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ABOUT COVER

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Retrospective Study

Six-year analysis of key monitoring for bacterial strain distribution and antibiotic sensitivity in a hospital

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Abstract

BACKGROUND

With the widespread use of antimicrobial drugs, bacterial resistance has become a significant problem, posing a serious threat to public health. The prevalence of clinical infection strains in hospitals and their drug sensitivities are key to the appropriate use of antibiotics in clinical practice.

AIM

To identify prevalent bacteria and their antibiotic resistance profiles in a hospital setting, thereby guiding effective antibiotic usage by clinicians.

METHODS

Specimens from across the institution were collected by the microbiology laboratory. The VITEK 2 compact fully automatic analyzer was used for bacterial identification and antibiotic sensitivity testing, and the WHONET5.6 software was utilized for statistical analysis.

RESULTS

A total of 12062 bacterial strains of key monitoring significance were detected. *Staphylococcus aureus* demonstrated widespread resistance to penicillin, but none of the strains were resistant to vancomycin or linezolid. Moreover, 219 strains of methicillin-resistant coagulase-negative staphylococci and 110 strains of methicillin-resistant *Staphylococcus aureus* were detected. *Enterococcus faecalis* showed moderate resistance to the third-generation quinolones ciprofloxacin and levofloxacin, but its resistance to nitrofurantoin and tetracycline was low. *Enterococcus faecium* displayed significantly lower resistance to third- and fourth-generation quinolones than *Enterococcus faecalis*. The resistance of two key monitoring strains, *Escherichia coli* and *Klebsiella pneumoniae*, to piperacillin/tazobactam was 5%-8%. However, none of the *Escherichia coli* and

Klebsiella pneumoniae strains were resistant to meropenem. The resistance of *Acinetobacter baumannii* to piperacillin/sulbactam was nearly 90%. Nonetheless, the resistance to tigecycline was low, and *Pseudomonas aeruginosa* demonstrated minimal resistance in the antibiotic sensitivity test, maintaining a resistance of < 10% to the cephalosporin antibiotics cefotetan and cefoperazone over the last 6 years. The resistance to amikacin remained at 0.2% over the past 3 years.

CONCLUSION

Our hospital's overall antibiotic resistance rate was relatively stable from 2017 to 2022. The detection rates of key monitoring strains are reported quarterly and their resistance dynamics are monitored and communicated to the entire hospital, which can guide clinical antibiotic selection.

Key Words: Antibiotic sensitivity test; Monitoring bacterial antibiotic resistance; Antimicrobial drugs; Antimicrobial stewardship; Combination therapies; Antibiotic stewardship

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Core Tip: This study provides essential insights into the distribution and drug resistance of key clinical bacteria in a hospital setting. The findings help clinicians to understand the prevalence of these strains and their resistance to antibiotics, which can guide effective treatment decisions. This contributes to the broader efforts to manage and combat antibiotic resistance, a significant global health challenge.

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INTRODUCTION

The widespread application of antimicrobial drugs has brought bacterial resistance to the forefront as a substantial public health threat[1]. To enhance the scientific management of these drugs, our hospital has initiated tracking tests in the microbiology laboratory to determine the distribution of key monitoring bacteria within its premises. This measure is in line with the State Council's "National Action Plan to Contain Antibacterial Resistance (2016-2020)", the National Health Commission's "Clinical Application Management Measures of Antibacterial Drugs", and the "Notice on Further Strengthening the Clinical Application Management of Antibacterial Drugs to Contain Antibacterial Resistance". The hospital has selected eight bacteria associated with hospital-acquired infections for key monitoring and summarized the changes in the antibiotic sensitivity of various multidrug-resistant strains. The intention is to aid clinicians in comprehending the prevalence of strains causing clinical infection within the hospital and serve as a reference for the judicious use of antibiotics.

MATERIALS AND METHODS

Bacterial sources

A total of 12062 clinical isolates were collected from the hospital during the period 2017-2022 from blood, sputum, urine, wound secretion, drainage fluid, cerebrospinal fluid, and pus samples.

