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ORIGINAL ARTICLE

Epidemiologic Distribution of Blood Culture Isolates in University-Affiliated Hospitals in Korea: a Multicenter Retrospective Study

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ABSTRACT

Background: **Blood culture is the most important diagnostic method for identifying bloodstream infections and guiding empirical antimicrobial therapy. Distribution and trends of blood culture isolates provides essential epidemiological information for the effective management of bloodstream infections.**
Methods: **We analyzed blood culture data collected from 14 university-affiliated hospitals across Korea in 2023. The survey investigated the most frequently isolated bacterial and fungal species, the polymicrobial and obligate anaerobic infections.**
Results: **Across 14 participating hospitals, *Escherichia coli* was the most frequently isolated bacterial species, followed by *Klebsiella pneumoniae* and *Staphylococcus aureus*. Among fungal isolates, *Candida albicans* predominated at most institutions, followed by *Candida parapsilosis* and *Candida tropicalis*. Notably, *Candida auris* was the third most common fungal isolate (9.3%) at one hospital. Data from 10 institutions showed that the median proportion of polymicrobi-al infections was 7.3% and obligate anaerobic infections accounted for 2.1%.**
Conclusions: **Gram-negative enterobacterales predominated over gram-positive cocci. Furthermore, new multidrug-resistant pathogen, such as *C. auris*, has emerged. Continuous monitoring and analysis are necessary to identify such new threats and to supply fundamental information for directing empirical antibiotic treatment for sepsis.**
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KEYWORDS

blood culture, sepsis, Enterobacterales, *Candida*, polymicrobial infection, anaerobic infection

INTRODUCTION

Blood culture is a key diagnostic method for intravascular infections such as febrile neutropenia, fever of unknown origin, central venous catheter-related bloodstream infections, infective endocarditis, sepsis, and unexplained leukocytosis [1]. Organisms isolated from blood cultures are subjected to identification and antimicrobial susceptibility testing to provide essential in-

formation for appropriate therapy. Sepsis, in particular, is a major cause of patient mortality and morbidity, hence requires prompt treatment; therefore, empirical antimicrobial therapy guided by pathogen distribution and susceptibility data from blood cultures is directly associated with patient survival [2,3]. Regular monitoring of changes in the distribution of blood culture isolates can serve as a fundamental reference for empirical antibiotic selection, and the corresponding antimicrobial susceptibility data provide an important clinical basis for effective treatment. In this study, we aimed to analyze the distribution of blood culture isolates from university-affiliated hospitals in Korea and to identify the recent trends.

MATERIALS AND METHODS

Data on the distribution of the most frequently isolated bacterial and fungal species isolated from blood cultures in 2023, the rate of polymicrobial detection, the isolation rate of obligate anaerobes were retrospectively collected from 14 university hospitals in Korea. The participants are the clinical microbiologists and extracted data throughout the electronic medical record (EMR) system. They submitted the most common 10 bacterial species and 5 fungal species isolated from blood cultures. Also, two or more isolates from a patient, defined as polymicrobial infections, as well as obligate anaerobic infections were manually counted from the EMR data during September - December, 2023.

MedCalc software was used to conduct statistical analyses of the data collected from participating institutions (MedCalc Software Ltd., Ostend, Belgium; version 23.2.6).

This study was approved by the Institutional Review Board of Gyeongsang National University Changwon Hospital (IRB No. 2024-09-011). Data from all participating institutions were provided with informed consent from the respondents.

RESULTS

Institutions were surveyed regarding the most frequently isolated bacterial and fungal species in blood cultures throughout 2023. Seven institutions (Hospitals A - G) reported data including duplicate isolates, whereas the remaining seven (Hospitals H - N) excluded duplicates. Of all institutions, *Escherichia coli* was the most frequently isolated bacterial species, followed by *Klebsiella pneumoniae* and *Staphylococcus aureus* (Table 1). For fungal isolates, *Candida albicans* was the most common species at all but one institution, followed by *Candida parapsilosis* and *Candida tropicalis*. The proportion of *E. coli* among all bacterial isolates ranged from 12.4 - 25.6%, whereas *C. albicans* accounted for 20.0 - 54.9% of fungal isolates across institutions. Notably, *Candida auris* was the 3rd common in one hospital. We did not add up all isolates, because each institution showed wide range of different isolates numbers.

