

ORIGINAL ARTICLE

A Twelve Year Retrospective Study Assessing the Prevalence of Bloodstream Infections Causing Pathogens at a Tertiary Care Hospital in Holy Makkah, Saudi Arabia

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ABSTRACT

Key words:
Critical care unit;
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Background: This study provides an important analysis of blood stream infections trends in a tertiary care setting. **Objective:** To determine the significant causative agents of morbidity in general inpatients and Critical Care Units (ICU & CCU) blood isolates, Makkah, Saudi Arabia, Makkah, Kingdom of Saudi Arabia. **Methodology:** This work was a retrospective study aiming to analyze the positive blood cultures trends from 1st January 2004 – 30th November 2015 recorded in a hospital information system at the Department of Clinical Microbiology at Al Noor Specialist Hospital. **Results:** Over the twelve years, bacteremia due to G^{-ve} bacteria (GNB) was found to be more prevalent than G^{+ve} bacteria (GPB) along with a persistent increasing trend of blood stream infections (BSIs) due to *Candida* spp. The prevalence of bacteremia due to Gram-negative bacteria was more than the Gram-positive bacteria in general medical wards and the CCU. In the CCU, *Acinetobacter* spp. (16.59%), *S. aureus* (15.57%), and *Klebsiella* spp. (14.69%) were the main causes of BSIs, while *S. aureus* (17.32%), *Streptococci* spp. (11.99%), *E. coli* (10.42%), and *Klebsiella* spp. (10.19%) were the main causes of bacteremia in general medical wards. **Conclusion:** In comparison to previous reports, our data suggests an upsurge in risk of Gram-negative bacteremia among CCU patients. These findings are also of key significance to epidemiologists and health policy makers in order to forecast the microbial trends.

INTRODUCTION

Bloodstream infections (BSIs) are significant causes of morbidity and mortality in hospitalized patients.^{1, 2} Accurate and timely identification of the causative organism is imperative for patient survival. Blood cultures are considered the “gold standard” in the diagnosis and treatment of BSIs.³ The positive blood culture either establishes or confirms that there is an infectious etiology for the patient’s illness. Moreover, it provides the etiologic agent for antimicrobial susceptibility testing which allows optimization of antibiotic therapy.⁴ The prognostic value of blood cultures is limited by contamination, which occurs when organisms that are not present in the blood are grown in culture.^{3,5} Al Noor Specialist Hospital is the largest tertiary care hospital in the holy city of Makkah, Kingdom of Saudi Arabia (KSA), with 600 beds. It provides healthcare services for adults including pediatric citizens, residents, pilgrims and visitors. It also receives most of Hajj and Umrah patients during Hajj

and Umrah seasons. This retrospective study was done to determine the prevalence of causative organisms detected in blood cultures [all inpatients hospitalized in general wards and the critical care unit (CCU)] during the last twelve years, from 1425 to 1436 Hijrah year (2004 – 2015 respectively).

METHODOLOGY

This was a retrospective study aiming to analyze the positive blood cultures trends from 1st January 2004 – 30th November 2015 recorded in a Hospital Information System at the Department of Clinical Microbiology at Al Noor Specialist Hospital. The blood cultures were processed using the BactT/ALERT (BioMérieux, France) continuous-monitoring blood culture systems, as per the manufacturer’s guidelines. Identification of species level was achieved by using the MICROSCAN and/or API 20NE systems (BioMérieux, France). According to clinical microbiology laboratory-approved policy, the samples were considered positive if growth

occurred within 5 days; otherwise they were considered: Negative if no growth observed after 5 days' incubation. Contaminant: Common skin contaminants (*Bacillus* spp, *Propionibacterium* spp, *Corynebacterium* spp, viridans group streptococci, *Aerococcus* spp, or *Micrococcus* spp) were detected in single bottle/set. Two or more organisms in a single bottle /set .Coagulase-negative staphylococci (CNS): as one skin contaminant if detected in single bottle /set as Organism causing bacteremia if detected in two or more sets within five days.

Statistical analysis

The results were expressed as percentages of distribution of different bacterial isolates. Microsoft Excel was used for the interpretation of these results.

Ethics approval

This study was first approved by the Institutional Review Board of the Faculty of Medical Sciences at Umm Al Qura University (Approval # AMSEC 15-26-12). In addition, study was approved by Directorate

General of Health Ministry of Health, Makkah region with reference number 47/300/ 43149 based on ethical approval from the Al-Noor Specialist Hospital Ethics Review Board.

