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Analysis of Pathogen Distribution and Drug Resistance Trends in Malignant Hematologic Disease Patients at a Tertiary Hospital in Jingzhou City from 2021 to 2025

Yongfeng Zhao[1,*], Ying Liu[1], Ying Zhu[1], Min Chen[2]

[1]*Department of Hematology, The First People's Hospital of Jingzhou, Jingzhou, Hubei, China*
[2]*Department of Pharmacy, The First People's Hospital of Jingzhou, Jingzhou, Hubei, China*
**Corresponding author: Yongfeng Zhao, zhaoyongfeng2529@163.com*

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Abstract: This study aims to investigate the pathogen distribution, antimicrobial resistance profiles, and risk factors for multidrug-resistant (MDR) infections in patients with malignant hematologic diseases, so as to inform empirical therapeutic decisions. A retrospective analysis of 168 infected patients (168 isolates) was performed. Susceptibility was tested by disc diffusion or automated systems per CLSI. Infection sites, pathogen profiles, resistance rates, and MDR detection were assessed. Univariate and multivariate logistic regression identified MDR risk factors, with ROC curve evaluation. The most frequent infection sites were anal swabs (32.7%) and urinary tract (30.4%), followed by bloodstream (13.7%) and respiratory tract (13.1%). The top four pathogens were Escherichia coli (E. coli) (41.7%), Enterococcus faecalis (11.3%), Staphylococcus epidermidis (7.7%), and Klebsiella pneumoniae (7.7%). E. coli exhibited high resistance to sulfonamides, levofloxacin, cefazolin, and cefoperazone-sulbactam (64.3-71.4%), but remained highly susceptible to meropenem (resistance 4.29%). MRSA was detected in 6.7% and was susceptible to vancomycin, linezolid, and tigecycline. The overall MDR detection rate was 30.36%, with ESBL-producers accounting for 88.2%. Multivariate analysis revealed that lower pre-infection lymphocyte count was an independent protective factor against MDR infection (OR = 0.170, 95% CI: 0.032–0.891, $P = 0.002$), with an AUC of 0.793. Infections in malignant hematologic patients mainly involve gastrointestinal and urinary tracts, with E. coli being the most common and carbapenem-sensitive pathogen. MDR prevalence is high, and lymphocytopenia is an independent risk factor. Clinicians should prioritize susceptibility testing and tailor antibiotics accordingly, especially in patients with low lymphocyte counts.

1. Introduction

Patients with malignant hematologic disorders—including leukemia, lymphoma, and multiple myeloma—frequently experience profound immune dysfunction, driven both by the disease itself and by intensive treatments such as chemotherapy, radiotherapy, and hematopoietic stem cell

transplantation. This immunosuppressed state predisposes them to a wide range of infections, particularly bacterial and fungal, which are among the most common and serious complications. Such infections not only complicate clinical management and escalate healthcare costs but also remain a leading cause of mortality in this population [1,2].

Over recent years, the extensive use of broad-spectrum antibiotics and antifungal agents has significantly shifted the distribution and resistance profiles of pathogenic microorganisms. The emergence and rapid spread of multidrug-resistant (MDR) and extensively drug-resistant (XDR) strains have posed formidable therapeutic challenges, especially in hematologic malignancy patients who require prolonged immunosuppressive therapy and are thus vulnerable to drug-resistant pathogens [3]. Current evidence reveals that Gram-negative bacteria, predominantly Escherichia coli, Klebsiella pneumoniae, and Pseudomonas aeruginosa, are the most frequently isolated organisms in these patients. Importantly, these pathogens display considerable resistance to penicillins and cephalosporins, with susceptibility rates declining steadily [4,5]. Hence, a clear and up-to-date understanding of the local epidemiological trends and resistance patterns is crucial for guiding empirical therapy, refining infection prevention measures, and ultimately improving patient prognosis [6,7].