Data from 10 institutions were analyzed to assess the proportion of cases with polymicrobial growth and those with obligate anaerobic organisms. Among positive blood culture cases, the median proportion of polymicrobial detections was 7.3% (IQR, 5.5 - 8.8%), and the median proportion of cases involving obligate anaerobes was 2.1% (IQR, 1.8 - 2.6%).

DISCUSSION

The spectrum of organisms isolated from blood cultures varies across age groups, geographic regions, and healthcare settings. In adults, however, *E. coli*, *Klebsiella* spp., and *S. aureus* are consistently reported as the most prevalent pathogens [4]. Similar patterns have been observed in Korea, where *E. coli*, *K. pneumoniae*, and *S. aureus* have been identified as the predominant blood culture isolates [5]. These findings are consistent with our study, in which *E. coli* emerged as the most frequently isolated organism among the 14 participating institutions. A review of blood culture trends over the past two decades indicates that since 2005, *E. coli* has become the leading pathogen, particularly in Europe and the Asia-Pacific region [6]. According to Diekema et al., the prevalence of methicillin-resistant *S. aureus* (MRSA) increased until 2008 but has since declined, whereas vancomycin-resistant *Enterococcus* (VRE) rates began to decrease after 2012. In contrast, multidrug-resistant *Enterobacterales* have shown a continuous upward trajectory [6]. A Korean surveillance study in 2023 reported a methicillin resistance rate of 49.2% for *S. aureus* and a vancomycin resistance rate of 39.5% for *Enterococcus faecium* [5]. Resistance rates for *E. coli* to ertapenem and imipenem were relatively low at 0.7% and 0.5%, respectively, whereas *K. pneumoniae* exhibited significantly higher resistance at 5.3% and 4.6%, respectively [5]. From 2016 to 2020, MRSA and VRE rates remained relatively stable, but carbapenem-resistant *Enterobacterales* demonstrated a sustained increase [5]. More recent multicenter data from Korea in 2025 confirmed similar resistance trends among blood culture isolates, reporting MRSA rates ranging from 39.1 - 47.4%, VRE rates in *E. faecium* from 33.6 - 37.8%, and a notably high carbapenem resistance rate in *K. pneumoniae*, ranging from 10.2 - 24.9% [7].

Staphylococcus epidermidis ranked third or fourth in frequency at most participating institutions in this study. According to a previous report, only 9.8% of blood cultures positive for *S. epidermidis* were deemed true infections, whereas 90.2% were classified as contaminants, emphasizing its common role as a skin commensal and contaminant in blood cultures [8]. The frequent isolation of such organisms has been linked to prolonged hospital stays and increased healthcare costs [9]. These findings emphasize the need for ongoing efforts to minimize contamination rates in blood culture prac-

Table 1. Most frequently isolated blood culture pathogens in Korea in 2023: (a) bacterial and (b) fungal species *.
(a)