RESULTS

During the study period, the total number of blood culture tests, positive and contamination results on set criteria are presented in table 1 from the CCU and general wards. The result indicates a grand total of 55481 cultures from CCU (9428) and general wards (46053). The percentage of positive cultures for BSIs from the CCU (14.5%) was higher than general wards (8.7%). The contaminated samples (16.8%) from the CCU were 12.3% CNS and 4.5% other contaminants, whereas for general wards the overall contamination level was 10.8%, with 7.4% CNS and 3.4% other contaminants.

Table 1: Frequencies of isolated microorganisms during twelve years (2004-2015)

	CCU N (%)	General Wards N (%)
Blood cultures results		
No growth	37072 (85.14)	6468 (14.86)
Coagulase negative Staphylococci	3417 (74.59)	1164 (25.41)
Positive cultures	1368 (25.42)	4012 (74.58)
Cultures declared having contaminants	428 (21.61)	1552 (78.39)
Bacteria type		
<i>S. aureus</i> +	213 (15.57)	695 (17.32)
<i>Streptococci spp.</i> +	77 (5.63)	481(11.99)
<i>Enterococcus spp.</i> +	87 (6.36)	164 (4.09)
<i>Acinetobacter spp.</i> -	227 (16.59)	365 (9.10)
<i>E. coli</i> -	104 (7.60)	418 (10.42)
<i>Enterobacter spp.</i> -	53 (3.87)	181(4.51)
<i>Klebsiella spp.</i> -	201 (14.69)	409 (10.19)
<i>Proteus spp.</i> -	52 (3.80)	66 (1.65)
<i>Pseudomonas spp.</i> -	124 (9.06)	361(9.00)
<i>Salmonella spp.</i> -	4 (0.29)	61(1.52)
<i>Serratia spp.</i> -	47 (3.44)	133 (3.32)
<i>Stenotrophomonas spp.</i> -	24 (1.75)	115 (2.87)
Others-	38 (2.78)	193 (4.81)
Fungi		
<i>Candida spp.</i>	117 (8.55)	370 (9.22)

Further sifting of positive cultures revealed a high percentage of bacterial presence (90.9%) compared to fungal presence i.e. *Candida spp.* (9.1%). The total percentage of Gram-negative bacteria (59%) surpassed Gram-positive bacteria (31.9%). In the CCU, the G-ve bacterial presence (63.9%) exceeded G+ve bacteria (27.6%), and in the general wards 57.4% of samples showed G-ve presence and 33.4% had G+ve bacteria (table 1). However, *Candida spp.* was more prevalent in

samples originating from general wards (76%) in comparison to the CCU (24%).

The frequencies data of isolated microorganisms (table 1) indicates that over the course of twelve years, there were more BSIs in general wards (n=4012) than the CCU (N=1368). However, given that the CCU is a single unit, the incidence level in the unit is quite high. These findings indicate the threat from these bacteria that have known resistance issues and thus reflect a

corresponding threat to public health. Keeping in mind the common practice as far as the treatments of infections is concerned, where antibacterial agents are prescribed empirically, it is necessary to culture the clinical samples, in particular the blood specimens. Average prevalence data over the entire study period shows *S. aureus* [methicillin sensitive staph. aureus (MSSA)] to be the main cause of G +ve bacteria (GPB) for general wards, followed by *Streptococci spp.*, MSSA remained the top microbe from general wards (17.32%) as well as the CCU (15.57%), followed by *Streptococci spp.* from general wards (11.99%) and *Enterococcus spp.* (6.36%) from the CCU. The report of these bacteria is notable in the perspective of resistance issues associated with these bacteria, especially MSSA and *Enterococcus spp.*

In case of G-ve bacteria's in general wards, *E. coli* (10.42%), *Klebsiella spp* (10.19%), *Acinetobacter spp.*

(9.10%) and *Pseudomonas spp.* (9%) remained the major contributors. There was also a fair amount of blood stream candidiasis (9.22%). As a whole GPBs were found to overwhelm GNBs in general wards. However, in comparison, G-ve bacteria *Acinetobacter spp.* (16.59%) was more prevalent than any bacteria in blood cultures from the CCU, followed by *Klebsiella spp.* (14.69%) in case of GNBs, while MSSA was the second-most prevalent bacterium from the CCU with 15.57% isolation. A significant presence of *Candida spp.* in cultures from general wards (n=370) as well as the CCU (n=117) is also of concern. *Candida spp.* prevailed in 8.55% of samples from the CCU, which is similar to general wards with a 9.22% incidence rate. As a whole, the most common encountered microorganisms during the study period were *S. aureus*, *Acinetobacter spp.*, *Klebsiella spp.*, and *Pseudomonas spp.*, with $\geq 9\%$ isolation from general wards as well as the CCU.