The present study was designed to investigate the epidemiological features of pathogenic infections, the distribution of common pathogens, and their contemporary antimicrobial resistance status in patients with malignant hematologic diseases. The findings are expected to serve as a practical reference for clinicians and to offer novel insights and strategies for infection control in this high-risk cohort, with the ultimate goal of reducing infection-related mortality and enhancing patients' quality of life.

2. Materials and Methods

2.1 Study Subjects

Patients with malignant hematologic diseases who were hospitalized in the Department of Hematology at The First Affiliated Hospital of Yangtze University from January 2021 to December 2025 were selected as the study subjects.

2.1.1 Inclusion Criteria

Patients were included if they met the following criteria: (1) a confirmed diagnosis of malignant hematologic disease (including acute leukemia, lymphoma, multiple myeloma, etc.) based on pathological or cytological evidence; (2) age of 18 years or older; and (3) development of infection-related signs or symptoms (such as fever, cough, or diarrhea) during hospitalization, with a definitive infectious etiology established by bacterial culture or molecular testing.

2.1.2 Exclusion Criteria

Patients were excluded if they met any of the following conditions: (1) severe impairment of major organ function (including cardiac, hepatic, or renal dysfunction); (2) incomplete clinical documentation, e.g., absence of microbiological findings or antimicrobial susceptibility testing results; or (3) a documented, unresolved infection existing before hospitalization.

2.2 Research Methods

2.2.1 Data Collection

The following clinical data were retrospectively collected from the hospital′ s electronic medical record system for each enrolled patient. General information included age, sex, body mass index (BMI), and history of underlying comorbidities. Disease-related variables comprised the type of hematologic malignancy (e.g., acute leukemia, lymphoma, multiple myeloma), disease status at admission (initial treatment, remission, or relapsed/refractory), and total disease duration. Treatment-related data encompassed chemotherapy regimens, history of hematopoietic stem cell transplantation, use of glucocorticoids or immunosuppressants, and recent antibiotic exposure (within 30 days prior to infection), with details on antibiotic types and duration.

Infection-related data covered the site of infection (respiratory tract, bloodstream, gastrointestinal tract, urinary system, or skin/soft tissues), associated clinical manifestations, and laboratory parameters (complete blood count, C-reactive protein, procalcitonin). Clinical outcomes were categorized as cured, improved, unchanged, or deceased. Etiological data consisted of bacterial culture and antimicrobial susceptibility testing results from various clinical specimens, including sputum, blood, stool, urine, and wound secretions.

2.2.2 Data Verification

The data collection process was conducted jointly by two investigators. One investigator was responsible for data extraction and entry, while the other performed cross-validation of the data, including verification of completeness, logical consistency, and compliance with original medical records. In cases of data inconsistencies or uncertainties, both investigators collaborated to discuss the matter and refer back to the original records for confirmation, ensuring the authenticity, accuracy, and reliability of the data.

2.2.3 Pathogen Identification and Drug Sensitivity Testing

Bacterial identification was performed using a fully automated microbial identification system (e.g., VITEK 2 Compact or equivalent). Antimicrobial susceptibility testing was carried out by the Kirby–Bauer disc diffusion method or broth microdilution, and the results were interpreted according to the current Clinical and Laboratory Standards Institute (CLSI) guidelines. Multidrug-resistant (MDR), extensively drug-resistant (XDR), and pandrug-resistant (PDR) strains were defined in accordance with international expert consensus recommendations.

2.2.4 Statistical Analysis

Data analysis was performed using SPSS 23.0. Categorical variables were presented as frequencies and percentages, while continuous variables were first tested for normality; normally distributed data were expressed as mean ± standard deviation (SD), and non-normally distributed data as median with interquartile range (IQR). For between-group comparisons, the chi-square test was used for qualitative variables. For quantitative variables, the independent-samples t-test was employed for normal data with homogeneous variances, Welch's corrected t-test for normal data with unequal variances, and the Mann–Whitney U test for non-normal distributions. To identify risk factors for multidrug-resistant infection, univariate analysis was first conducted with a threshold of $P < 0.10$ for variable inclusion; subsequently, selected variables were entered into a multivariate logistic regression model using a stepwise forward selection approach, with odds ratios (OR) and 95%

confidence intervals (CI) calculated, and $P < 0.05$ considered statistically significant.