Hospitals **	Ranking of the most frequently isolated bacterial species from blood cultures (%)					
	1	2	3	4	5	Number of total bacterial isolates
A	*E. coli* (23.1)	*K. pneumoniae* (11.4)	*S. epidermidis* (7.8)	*A. baumannii* (7.0)	*E. faecium* (6.1)	3,274
B	*E. coli* (20.7)	*K. pneumoniae* (14.3)	*S. aureus* (9.7)	*S. epidermidis* (8.2)	*S. capitis* (6.2)	4,980
C	*E. coli* (14.6)	*K. pneumoniae* (10.7)	*S. epidermidis* (7.3)	*S. aureus* (5.4)	*E. faecium* (5.4)	5,375
D	*E. coli* (21.4)	*K. pneumoniae* (13.8)	*S. epidermidis* (9.4)	*S. aureus* (8.1)	*E. faecium* (5.1)	3,526
E	*E. coli* (17.7)	*S. aureus* (15.6)	*K. pneumoniae* (8.7)	*S. epidermidis* (8.4)	*C. striatum* (4.5)	5,146
F	*E. coli* (20.2)	*E. faecium* (12.8)	*K. pneumoniae* (12.3)	*S. aureus* (11.4)	*S. epidermidis* (6.1)	6,313
G	*E. coli* (19.2)	*S. epidermidis* (14.5)	*K. pneumoniae* (13.1)	*E. faecium* (8.8)	*S. aureus* (8.7)	4,164
H	*E. coli* (12.4)	*K. pneumoniae* (6.1)	*S. epidermidis* (5.5)	*S. aureus* (4.3)	*E. faecium* (2.2)	7,920
I	*E. coli* (25.6)	*S. aureus* (11.5)	*S. epidermidis* (10.5)	*K. pneumoniae* (9.8)	*E. faecium* (3.3)	2,029
J	*E. coli* (24.3)	*K. pneumoniae* (19.8)	*S. aureus* (8.2)	*E. faecium* (5.8)	*S. epidermidis* (4.4)	3,088
K	*E. coli* (24.9)	*K. pneumoniae* (11.9)	*S. aureus* (7.1)	*S. epidermidis* (6.1)	*E. faecium* (3.3)	1,227
L	*E. coli* (23.3)	*K. pneumoniae* (9.4)	*S. epidermidis* (8.2)	*S. aureus* (6.4)	*E. faecium* (5.4)	1,417
M	*E. coli* (21.8)	*K. pneumoniae* (21.0)	*E. faecium* (13.3)	*S. epidermidis* (5.9)	*S. aureus* (5.7)	10,332
N	*E. coli* (17.0)	*K. pneumoniae* (12.9)	*S. epidermidis* (10.0)	*S. aureus* (9.5)	*E. faecium* (7.7)	3,513

Hospitals **	Ranking of the most frequently isolated bacterial species from blood cultures (%)					
	6	7	8	9	10	Number of total bacterial isolates
A	*S. aureus* (5.4)	*S. capitis*/*P. aeruginosa* (3.2/3.2) ***		*S. hominis* (2.5)	*E. faecalis* (2.4)	3,274
B	*E. faecium* (6.2)	*E. faecalis* (3.1)	*C. striatum* (2.6)	*S. hominis* (1.8)	*P. aeruginosa* (1.5)	4,980
C	*A. baumannii* (2.6)	*E. faecalis* (1.6)	*P. aeruginosa* (0.9)	*E. cloacae* (0.9)	*B. cereus* (0.7)	5,375
D	*S. capitis* (3.7)	*E. faecalis* (3.2)	*P. aeruginosa* (2.4)	*C. striatum* (2.3)	*S. hominis* (2.2)	3,526
E	*E. faecium* (3.5)	*S. capitis* (3.2)	*S. hominis* (2.8)	*A. baumannii* (2.7)	*B. cereus* (2.4)	5,146
F	*E. faecalis* (3.4)	*P. aeruginosa* (2.7)	*A. baumannii* (1.8)	*E. cloacae*/*C. striatum* (1.6/1.6) ***		6,313
G	*C. striatum* (4.9)	*E. faecalis* (4.8)	*S. capitis* (4.0)	*A. baumannii* (3.5)	*P. aeruginosa* (2.2)	4,164
H	*S. hominis* (2.0)	*E. faecalis* (1.9)	*S. capitis* (1.6)	*A. baumannii* (1.4)	*P. aeruginosa* (1.3)	7,920
I	*E. faecalis* (2.7)	*C. striatum*/*P. aeruginosa* (1.8/1.8) ***		*P. mirabilis* (1.3)	*S. marcescens* (1.0)	2,029
J	*P. aeruginosa* (4.3)	*E. faecalis* (2.8)	*A. baumannii* (1.8)	*C. striatum*/*S. maltophilia* (1.1/1.1) ***		3,088
K	*S. hominis*/*S. capitis* (2.9/2.9) ***		*P. aeruginosa* (2.3)	*E. faecalis* (2.2)	*M. luteus* (2.0)	1,227
L	*S. capitis* (4.4)	*A. baumannii* (3.1)	*P. aeruginosa* (2.4)	*C. striatum* (2.3)	*E. faecalis* (1.9)	1,417
M	*E. faecalis* (3.4)	*P. aeruginosa* (3.3)	*S. maltophilia* (2.0)	*C. freundii* (1.9)	*A. baumannii* (1.7)	10,332
N	*E. faecalis* (3.9)	*S. capitis* (3.0)	*C. striatum* (2.6)	*P. aeruginosa* (2.5)	*S. hominis* (2.1)	3,513

