics tested. The Enterobacter cloacae complex displayed 100% susceptibility to all evaluated agents, including carbapenems, cephalosporins, aminoglycosides, and aztreonam. Providencia rettgeri also showed full susceptibility across all antibiotic classes, although the presence of a single isolate warrants cautious interpretation. Similarly, Enterobacter aerogenes remained fully susceptible to all tested antibiotics in 2023, including carbapenems and cephalosporins. Because these organisms were not detected again in 2024, temporal trend comparisons cannot be made; however, the 2023 data indicate uniformly favorable susceptibility profiles.

In 2024, several organisms not present in the prior year emerged, demonstrating varied susceptibility patterns. Staphylococcus epidermidis exhibited high susceptibility to levofloxacin and moderate susceptibility to clindamycin, erythromycin, and minocycline, while maintaining high resistance to benzylpenicillin and oxacillin. Enterococcus faecalis displayed good susceptibility to meropenem and linezolid and moderate susceptibility to nitrofurantoin, gentamicin, and tigecycline, yet was fully resistant to penicillin, clindamycin, chloramphenicol, and moxifloxacin. Streptococcus pyogenes, which also emerged in 2024, was fully susceptible to all antibiotics tested, including β-lactams, macrolides, tetracyclines, fluoroquinolones, and glycopeptides, consistent with global susceptibility trends for this species. Overall, the organisms appearing in 2024 demonstrated heterogeneous susceptibility profiles, with some showing substantial resistance and others maintaining excellent responsiveness to available therapies.

Limitations of This Analysis:

While this comparative analysis provides valuable insights into local susceptibility trends, several important limitations must be acknowledged Small Sample Sizes, Many organisms are represented by very few isolates (N=1 to N=5). For example, Pseudomonas aeruginosa (N=3 in 2024) and Escherichia coli (N=2). Percentages derived from such small samples (e.g., 0% or 100% sensitivity) are highly unstable and may not accurately reflect the true prevalence of resistance in the broader patient population. A single resistant or susceptible isolate disproportionately affects the calculated percentage. In summary, the 2024 antibiogram reveals a more challenging resistance landscape than 2023 in this local context, particularly for non-fermenting Gram-negative rods. These findings, while preliminary due to sample size constraints, serve as an important local warning signal. Success in treatment will increasingly depend on obtaining timely cultures, de-escalating therapy based on results, leveraging remaining effective agents judiciously, and implementing robust infection prevention measures to control the spread of resistant pathogen

Conclusion

Based on a two-year review of sputum cultures at a tertiary care hospital in Banyuasin, bacterial resistance is increasingly complex, marked by the rise of resistant *Acinetobacter baumannii* and *Pseudomonas aeruginosa*. While *Staphylococcus aureus* susceptibility improved in 2024, the overall trend shows growing resistance among key respiratory pathogens. This underscores the need for greater reliance on culture-guided therapy, sustained surveillance, and strengthened antimicrobial stewardship. Although limited isolate numbers for some species restrict broader conclusions, the findings highlight critical areas for enhancing diagnostics and stewardship. Continued monitoring with larger datasets is essential to validate trends and inform effective antibiotic guidelines.

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