3 Results

3.1 Distribution Characteristics of Pathogenic Bacteria in Patients with Malignant Hematologic Diseases

A total of 168 patients with malignant hematologic diseases complicated by infections were enrolled, from whom 168 pathogenic strains were isolated. The most common infection sites were anal swabs (55 cases, 32.7%), followed by the urinary tract (51 cases, 30.4%), bloodstream (23 cases, 13.7%), and respiratory tract (22 cases, 13.1%). Regarding pathogen distribution, Escherichia coli was the most frequently isolated organism (70 strains, 41.7%), followed by Enterococcus faecalis (19 strains, 11.3%), Staphylococcus epidermidis (13 strains, 7.7%), and Klebsiella pneumoniae subsp. pneumoniae (13 strains, 7.7%). Detailed distribution is shown in Figure 1.

Among the 168 infected patients, 24 (14.3%) were diagnosed with acute myeloid leukemia, 16 (9.5%) were on maintenance chemotherapy for other malignancies, 10 (6.0%) had multiple myeloma, and 5 (3.0%) had chronic myeloid leukemia.

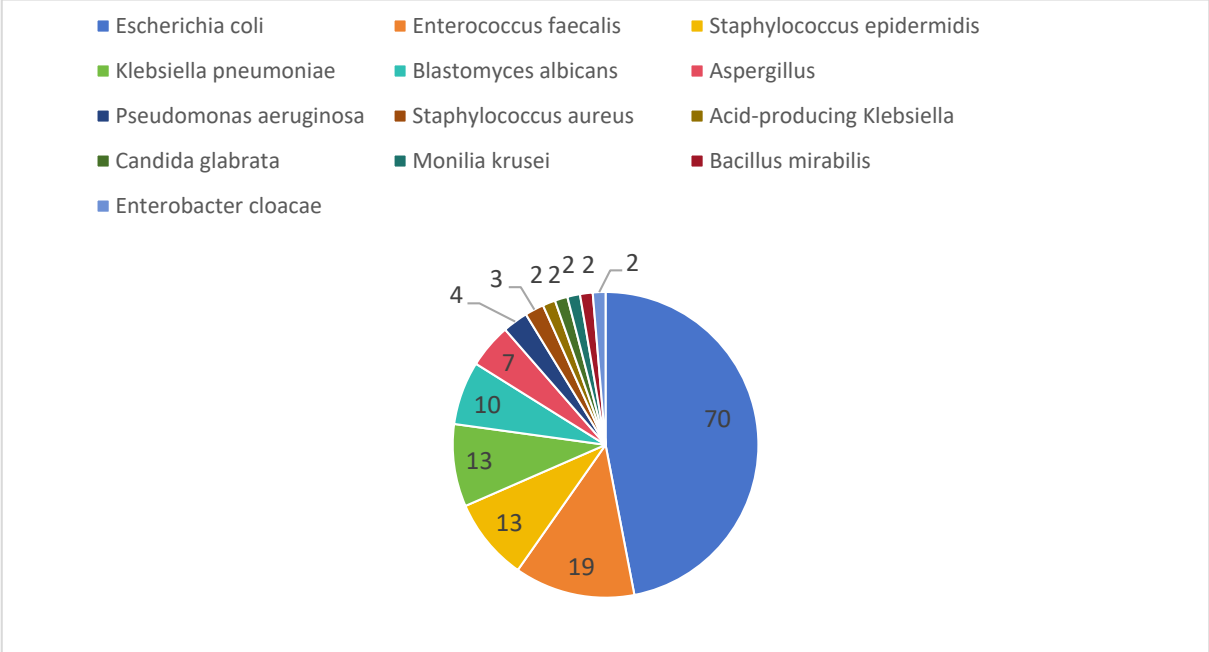

Figure 1 Distribution Map of Pathogenic Bacteria

3.2 Analysis of Drug Resistance among Major Pathogenic Microorganisms

Among the isolated Gram-negative bacteria, Escherichia coli showed the highest resistance rate to compound sulfonamides (71.43%), followed by levofloxacin (70%), cefazolin (65.71%), and cefoperazone-sulbactam (64.29%), whereas the resistance rate to meropenem was the lowest (4.29%). Regarding Gram-positive cocci, methicillin-resistant Staphylococcus aureus (MRSA) was detected at a rate of 6.7%, and all MRSA isolates remained susceptible to vancomycin, linezolid, and tigecycline (resistance rate: 0%). In contrast, MRSA exhibited resistance rates of 83.3% to ciprofloxacin, 23.3% to gentamicin, and only 3.3% to rifampicin.

3.3 Risk Factor Analysis of Multidrug-Resistant Bacteria