Bacterial identification and antibiotic sensitivity testing

The VITEK 2 compact fully automatic analyzer was used to identify the bacteria in the collected samples and determine their antibiotic sensitivity. The analysis and interpretation of the results complied with the Clinical and Laboratory Standards Institute 2017 guidelines. The WHONET5.6 software was used to statistically analyze the results.

Definition of multidrug-resistant bacteria

According to the "Guidelines for Prevention and Control of Multidrug-Resistant Bacterial Hospital Infections (Trial)" issued by the Ministry of Health in 2011[2], multidrug-resistant bacteria are those that demonstrate resistance to three or more types of clinically used antimicrobial drugs.

Quality control strains

The quality control strains used in this study were *Staphylococcus aureus* (*S. aureus*) (ATCC6538); *Pseudomonas aeruginosa* (

P. aeruginosa (ATCC27853); *Escherichia coli* (*E. coli*) (ATCC25922); *Acinetobacter baumannii* (*A. baumannii*) (ATCC19606); *Staphylococcus epidermidis* (*S. epidermidis*) (ATCC12228); *Klebsiella pneumoniae* (*K. pneumoniae*) (ATCC700603); *Enterococcus faecium* (*E. faecium*) (ATCC29212); *Enterococcus faecalis* (*E. faecalis*) (ATCC51558).

RESULTS

Overview of key pathogens linked to hospital-acquired infections from 2017 to 2022

Between 2017 and 2022, the principal pathogens linked to hospital-acquired infections were: *S. aureus*, *P. aeruginosa*, *A. baumannii*, *S. epidermidis*, *K. pneumoniae*, *E. coli*, *E. faecalis*, and *E. faecium*. A rising trend in the detection rate of these eight key pathogens was observed from 2017 to 2019. However, in 2020, a significant reduction was noted in the overall detection rate, which could be attributed to decreased hospital visits owing to the impact of the pandemic. In 2021 and 2022, the rate returned to nearly the 2019 level. Of these, the three most commonly detected strains were *E. coli* (3384, 28%), *K. pneumoniae* (3326, 27.6%), and *A. baumannii* (1861, 15.4%). Following these strains, in descending order, were *P. aeruginosa*, *S. aureus*, *S. epidermidis*, *E. faecium*, and *E. faecalis* (see Figure 1). The incidence of multidrug-resistant bacteria was 20%-27% (see Table 1).

Analysis of antimicrobial resistance trends for key pathogens from 2017 to 2022

Staphylococcus: A total of 944 *S. aureus* strains and 812 *S. epidermidis* strains were identified. Of these, there were 219 methicillin-resistant coagulase-negative staphylococci (MRCNS) and 110 methicillin-resistant *S. aureus* (MRSA). *S. aureus* exhibited a high penicillin resistance rate of nearly 100%. Over the 6 years, the erythromycin resistance rate was high and increased gradually from 71.8% in 2017 to 90% in 2022. Concurrently, golden staphylococcus demonstrated significant clindamycin resistance, reaching 64.0% in 2022. Gentamicin remained relatively effective against *S. aureus*, with a stable resistance rate of approximately 11% over the period. Notably, no *S. aureus* strains resistant to vancomycin or linezolid were detected (refer to Figure 2A).

Enterococcus: A total of 191 *E. faecium* and 114 *E. faecalis* strains were identified in this study, both of which exhibited resistance to penicillin G. *E. faecium* showed resistance to the third-generation quinolones ciprofloxacin and levofloxacin, with resistance rates of 60.38%-68.9% and 66.28%-70.38%, respectively. Resistance to the fourth-generation fluoroquinolone moxifloxacin was slightly less, at approximately 60%. *E. faecium* demonstrated lower resistance to nitrofurantoin and tetracycline. Importantly, a few vancomycin-resistant *E. faecium* were detected from 2017 to 2022, although the resistance rate decreased gradually from 2.7% in 2017 and stabilized at approximately 1% (refer to Figure 2B).

In contrast, *E. faecalis* displayed a lower overall detection rate and demonstrated less resistance. The resistance rate to penicillin G exceeded 90%, the resistance rate to gentamicin remained between 15% and 20%, and the resistance rates to third- and fourth-generation quinolones were significantly lower than those of *E. faecium*. No vancomycin-resistant *E. faecalis* were detected (refer to Figure 2C).