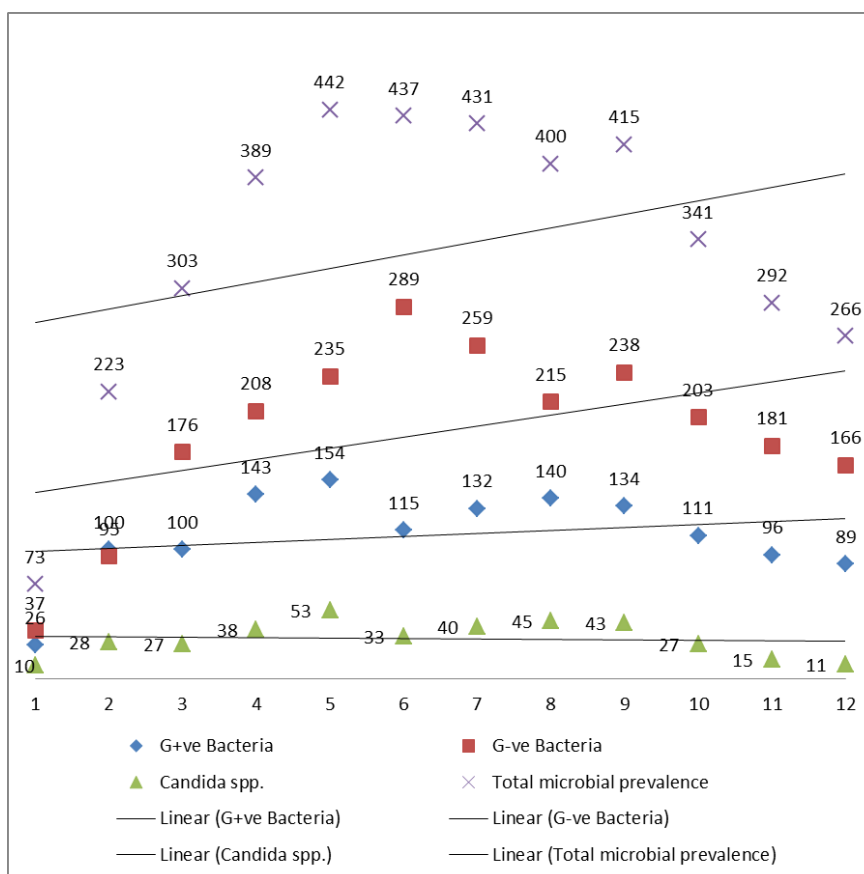


Figure 1: Trends in total microbial, G+ve bacteria, G-ve bacteria and Candida spp. prevalence in general wards for twelve years study period (2004 – 2015)

The twelve-year study data from the general wards shows an overall increasing trend in BSIs (Figure 1). The prevalence of GNBs and GPBs were approximately equal at the start of the study but gradually GNBs doubled over the whole period compared to GPBs, which is evident from their respective trend lines.

However, the prevalence of BSIs due to *Candida spp.* increased in the first five years of the study, followed by constant reports for following four years, and thereafter showed a declined prevalence. Overall, the BSIs resulting from *Candida spp.* show a constant trend.