Among all isolated strains, 51 MDR strains were detected, accounting for 30.36%; 45 ESBL-producing strains were identified, representing 88.2%; 2 D-test-positive strains were detected, yielding a detection rate of 3.9%; 2 MRSA strains were identified, also at a detection rate of 3.9%; and 1 CRE strain and 1 β-lactamase-positive strain were each detected, with a combined detection rate of 2.0%.

Univariate analysis results showed that the pre-detection lymphocyte count levels were 0.46×10^9/L in patients with multidrug resistance and 0.73×10^9/L in those with sensitivity, with a statistically significant difference between the two groups (P=0.038). The pre-detection PCT levels were 0.24 ng/mL and 0.50 ng/mL respectively, also demonstrating a statistically significant difference (P=0.023) (Table 1).

Table 1 Differences in Clinical Manifestations among Patients with Varying Levels of Drug Resistance

	Total	Non-resistant (n=117)	Multidrug resistance (n=51)	P
Sex				
female	99(58.9)	67(57.3)	32(62.7)	0.507
male	69(41.1)	50(42.7)	19(37.3)	
Age	67(52,74)	69(49,74)	60(54,70)	0.109
Chemotherapy				
No	92(54.8)	62(53.0)	30(58.8)	0.485
Yes	76(45.2)	55(47.0)	21(41.2)	
Transplant				
No	164(97.6)	113(96.0)	51(100)	0.181
Yes	4(2.4)	4(3.4)	0(0)	
Lymphocytes	0.67(0.31,1.15)	0.73(0.33,1.24)	0.46(0.28,0.80)	0.038
Monocytes	0.37(0.16,0.59)	0.38(0.16,0.57)	0.35(0.17,0.59)	0.762
Platelets	95(24,180)	91(21,170)	115(30,211)	0.121
Hemoglobin	83(68,105)	80(67,104)	90(75,106)	0.148
CRP	38.71(10.60,87.59)	41.65(13.00,91.72)	36.42(9.59,62.34)	0.574
PCT	0.46(0.23,1.00)	0.50(0.32,1.35)	0.24(0.15,0.63)	0.023
IL-6	29.22(12.35,105.80)	45.69(16.40,114.05)	22.68(8.94,102.73)	0.471

3.4 Independent Risk Factors for Combined Multidrug-Resistant Bacterial Infections

Table 2 Multivariate Logistic Regression Analysis for Malignant Hematologic Diseases Complicated by Multidrug-Resistant Bacterial Infections

