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Original Article

Distribution and drug resistance of pathogens isolated from patients with hematological malignancies in three-year period

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Abstract

Objective: This study aimed to retrospectively analyze the 3-year findings of bacterial and fungal pathogens isolated from infections in patients with hematological malignancies.

Methods: A retrospective analysis of 158 patients with hematological malignancies treated between January 2015 and December 2017 in Okmeydanı Training and Research Hospital, Istanbul, Turkey. A total of 3374 non-consecutive blood samples (n=1954) from 158 patients, urine samples (n=1024), wound swabs (n=94), respiratory samples (n=87), and other samples (CSF, body fluids, etc.) (n=215) were collected.

Results: Pathogen growth was detected in 6% (203/3374) of the samples. The most frequently isolated pathogens are coagulase-negative *staphylococci* (CNS, 20%), *E. coli* (19%), *Klebsiella sp*. (17%), and yeasts (16%), followed by *Pseudomonas sp*., *Acinetobacter sp*. and *Enterococcus sp*. (7%, 6%, and 6%, respectively). Candida species were dominant in fungal isolates (26/32; 81.2%). The most commonly detected antibiotic resistance patterns and organisms are carbapenem-resistant *Acinetobacter sp.* (92%), methicillin-resistant CNS (83%), carbapenem-resistant *Klebsiella sp*. (65%), MRSA (57%), and vancomycin-resistant *Enterococci* (VRE, 42%).

Conclusion: Bloodstream infections accounted for more than half of all infection episodes. Periodic examination of the clinical and microbiological profiles of infections developing in patients with malignancy is essential for successful treatment management.

Keywords: Antimicrobial resistance, hematological malignancy, infection.

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INTRODUCTION

Patients with hematological malignancies frequently suffer chemotherapy-related neutropenia, mucositis, and disease-related immunosuppression. Despite improvements in the treatment modalities, including effective empirical broad-spectrum antibiotics, antifungals, and cell-stimulating factors, infections represent a major threat for this patient population and contribute to morbidity and mortality. Infections are related to a prolonged hospital stay, increased health-system costs, and compromised efficacy of chemotherapeutics in these patients (1, 2). Previous epidemiological studies have shown a significant change in the spectrum of pathogens isolated from febrile neutropenic patients. Forty years ago Gram-negative bacteria were the most frequent organisms, then Gram-positive cocci were outweighed. In recent years, antibiotic-resistant gram-negative bacilli are become the predominated causative agents in febrile neutropenia. The empiric therapy decision should be based on the information on geographically prevalent pathogens and their susceptibility patterns, potential infection sites, patients' characteristics, and the cost of treatment regimens (3).

MATERIALS AND METHODS

We conducted a retrospective analysis of 158 patients with hematological malignancies treated at the Okmeydanı Research and Training Hospital, Istanbul, Turkey between January 2015 and December 2017. Clinical specimens were collected and bacterial and fungal cultures were performed in case of fever or other signs of infection if indicated by the physicians. When cultures revealed positive growth, pathogen identification was performed with conventional methods (such as colony morphology, Gram stain characteristics, and biochemical reactions) and an automated system (BD Phoenix 100, Becton Dickinson, USA). The same automated analyzer was used for antibiotic susceptibility testing.

Table 1. Distribution of clinical specimens and pathogens

Pathogen	Clinical specimens					
	Blood	Urine	Skin/soft tissue	Respiratory	Other	Total
E.coli	19	16	2	0	1	38
Klebsiella sp.	22	8	3	1	0	34
Acinetobacter sp.	6	2	3	1	0	12
Pseudomonas sp.	10	1	4	0	0	15
S.aureus	5	1	1	0	0	7
CNS*	36	0	0	0	5	41
Enterococcus sp.	6	6	0	0	0	12
Fungi	12	11	0	6	3	32
Others	5	2	1	1	3	12
Total	121	41	14	9	12	203
Culture negative	1954	1024	94	87	215	3374

*Coagulase negative *Staphylococci*

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RESULTS

In a 3-year period, a total of 3374 non-consecutive specimens were collected from 158 patients. Specimen distribution was as follows: blood samples (n=1954), urine samples (n=1024), wound swabs (n=94), respiratory samples (n=87), other samples (CSF, body fluids, etc.) (n=215). Pathogen growth was revealed in 6% (203/3374) of specimens; growth in blood and urine samples were predominant (80%; 162/203). The most common isolated pathogens were coagulase-negative *staphylococci* (CNS, 20%), *E. coli* (19%), *Klebsiella sp.* (17%), and yeasts (16%) followed by *Pseudomonas sp.*, *Acinetobacter sp*. and *Enterococcus sp*. (7%, 6%, and 6%, respectively) (Table 1). Candida species were predominant (26/32; 81.2%) in fungal isolates. Most frequently detected antibiotic resistance patterns and organisms were carbapenem-resistant *Acinetobacter sp*. (92%), methicillin-resistant CNS (83%), carbapenem-resistant *Klebsiella sp.* (65%), MRSA (57%), and vancomycin-resistant *Enterococci* (VRE, %42) (Table 2). The distribution of clinical specimens and pathogens (numbers and percentages) is presented in Figure 1.