Enterobacteriales: *E. coli* and *K. pneumoniae* were the top two pathogens monitored and accounted for 28.1% and 27.6% of the total strains detected, respectively. The overall resistance rate to the compound sulfamethoxazole exceeded 50% for both *E. coli* and *K. pneumoniae*, with no increasing trend over the 6 years. Both pathogens showed a high resistance rate to cefotaxime, which fluctuated around 50%. However, the pathogens demonstrated high sensitivity to cefotaxime, a third-generation cephalosporin, with a sensitivity rate of approximately 78% for *E. coli* and 76% for *K. pneumoniae*. Both pathogens displayed slightly higher sensitivity to fourth-generation cephalosporins. Cefoperazone/sulbactam, a key antibiotic combination, was effective against these two predominant strains of *Enterobacteriales*. Their resistance to the drug remained at approximately 9%. The pathogens depicted even lower resistance to piperacillin/tazobactam, which hovered in the range of 5%-8%. Notably, no *E. coli* or *K. pneumoniae* resistant to meropenem were detected, and their resistance rate to imipenem was a mere 0.2% (refer to Figures 2D and E).

Nonfermenting bacteria: *A. baumannii* and *P. aeruginosa* were the third and fourth most frequently detected bacterial strains in this study. The monitoring of *A. baumannii* revealed a high resistance rate to piperacillin/tazobactam of almost 90%. The pathogen's resistance rates to cefotaxime, cefoperazone, and levofloxacin hovered at approximately 75%. The resistance rate to tigecycline was relatively low and stabilized at approximately 6% in recent years (refer to Figure 2F).

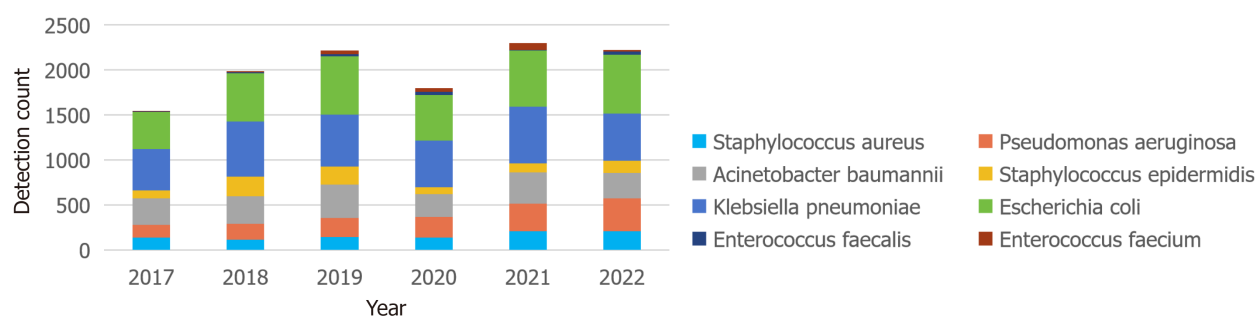
When compared with *A. baumannii*, *P. aeruginosa* exhibited lower antimicrobial resistance in susceptibility tests. Over the past 8 years, its resistance to imipenem fluctuated between 18.4% and 21.4%. Resistance to cephalosporins, such as cefotaxime and cefoperazone, was maintained at < 10% in the past 6 years. *P. aeruginosa* consistently demonstrated the lowest resistance to amikacin, maintaining a rate of 0.2% over the past 3 years (refer to Figure 2G).

