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ORIGINAL ARTICLE

Epidemiology and Prevalence of Bloodstream Infections in a Regional Hospital in Northern Taiwan During 2008–2013

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Background: Diagnosing bloodstream infections (BSIs) is a critical function of clinical microbiology laboratories. To reveal the prevalence of BSIs in a hospital in Northern Taiwan, which was established in July 2008, we investigated the clinical characteristics of patients with positive blood cultures from July 2008 to December 2013.
Methods: The medical records of the patients were retrospectively reviewed. In total, 104,641 blood culture sets were collected and analyzed.
Results: Microorganisms grew on 10.28% of these sets, as follows: 5.48% exhibited growth of a single microorganism; 1.56% exhibited growth of more than one microorganism; and 3.24% exhibited growth of contaminants. Furthermore, 5739 monomicrobial isolates included: Gram-positive cocci (22.02%); Enterobacteriaceae (56.51%); glucose nonfermentative Gram-negative bacteria (7.27%); yeast (6.22%); and anaerobic bacteria (6.64%). Most microorganisms were identified as follows: *Escherichia coli* (33.80%); *Staphylococcus aureus* (14.20%); *Klebsiella pneumoniae* (11.41%); *Pseudomonas aeruginosa* (3.17%); and the *Acinetobacter calcoaceticus–Acinetobacter baumannii* (*Acb*) complex (2.68%). Furthermore, among infants aged ≤3 months, Group B *Streptococcus* (GBS) and *S. aureus* were the leading pathogens causing bacteremia, whereas among infants 3–12 months old and children 1–4 years old, *Salmonella* species were the leading pathogens causing bacteremia. The prevalence of *Streptococcus pneumoniae* increased from the 3–12-month-old age group and reached a peak in the 5–12-year-old age group. For patients aged >13 years, the most common pathogens were *E. coli*, *S. aureus*, and *K. pneumoniae*.
Conclusion: We propose that the types and prevalence of BSIs vary according to age group and exhibit substantial geographical differences.

1. Introduction

Because bloodstream infections (BSIs) incur high health care costs, surveillance and detection of BSIs are a high priority in hospital settings.[1,2] Early diagnosis with structured management and treatment of patients with BSIs is essential to prevent fatalities. Broth blood culture is the gold standard test for detecting BSIs. This study was conducted at Shuang Ho Hospital, an 850-bed regional hospital in New Taipei City, Taiwan. The hospital's computerized patient database was used to identify and collect positive blood cultures that were recorded from July 2008 (when the hospital was established) to December 2013. The medical records of all patients were retrospectively reviewed to collect the following information: age, sex, laboratory data, microbiological findings, and antimicrobial susceptibility test results.

The research aim was to reveal the prevalence of BSIs in a hospital, which was established in July 2008 in Northern Taiwan. We investigated the clinical characteristics of patients with positive blood cultures from July 2008 to December 2013.

2. Methods

2.1. Bacterial isolates and antimicrobial susceptibility

Blood samples were inoculated into BACTEC culture bottles using the BACTEC FX system (Becton Dickinson, Cockeysville, MD, USA).

Conflicts of interest: The authors have no conflicts of interest to declare.

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All strains and antimicrobial susceptibility were identified using the BD Phoenix Automated Microbiology System (Becton Dickinson).

2.2. Statistical analysis

Comparisons between each variable and category were performed using the Chi-square test. Paired Student *t* tests were used to test the mean time to detection (TTD) difference. All statistical analyses were conducted using SPSS for Windows (Version 19.0; SPSS Inc., Chicago, Illinois, USA); A p value < 0.05 was considered statistically significant.

2.3. Ethics statement

All data used in this study were retrospectively obtained from the laboratory information system (LIS), which waived the right to informed consent.

3. Results

We collected and analyzed 104,641 blood culture sets from July 2008 to December 2013 (Table 1). Of these sets, 10.28% exhibited the growth of microorganisms: 5.48% exhibited growth of a single microorganism; 1.56% exhibited growth of more than one microorganism; and 3.24% exhibited growth of contaminants. Furthermore, among 5,739 monomicrobial isolates: 22.02% of isolates were Gram-positive cocci; 56.51% of isolates were Enterobacteriaceae; 7.27% of isolates were glucose nonfermentative Gram-negative bacteria (GNB); 6.22% of isolates were yeast; and 6.64% of isolates were anaerobic bacteria. The most frequently identified microorganisms were (in descending order): *Escherichia coli* (33.80%); *Staphylococcus aureus* (14.20%); *Klebsiella pneumoniae* (11.41%); *Pseudomonas aeruginosa* (3.17%); and the *Acinetobacter calcoaceticus*–*Acinetobacter baumannii* (*Acb*) complex (2.68%).