(b)

Hospitals **	Ranking of the most frequently isolated fungal species from blood cultures (%)					
	1	2	3	4	5	Number of total fungal isolates
A	*C. albicans* (54.9)	*C. parapsilosis* (14.7)	*C. tropicalis* (11.8)	*C. glabrata* (11.1)	*C. utilis* (4.6)	306
B	*C. albicans* (33.9)	*C. parapsilosis* (17.9)	*C. glabrata* (16.1)	*C. jadinii* (12.1)	*K. ohmeri* (10.3)	58
C	*C. albicans* (39.0)	*C. parapsilosis* (22.9)	*C. glabrata* (19.3)	*C. tropicalis* (16.2)	-	462
D	*C. albicans* (40.7)	*C. tropicalis* (27.2)	*C. parapsilosis* (17.9)	*T. asahii* (6.2)	*C. glabrata* (4.6)	324
E	*C. albicans* (40.5)	*C. tropicalis* (28.0)	*C. glabrata/C. auris* (9.3/9.3) ***		*C. parapsilosis* (6.2)	257
F	*C. tropicalis* (20.4)	*C. albicans* (20.0)	*C. glabrata* (19.1)	*C. parapsilosis* (17.8)	*C. guilliermondii* (6.2)	550
G	*C. albicans* (39.5)	*C. glabrata* (27.0)	*C. tropicalis* (21.7)	*C. guilliermondii* (6.8)	*C. parapsilosis* (4.2)	263
H	*C. albicans* (34.6)	*C. glabrata* (26.9)	*C. parapsilosis* (16.7)	*C. tropicalis* (14.1)	*C. dubliniensis* (3.8)	78
I	*C. albicans* (43.8)	*C. tropicalis* (28.1)	*C. glabrata* (18.8)	*C. parapsilosis/ C. guilliermondii/C. lusitaniae* (3.1/3.1/3.1) ***		32
J	*C. albicans* (45.6)	*C. parapsilosis* (19.9)	*C. glabrata* (19.5)	*C. tropicalis* (12.9)	*C. krusei* (1.4)	287
K	*C. albicans* (41.1)	*C. parapsilosis* (26.8)	*C. tropicalis* (14.3)	*C. glabrata* (8.9)	*S. cerevisiae* (5.4)	56
L	*C. albicans* (31.0)	*C. parapsilosis* (22.6)	*C. glabrata* (19.0)	*S. cerevisiae* (8.3)	-	84
M	*C. albicans* (29.1)	*C. tropicalis* (21.7)	*C. glabrata* (19.3)	*C. parapsilosis* (15.0)	*C. guilliermondii* (5.5)	618
N	*C. albicans* (42.9)	*C. parapsilosis* (22.1)	*C. tropicalis* (20.7)	*C. glabrata* (8.8)	*S. cerevisiae* (2.3)	217

[*] **Data collected from January to December 2023.**
[**] **Data from hospitals A - G were duplicated and may include repeated isolates from the same patient, whereas hospitals H - N submitted the non-duplicate data.**
[***] **Organisms with identical isolation counts.**
A. baumannii: Acinetobacter baumannii, B. cereus: Bacillus cereus, C. albicans: Candida albicans, C. auris: Candida auris, C. dubliniensis: Candida dubliniensis, C. glabrata: Candida glabrata, C. guilliermondii: Candida guilliermondii, C. jadinii: Candida jadinii, C. krusei: Candida krusei, C. lusitaniae: Candida lusitaniae, C. parapsilosis: Candida parapsilosis, C. tropicalis: Candida tropicalis, C. utilis: Candida utilis, C. striatum: Corynebacterium striatum, E. faecium: Enterococcus faecium, E. faecalis: Enterococcus faecalis, E. coli: Escherichia coli, E. cloacae: Enterobacter cloacae, K. pneumoniae: Klebsiella pneumoniae, K. ohmeri: Kodamaea ohmeri, M. luteus: Micrococcus luteus, S. cerevisiae: Saccharomyces cerevisiae, S. aureus: Staphylococcus aureus, S. capitis: Staphylococcus capitis, S. epidermidis: Staphylococcus epidermidis, S. hominis: Staphylococcus hominis, S. marcescens: Serratia marcescens, S. maltophilia: Stenotrophomonas maltophilia, T. asahii: Trichosporon asahii.