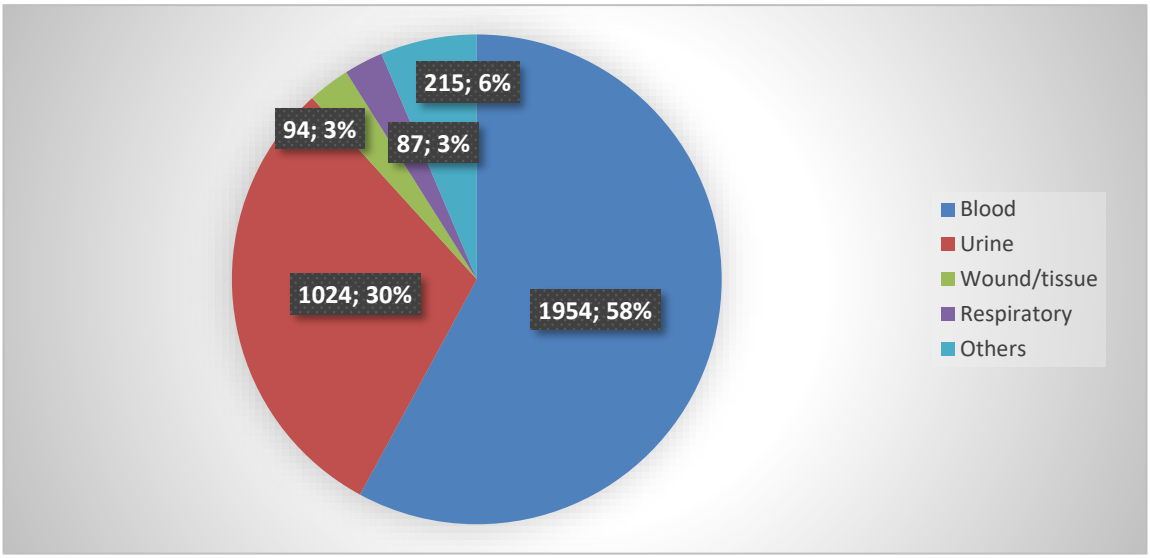

Figure 1: Distribution of clinical specimens and pathogens (numbers and percentages)

Table 2. Frequent antibiotic resistance patterns and pathogens

Antibiotic-resistant pathogen	Rate
ESBL (+) *E.coli* (n:18)	47%
ESBL (+) *Klebsiella sp.* (n:4)	12%
Carbapenem resistant *Klebsiella sp.* (n:22)	65%
Carbapenem resistant *Acinetobacter sp*. (n:11)	92%
Carbapenem resistant *Pseudomonas sp.* (n:5)	33%
Methicillin-resistant *S. aureus* (n:4)	57%
Methicillin-resistant CNS* (n:34)	83%
Vancomycin-resistant *Enterococcus sp.* (n:5)	42%

*Coagulase-negative Staphylococci

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DISCUSSION

Infection in cancer patients is one of the most important complications. Pathogens that can cause infection in immunocompromised cancer patients are quite different. In this study, we retrospectively analyzed the bacterial and fungal pathogens isolated from infections in patients with hematological malignancies over a 3-year period. Bloodstream infections (BSI) accounted for more than half of all infection episodes. In a similar study published in 2014, BSIs were found to be predominant compared to other sites and the rate of Gram-negative organisms (47%) was higher than Gram-positive pathogens (40%). Our results are concordant with the detection rates of Gram negatives and gram positives at 51% and %32, respectively. They have isolated fungal pathogens in a higher percentage (25.5%) compared to our results (15.7%) (4). Demirkaya et al. published a study evaluating pathogens isolated from immunocompromised patients and their antibiotic susceptibility. E.coli is detected in the first rank (30.8%) followed by CNS (15.1%). We isolated these two pathogens at equal rates such as 20.2% for CNS and 18.7% for *E.coli*. Regarding antibiotic resistance, they reported that 51% of the *E. coli* isolates were extended-spectrum β-lactamase positive, and the ratio of multiple drug resistant (MDR) isolates among *Acinetobacter sp.* was 73% (5). Our results indicated a similar ESBL producer rate in *E.coli* isolates (47%) but carbapenem resistance in *Acinetobacter sp.* is much higher (92%). The antibiotic susceptibility and spectrum of pathogens isolated from patients with hematological malignancies are subjected to change over time as with other inflammatory and infectious diseases (6-8). Surveillance of those infections is an important task and should be performed on a regular basis. Moreover, exploring the responsible resistance mechanisms in antibiotic-resistant pathogens would be beneficial for further epidemiological analysis.

Limitations: The present research has a limitation. This study was planned as retrospectively. In our study, malignancy-related microorganisms were examined, but no classification was made according to malignancy types. In advanced studies, different treatment methods and clinical approaches can be developed by examining the microorganisms that reproduce according to the type of malignancy.

CONCLUSION

Bloodstream infections accounted for more than half of all infection episodes. Periodic examination of the clinical and microbiological profiles of infections developing in patients with malignancy is essential for successful treatment management.

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