In the 0–3-month-old age group, the leading pathogen-causing bacteremia were Group B *Streptococcus* (GBS, 23.5%) and *S. aureus* (23.5%), followed by *E. coli* (17.6%) and *K. pneumoniae* (11.80%) (Figure 1A). In addition, in the 0–6-day-old age group, two cases of *E. coli*, one case of GBS, one case of *S. aureus*, and one case of *Enterococcus* infection were identified. By contrast, in the 7–30-day-old age group, three cases of GBS, one case of *S. aureus*, one case of *Serratia marcescense*, and one case of *Campylobacter* infection were identified (Figure 1B). Furthermore, *Salmonella* species accounted for 61.5% of BSIs in the 3–12-month-old age group (Figure 1A). In the 1–4-year-old age group, the most common pathogens were *Salmonella* species (45.45%), followed by *Streptococcus pneumoniae* (18.18%). In the 5–12-year-old age group, the most common pathogens were *S. aureus* (31.25%) and *S. pneumoniae* (31.25%), followed by *Salmonella* species (18.75%) and *E. coli* (12.50%).

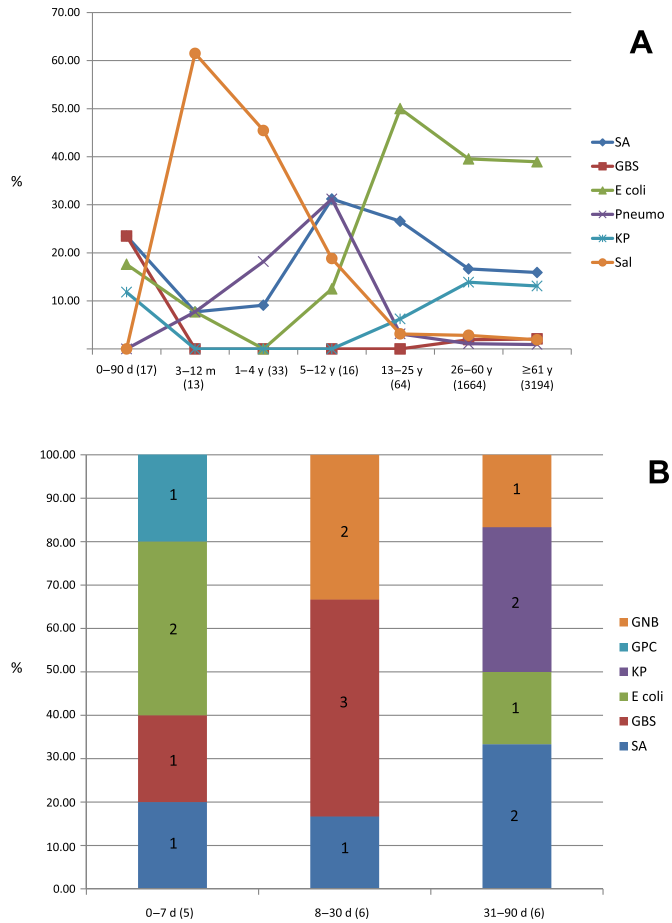

Figure 1 (A) The causes of bacteremia by age group. (B) The 0–90-day-old age group is further divided into 0–7-day-old, 8–30-day-old, and 31–90-day-old age groups. *E. coli* = *Escherichia coli*; GBS = Group B *Streptococcus;* GNB = Gram-negative bacteria; GPC = Gram-positive cocci; KP = *Klebsiella pneumoniae*; Pneumo = Streptococcus pneumoniae; SA = *Staphylococcus aureus*; Sal = Salmonella species.

Table 1 The number of each microorganism identified in the blood culture bottles

Gram-positive bacteria (n = 1,270)	(%)	Gram-negative bacteria (n = 3,731)	(%)
Staphylococcus aureus	64.17	*Escherichia coli*	52.00
Streptococcus pneumoniae	4.80	*Klebsiella pneumoniae*	17.56
GAS	3.78	*Enterobacter cloacae*	3.59
GBS	8.03	*Salmonella*	3.65
beta-*Streptococcus*	4.72	*Vibrio*	0.03
Enterococcus	14.02	*Aeromonas*	0.86
Listeria	0.47	*Campylobacter*	0.38
		Yersinia	0.03
		GNB	10.10
		Pseudomonas aeruginosa	4.88
		Acb complex	4.13
		Haemophilus influenzae	0.38
		Haemophilus parainfluenzae	0.19
		Moraxella catarrhalis	0.05
		Neisseria meningitidis	0.03

Acb = *Acinetobacter calcoaceticus*–*Acinetobacter baumannii*; GAS = Group A streptococcal bacteria; GNB = other Gram-negative bacteria.