tices. Emphasis should be placed on strict adherence to aseptic blood collection techniques and the appropriate use of skin disinfectants to ensure specimen integrity and improve diagnostic accuracy.

Fungal bloodstream infections are predominantly caused by species of the genus *Candida*, accounting for > 90% of cases, with *C. albicans* being the most common and clinically significant species [10,11]. Candidemia primarily affects high-risk patient populations, including those with burns, malignancies, hematologic disorders, or immunocompromised conditions. Given the variability in species distribution and antifungal resistance, surveillance of local epidemiology is essential to guide appropriate antifungal therapy [11]. In our study, *C. albicans* was the most frequently isolated fungal species across all participating institutions except one. Notably, one center reported *Candida auris* - a multidrug-resistant yeast of increasing global concern - as the third most common fungal isolate. The detection rate of *C. auris*, which was below 0.1% prior to 2018, rose to 1.6% in 2022. Reported antifungal resistance rates for *C. auris* include 82.1% to fluconazole, 17.9% to ampho-

tericin B, and 1.3% to echinocandins, with 17.9% of isolates exhibiting resistance to fluconazole and amphotericin B [12]. Considering the high mortality associated with fungal sepsis, the emergence of *C. auris* warrants heightened vigilance. Koleri et al. reported a mortality rate of 41.6% in cases of *C. auris* fungemia, emphasizing the importance of continuous surveillance, early detection strategies, enhanced awareness among healthcare providers, targeted education, and rigorous infection control measures [13].

In our study, the proportion of polymicrobial isolates from blood cultures was 7.3%, which is lower than that reported in a previous domestic study (11.2%) [14]. The isolation rate of obligate anaerobic bacteria was 2.1%, comparable to that reported in another study (2.9%) [15]. These variations may be attributable to various factors, including differences in patient illness severity and detection methods for obligate anaerobes.

Our study has several limitations. First, results pertaining to the distribution of isolated organisms may have been impacted by the inclusion of pediatric blood culture data, but this proportion might be trivial considering the proportion of pediatric patients. Second, the reported frequency of isolates may have been affected by duplicate cultures, as approximately half of the participating institutions included data from duplicate samples. As this is the retrospective study, we could not control the duplicates issue. Third, considering the complexity of the dataset, only the top ten most frequently isolated pathogens were presented to provide an overview of the current etiological agents of sepsis. Fourth, this study presented only the distribution of isolates recovered from blood cultures and did not include an analysis of antimicrobial susceptibility results. Finally, there is a possibility that isolates defined as contaminants by each institution were neither standardized nor fully excluded during data collection of blood culture isolates. In addition, clinical relevance of the blood isolates was not analyzed by reviewing medical records.

In conclusion, although the distribution of frequently isolated organisms in blood cultures has not shown substantial changes, such analyses provide fundamental epidemiological data to guide empirical antibiotic selection in patients with bloodstream infections. Also, it can help monitor the emergence of new pathogens and identify their epidemiological patterns. Therefore, periodic evaluation of these trends and continuous efforts to strengthen surveillance systems for bloodstream infection pathogens are needed.

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Ethical Approval:

This study was approved by the Institutional Review Board of Gyeongsang National University Changwon Hospital (IRB No. 2024-09-011). Data from all participating institutions were provided with informed consent from the respondents.

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The authors confirm that no generative AI or AI-based tools were used in the writing, editing, or data analysis of this manuscript.

Declaration of Interest:

The author(s) declare that there are no conflicts of interest.

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