						95.0% CI	
	B	S.E.	Wald	P	Exp(B)	Lower	Upper
leukomonocyte	-1.774	0.846	4.397	0.036	0.170	0.032	0.891
PCT	-0.921	0.657	1.963	0.161	0.398	0.110	1.444
chemotherapy	-1.087	0.834	1.701	0.192	0.337	0.066	1.727
transplant	-19.500	21,188.488	0.000	0.999	0.000	0.000	

Variables with $P < 0.05$ in the univariate analysis, along with prior chemotherapy and transplantation status, were entered into the multivariate logistic regression model. The results showed that the pre-infection lymphocyte count was an independent protective factor against

multidrug-resistant bacterial infections in patients with malignant hematologic diseases (OR = 0.170, 95% CI: 0.032–0.891; see Table 2). The area under the ROC curve (AUC) for this model was 0.793 (P = 0.002) (Figure 2).

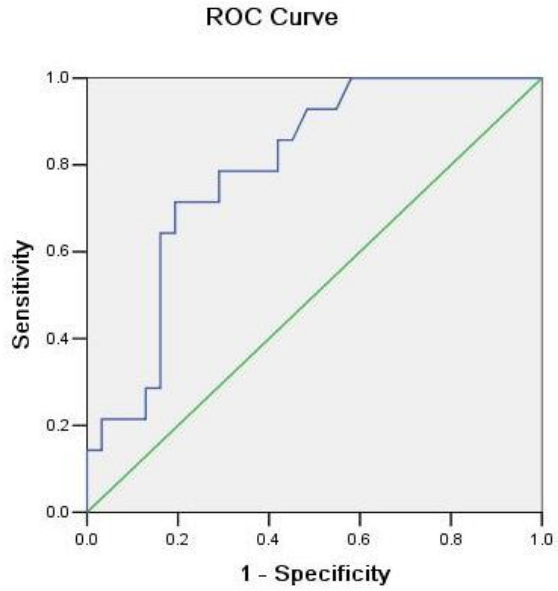

Figure 2 ROC Curve of the Multivariate Logistic Regression Analysis Model

4. Discussion

In this cohort of patients with malignant hematologic diseases complicated by infections, the gastrointestinal tract (anal swabs) was the most common site of infection, accounting for 55 cases (32.7%), followed by the urinary tract (51 cases, 30.4%), bloodstream (23 cases, 13.7%), and respiratory tract (22 cases, 13.1%). This distribution differs from the respiratory tract predominance reported in many other studies, which may be attributable to variations in underlying disease profiles, antibiotic exposure histories, and specimen collection practices at our center. Among the 168 isolated pathogenic strains, Escherichia coli was the most prevalent (70 cases, 41.7%), followed by Enterococcus faecalis (19 cases, 11.3%), Staphylococcus epidermidis (13 cases, 7.7%), and Klebsiella pneumoniae subsp. pneumoniae (13 cases, 7.7%). The high frequency of E. coli in urinary and gastrointestinal specimens underscores the importance of monitoring intestinal colonization patterns and implementing preventive measures against catheter-associated infections.

Regarding disease type distribution, the majority of patients had acute myeloid leukemia (24 cases, 14.3%) or were receiving maintenance chemotherapy for other malignancies (16 cases, 9.5%), followed by multiple myeloma (10 cases, 6.0%) and chronic myeloid leukemia (5 cases, 3.0%). Since no stratified analysis was performed to examine differences in pathogenic bacteria across disease types, we cannot conclude that significant variations exist among different hematologic disorders. Nonetheless, individualized empirical anti-infective therapy should be tailored according to each patient's immune status and prior medication history [8-13].