Table 2 Average time to detection of bacteria growing in aerobic and anaerobic bottles

Microorganism	Aerobic	Anaerobic
Staphylococcus aureus	23.4	25.2*
Streptococcus pneumoniae	17.5	18.3
GAS	19.7	17.6
GBS	20.4	17.7
Enterococcus faecalis	20.1	22
Escherichia coli	22.4	17.8**
Klebsiella pneumoniae	24.5	20**
Enterobacter cloacae	20.8	20.6
Serratia marcescens	26.6	24.1
Salmonella species	27.7	22.7
Proteus mirabilis	28.6	21.1*
Pseudomonas aeruginosa	23.6	31.4*
Acb complex	16.4	23.3**

*$p < 0.05$, paired Student t test.
**$p < 0.001$, paired Student t test.
Acb = *Acinetobacter calcoaceticus*–*Acinetobacter baumannii*; GAS = Group A streptococcal bacteria; GBS = Group B *Streptococcus*.

In the 13–25-year-old, 26–60-year-old, and >61-years-old age groups, *E. coli* was the leading cause of bacteremia (50.00%, 39.54%, and 38.95%, respectively), and *S. aureus* was the second most common agent (25.65%, 16.65%, and 15.90%, respectively), followed by *K. pneumoniae* (6.25%, 13.88%, and 13.09%, respectively). In addition, four cases of *Haemophilus influenzae* type b bacteremia and one case of *Neisseria meningitides* bacteremia were identified.

The average TTD, which is defined as the period from the insertion of a blood culture bottle into the monitoring instrument to the detection of microorganisms, is an accurate indicator for evaluating the performance of automatic blood culture machines or media. In this study, the recovery of aerobic bottles was compared with the recovery of anaerobic bottles (Table 2). A significantly greater number of *Enterococci*, glucose nonfermentative GNB, and yeast were recovered from the aerobic bottles. In addition, a greater number of isolates of *S. aureus* and Enterobacteriaceae (except for *Serratia* species) were recovered from the anaerobic bottles than from the aerobic bottles ($p < 0.001$). Regarding initial detection, the anaerobic bottles revealed earlier detection of microbial growth, compared to the aerobic bottles for *E. coli*, *K. pneumoniae*, and *Proteus mirabilis* ($p < 0.001$). By contrast, the aerobic bottles had earlier microbial growth, compared to the anaerobic bottles, for *S. aureus*, *P. aeruginosa*, and the *Acb* complex ($p < 0.001$). No statistically significant sex differences between the samples from female and male patients were observed in the blood cultures; however, the *E. coli* and *P. mirabilis* bacteremia rates were significantly higher for females than for males ($p < 0.001$).

4. Discussion

In this study, early-onset bacteremia comprised 20% (1/5) of GBS infections, whereas late-onset bacterial infections comprised 50% (3/6) of GBS infections. In Taiwan, GBS screening during pregnancy has been promoted since 1996. Studies have reported that intrapartum antibiotic prophylaxis can reduce the early incidence of GBS infection, but may increase the risk of late-onset serious bacterial infections.[3,4] In this study, the leading pathogens causing bacteremia were *S. aureus* and *K. pneumoniae* for the 1–3-month-old age group, and *Salmonella* species for the 3–12-month-old and 1–4-year-old age groups.

In a previous study of a medical center in Northern Taiwan,[5] the leading pathogens causing bacteremia in 0–6-day-old infants are GBS and *E. coli*. In the 7–90-day-old and 4–6-month-old age groups, the most common pathogens were *E. coli* and GBS. For the 7–12-month-old age group, the leading pathogens causing bacteremia are *Salmonella* species and *E. coli*. Furthermore, based on the largest and most geographically diverse study in the United States that examined the epidemiology of bacteremia in children older than 7 years, *E. coli* (42%) is the most common cause of bacteremia in previously healthy febrile infants (≤90 days) admitted to a general inpatient unit, followed by GBS (23%).[6] Therefore, we propose that the types and prevalence of BSIs vary according to age groups and exhibit substantial geographical differences.

Studies have proposed that the risk groups for serious invasive pneumococcal infections are in children (i.e., <2 years) and in elderly people (i.e., >65 years).[7,8] In this study, the prevalence of *S. pneumoniae* increased from the 3–12-month-old age group and reached a peak for the 5–12-year-old age group and subsequently decreased in the patients aged older than 13 years.

The 23-valent and 7-valent conjugate vaccines against pneumococcal infection were introduced in Taiwan in 1998 and 2005, respectively. Population differences have been recognized in the bacteremia caused by *S. pneumoniae* in Taiwan.

In patients aged older than 13 years, *E. coli*, *S. aureus*, and *K. pneumoniae* are the most prevalent pathogens. Geographical differences have been recognized in the disease spectrum of *K. pneumoniae*, are occurs almost exclusively in Taiwan and South Africa.[9] Excluding the 1–3-month-old age group (33.3%, 2/6), the prevalence of *K. pneumoniae* increased from the 13–25-year-old age group and became the third leading cause of bacteremia among age groups older than 13 years.

Our study had some limitations in that it was not a multicenter study; therefore, the results may not accurately represent all disease patterns observed nationwide.

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