DISCUSSION

From 2017 to 2022, the distribution and drug sensitivity of eight key pathogens, namely, *S. aureus*, *P. aeruginosa*, *A. baumannii*, *S. epidermidis*, *K. pneumoniae*, *E. coli*, *E. faecalis*, and *E. faecium*, were continuously monitored and analyzed. The empirical use of penicillin has culminated in widespread drug resistance in the detected *S. aureus* strains[3]. Although the detection rate of MRSA is lower than that in similar studies conducted previously[4,5], the overall resistance rate of *S.*

Table 1 The proportion of multi-drug resistant bacteria

Year	Count of multi-drug resistant bacteria	Count of key surveillance strains	Percentage of multi-drug resistant bacteria
2017	438	1547	28.31%
2018	447	1980	22.58%
2019	459	2215	20.72%
2020	455	1797	25.32%
2021	542	2298	23.59%
2022	526	2225	23.64%



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Figure 1 Trend in key pathogens' distribution from 2017-2022.

aureus agrees with national bacterial resistance monitoring data[6,7]. Hospitals need to pay attention to the detection of MRCNS. Research on hospital-acquired Methicillin-resistant non-staphylococci indicates that infections are concentrated in the lower respiratory tract and surgical sites. Clinical departments should strengthen disinfection and prevention measures. Patients with two consecutive MRCNS detections should be placed under preventive isolation to mitigate the spread of hospital-acquired infections[8]. Coagulase-negative staphylococci possess fewer virulence properties than *S. aureus*, which results in different disease spectrums. Hence, host susceptibility becomes significantly more critical[9].

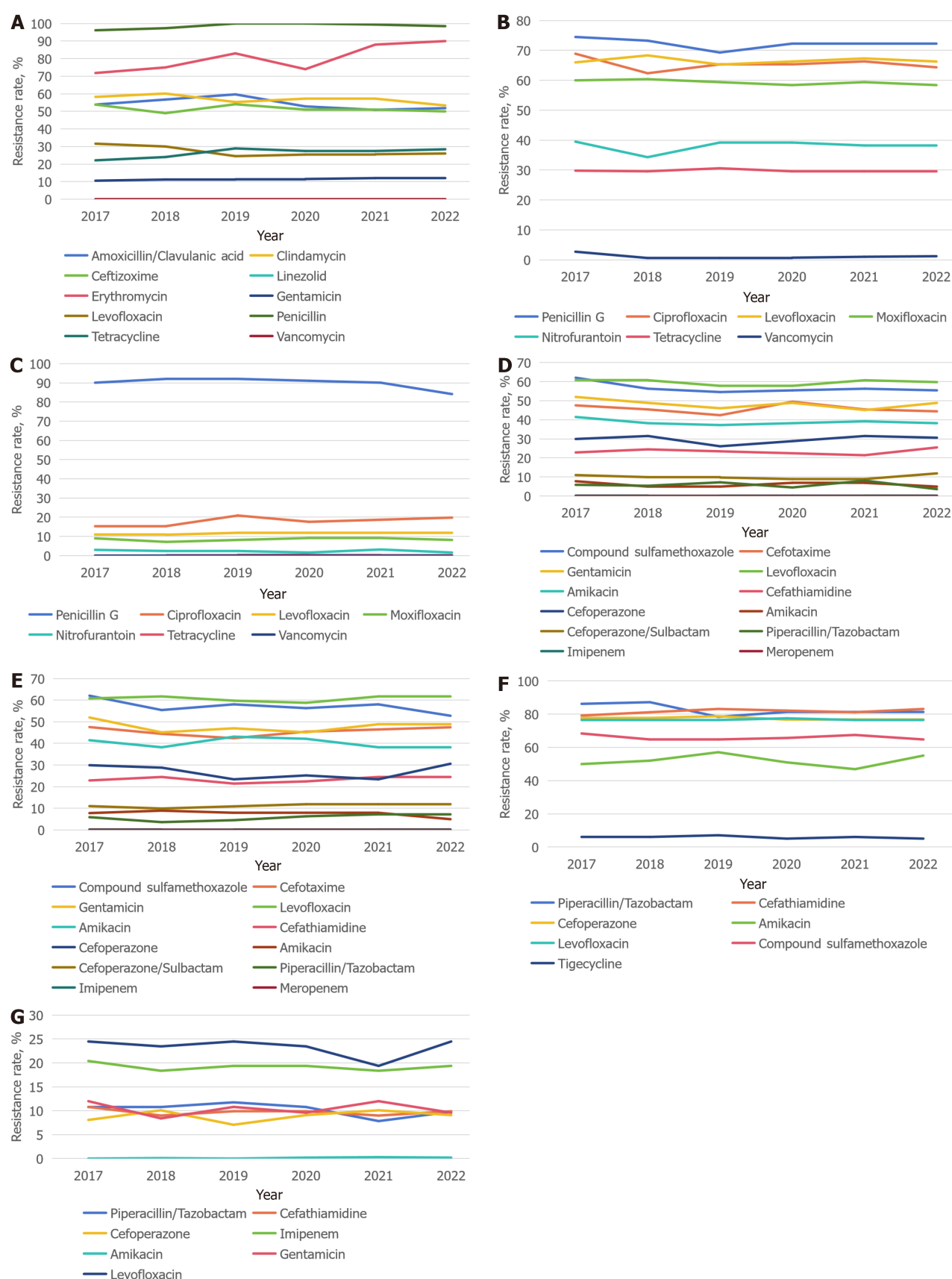
Of the eight key surveillance strains, the total number of *E. faecium* and *E. faecalis* identified in our hospital is relatively low. A few vancomycin-resistant enterococci (VRE) have been detected over the past 6 years. For VRE, experts suggest selecting the corresponding antibiotic based on the results of the strain's drug sensitivity test and combining antibiotics with different mechanisms of action to avoid resistance[10-12].