As the most prevalent Gram-negative bacterium, E. coli exhibited the highest resistance rate to compound sulfonamides (71.43%), followed by levofloxacin (70%), cefazolin (65.71%), and cefoperazone-sulbactam (64.29%), highlighting the need for cautious empirical use of these agents. However, E. coli remained highly susceptible to meropenem (resistance rate: 4.29%), consistent with trends reported by domestic bacterial resistance surveillance networks in recent years. Among Gram-positive bacteria, MRSA was detected in 6.7% of cases (2 strains), a rate lower than that

reported in some hematology-focused studies. All isolated staphylococci were susceptible to vancomycin, linezolid, and tigecycline (resistance rate: 0%), indicating that these agents remain viable options for empirical treatment of severe Gram-positive infections. Additionally, MRSA showed high resistance to ciprofloxacin (83.3%) and gentamicin (23.3%), but only 3.3% to rifampicin, providing valuable insights for combination therapy strategies.

A total of 51 multidrug-resistant (MDR) strains were identified, with a detection rate of 30.36%. Among these, ESBL-producing strains accounted for 88.2% (45/51). Two strains each were positive for the D-test and MRSA (both 3.9%), while one strain each was positive for CRE and β-lactamase (both 2.0%). ESBL-producing E. coli was the predominant MDR type. No extensively drug-resistant (XDR) or pandrug-resistant (PDR) strains were detected, possibly due to the limited sample size or stringent antimicrobial stewardship policies at our hospital. The high MDR prevalence underscores the urgent need to enhance rational antibiotic use and conduct regular resistance surveillance in patients with hematologic malignancies [14-15].

Univariate analysis revealed that the pre-infection lymphocyte count in the MDR group (0.46×10^9/L) was significantly lower than that in the susceptible group (0.73×10^9/L; $P = 0.038$), and pre-infection PCT levels also differed significantly between the two groups (0.24 vs. 0.50 ng/mL; $P = 0.023$). Multivariate logistic regression incorporating variables with $P < 0.05$ along with prior chemotherapy and transplantation status demonstrated that the pre-infection lymphocyte count was an independent protective factor against MDR infection (OR = 0.170, 95% CI: 0.032–0.891, $P = 0.002$), indicating that lower lymphocyte counts are associated with higher MDR infection risk. The ROC curve yielded an area under the curve (AUC) of 0.793 ($P = 0.002$), demonstrating adequate discriminative power.

Low lymphocyte counts reflect profound suppression of cellular immune function, commonly observed after intensive chemotherapy, in relapsed/refractory states, or when the disease itself involves the immune system. Such patients often exhibit compromised intestinal mucosal barrier integrity, increased susceptibility to opportunistic pathogen translocation, and prolonged hospitalization with extensive antibiotic exposure, collectively predisposing them to MDR infections. Notably, this study did not identify associations between traditional risk factors—such as age, relapsed/refractory status, prior carbapenem use, or duration of agranulocytosis—and MDR infections, likely due to limited sample size or incomplete data collection. Future investigations with larger cohorts are warranted to further validate these findings [16-17].

Several limitations of this study should be acknowledged. First, it was a single-center retrospective study with a relatively small sample size, which may introduce selection bias. Second, the pathogen positivity rate was low in some patients, potentially underestimating the prevalence of infections caused by rare pathogens. Third, different susceptibility testing methods were employed, which may introduce methodological variability. Fourth, the impact of antimicrobial dosage and treatment duration on resistance development was not analyzed. Fifth, the absence of long-term follow-up data precludes evaluation of the effect of MDR infections on overall survival. These findings should be further validated through multicenter, prospective studies.

5. Conclusion

In conclusion, among patients with malignant hematologic diseases complicated by infections in this cohort, the gastrointestinal and urinary tracts were the most common infection sites, and Escherichia coli was the predominant pathogen. E. coli remained highly susceptible to carbapenems but exhibited considerable resistance to cephalosporins and quinolones. The overall detection rate of multidrug-resistant strains was 30.36%, with ESBL-producers accounting for the majority. Notably, a low pre-infection lymphocyte count was identified as an independent protective

factor against MDR infection. Clinically, closer attention should be paid to patients with reduced lymphocyte counts, and carbapenem antibiotics should be used judiciously based on susceptibility testing results to optimize therapeutic outcomes.

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