The unique cell wall structure of gram-negative bacteria makes them more likely to acquire drug resistance than gram-positive bacteria[13,14]. *E. coli* and *K. pneumoniae* are the top two key surveillance strains. Our hospital's *K. pneumoniae* drug resistance situation is serious, which mirrors the conclusions of drug resistance analysis conducted by other tertiary hospitals[15]. The resistance rates to gentamicin, cefotaxime, and the compound sulfamethoxazole exceed 50%. Cefoperazone/sulbactam and piperacillin/tazobactam are viable alternatives to treat infections caused by drug-resistant bacteria, but their adverse reactions warrant the special attention of clinical doctors and pharmacists[16,17].

The increase in the antibiotic resistance rate of *A. baumannii* isolates has altered the epidemiology of hospital-acquired severe infections. A systematic review has identified that carbapenem-resistant and multidrug-resistant *A. baumannii* account for 65% and 59%, respectively, of all hospital-acquired infections among patients admitted to the intensive care unit in Southeast Asia[18]. Of the key surveillance strains in our hospital, *A. baumannii* also exhibited a relatively high overall resistance rate. Clinically, strategies to handle the primary drug resistance of isolates are limited, and the main alternative is to combine polymyxin with tigecycline, a tetracycline derivative[19]. Our hospital has detected a few tigecycline-resistant strains, which warrant clinicians' attention.

The global burden of antibiotic resistance is high in clinical isolates of *P. aeruginosa*[20]. Nonetheless, national monitoring data should be interpreted with caution because local resistance rates vary greatly and are closely related to local antibiotic usage patterns and patient types. The resistance rate of *P. aeruginosa* detected in our hospital is relatively low. An observational study found that the drug resistance risk was the lowest for cefoperazone and the highest for imipenem in patients treated with a single antipseudomonal agent[21]. This finding is consistent with the conclusions drawn from the drug resistance rate detected in our hospital.

The present study, while providing valuable insights into bacterial strain distribution and antibiotic sensitivity over a six-year period in a single hospital, is subject to several limitations. First, the geographic scope of the research is limited to one hospital, potentially constraining the generalizability of the findings. Second, the methods employed, including the use of the VITEK 2 compact analyzer for bacterial identification and WHONET5.6 software for statistical analysis, may have inherent limitations in terms of accuracy and analytical capabilities. Third, although the study spans six years, bacterial resistance patterns can evolve rapidly, rendering the data less applicable in the future. Fourth, the absence of a control group for comparative analysis poses a limitation in the interpretative strength of the results. Additionally, the



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Figure 2 Analysis of antimicrobial resistance trends for key pathogens from 2017 to 2022. A: Trend in *Staphylococcus aureus* resistance rate from 2017 to 2022; B: Trends in *Enterococcus faecium* resistance rate from 2017 to 2022; C: Trends in *Enterococcus faecalis* resistance Rate from 2017 to 2022; D: Trends in *Escherichia coli* resistance rate from 2017 to 2022; E: Trends in *Klebsiella pneumoniae* resistance rate from 2017 to 2022; F: Trends in *Acinetobacter baumannii* drug resistance from 2017 to 2022; G: Trends in *Pseudomonas aeruginosa* drug resistance from 2017 to 2022.

possibility of human error or subjectivity in interpreting cultures and tests cannot be ruled out. Financial constraints may have also influenced the comprehensiveness of the study, and any gaps or omissions in the data further limit the scope of our conclusions.

CONCLUSION

Collection of samples from the entire hospital and summarizing the detection volume and drug sensitivity results of key strains can serve as a reference for the clinical use of antibiotics. Over the past 6 years, the antibiotic resistance rate in our hospital has remained relatively stable, with no large-scale drug-resistant strain outbreak. The findings of hospital-acquired infection management and the rational use of antibiotics are the result of collaboration among clinical departments, microbiology laboratories, pharmacy departments, hospital-acquired infection management departments, and medical affairs. The ultimate goal is to reduce patient infection risk, prevent antibiotic abuse, and curb superbug production from multiple perspectives, such as infection prevention and diagnosis, rational use of antibiotics, and long-term monitoring.

ARTICLE HIGHLIGHTS

Research background

This research focuses on the critical public health issue of bacterial resistance due to prevalent antimicrobial drug use. The study's objective is to understand the prevalent bacterial strains and their resistance patterns within a hospital setting. Advanced analytical tools and software were employed for comprehensive analysis. This initiative aims to guide clinicians in effective antibiotic selection, addressing the growing concern of antimicrobial resistance.

Research motivation

The motivation behind this research is the urgent need to address the escalating problem of bacterial resistance in hospitals. By understanding the prevalent strains and their antibiotic resistance profiles, this study provides essential insights to clinicians. The findings assist in making informed decisions on antibiotic usage, contributing significantly to managing antimicrobial resistance effectively.

Research objectives

The main goal of this research is to identify prevalent bacteria in hospitals and assess their antibiotic resistance profiles. The research focuses on key strains and evaluates their resistance to common antibiotics, aiming to guide clinical antibiotic selection. The establishment of a regular reporting system is also a crucial objective, ensuring the continuous monitoring of resistance data to aid clinical decisions.

Research methods

The study involves collecting specimens from varied sources within the hospital, utilizing the VITEK 2 compact analyzer for bacterial identification and antibiotic sensitivity testing. WHONET5.6 software facilitated effective data analysis and interpretation. The methodologies ensured accurate and reliable findings, providing critical insights for appropriate antibiotic selection in clinical practice.

Research results

The study identified 12062 bacterial strains, revealing diverse resistance patterns among them. Notable findings include *Staphylococcus aureus*'s resistance to penicillin and *Pseudomonas aeruginosa*'s minimal resistance to certain antibiotics. Regular reporting and monitoring of these strains and their resistance dynamics are conducted to continually inform and guide clinical antibiotic selection within the hospital.

Research conclusions

The findings of this study disclose significant insights into bacterial resistance within a hospital. It outlines specific resistance patterns of various bacteria, emphasizing the importance of regular reporting and monitoring. These conclusions are pivotal in guiding clinicians in optimizing antibiotic selection and contribute to the broader goal of managing antimicrobial resistance effectively.

Research perspectives

This study underscores the need for continuous surveillance of antibiotic resistance and encourages further research into the mechanisms behind resistance development. Investigating the effects of interventions and focusing on collaborative efforts to implement effective infection control measures are pivotal. Long-term studies and public awareness campaigns are essential for developing guidelines and promoting responsible antibiotic usage, aiming to curb the spread of bacterial resistance.

FOOTNOTES

Author contributions: Li ZY proposed the concept of this study; Yang D has contributed to data collection and formal analysis; Li ZY and Hao CH participated in the research; Hao CH has contributed to these methods; Li ZY, Yang D, and Hao CH validated this study; Yang D and Li ZY contributed to the visualization of this study; Li ZY drafted the first draft; Li ZY, Yang D, and Hao CH jointly reviewed and edited the manuscript.

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