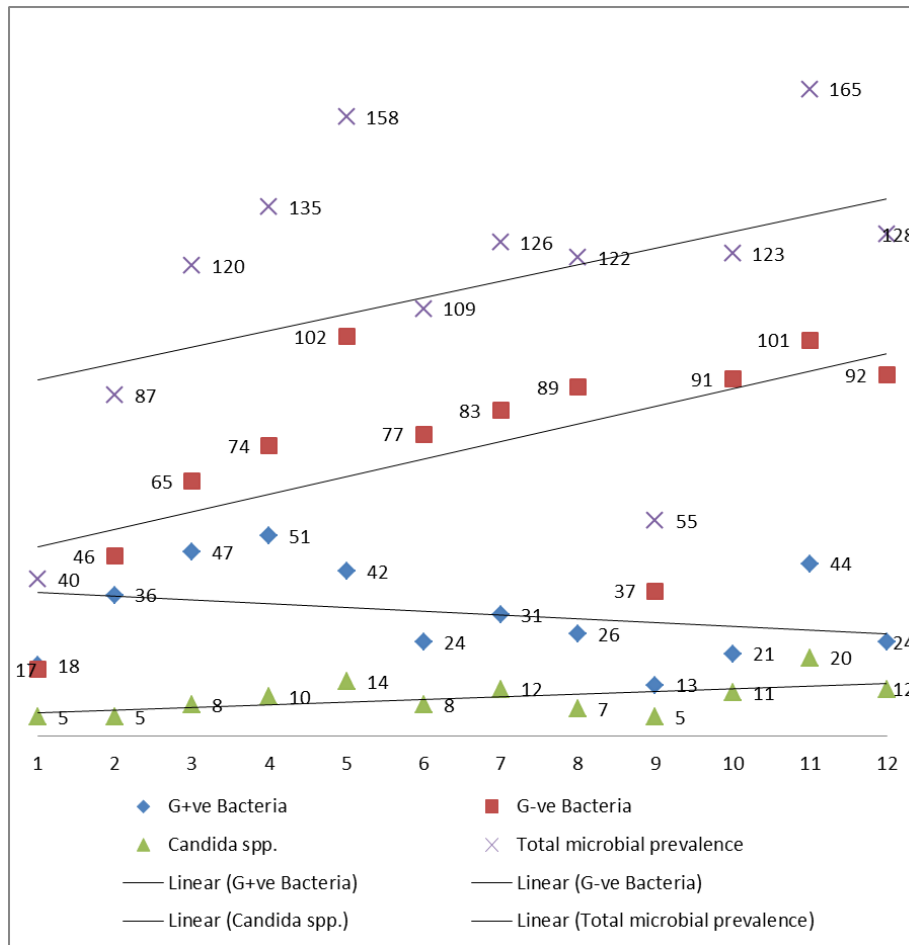


Figure 2: Trends in total microbial, G+ve bacteria, G-ve bacteria and Candida spp. prevalence in critical care unit (CCU) for twelve years study period (2004 – 2015)

As far as CCU is concerned, the data over the twelve years suggests a rapidly increasing trend in BSIs (Figure 2), especially due to GNBs. The prevalence of GNBs was observed to be higher than GPBs and the trend continued during the whole period of study. Although there was a rapid decline in total microbial, bacterial and fungal prevalence in 2012, later on the data became consistent again. As a whole, the prevalence of GNBs

remained high in the CCU and the trend shows an upsurge that is a major influencing factor for total microbial prevalence, whilst for GPBs the situation is reversed and a declining trend was observed for the study period. The prevalence of BSIs due to *Candida spp.* gradually increased in the first five years and then the prevalence is nearly constant as indicated from the trend line.

Table 2: Frequencies of isolated microorganism from general wards during twelve years (2004-2015)

Microorganisms from general wards		2004 N (%)	2005 N (%)	2006 N (%)	2007 N (%)	2008 N (%)	2009 N (%)	2010 N (%)	2011 N (%)	2012 N (%)	2013 N (%)	2014 N (%)	2015 N (%)
Gram positive bacteria	<i>S. aureus</i>	18 (24.7)	45 (20.2)	39 (12.9)	74 (19)	71 (16.1)	54 (12.4)	61 (14.2)	77 (19.3)	72 (17.3)	58 (17)	57 (19.5)	69 (25.9)
	Streptococci spp.	7 (9.6)	39 (17.5)	50 (16.5)	56 (14.4)	68 (15.4)	45 (10.3)	57 (13.2)	53 (13.3)	45 (10.8)	33 (9.7)	18 (6.2)	10 (3.8)
	Enterococcus spp.	1 (1.4)	16 (7.2)	11 (3.6)	13 (3.3)	15 (3.4)	16 (3.7)	14 (3.2)	10 (2.5)	17 (4.1)	20 (5.9)	21 (7.2)	10 (3.8)
Gram negative bacteria	Acinetobacter spp.	9 (12.3)	14 (6.3)	30 (9.9)	20 (5.1)	62 (14)	45 (10.3)	19 (4.4)	27 (6.8)	52 (12.5)	30 (8.8)	31 (10.6)	26 (9.8)
	<i>E. coli</i>	8 (11)	21 (9.4)	32 (10.6)	39 (10)	26 (5.9)	26 (5.9)	36 (8.4)	49 (12.3)	39 (9.4)	55 (16.1)	43 (14.7)	44 (16.5)
	Enterobacter spp.	1 (1.4)	7 (3.1)	11 (3.6)	15 (3.9)	25 (5.7)	33 (7.6)	24 (5.6)	12 (3)	9 (2.2)	16 (4.7)	14 (4.8)	14 (5.3)
	Klebsiella spp.	7 (9.6)	10 (4.5)	23 (7.6)	41 (10.5)	30 (6.8)	55 (12.6)	60 (13.9)	38 (9.5)	48 (11.6)	27 (7.9)	35 (12)	35 (13.2)
	Proteus spp.	0 (0)	3 (1.3)	1 (0.3)	3 (0.8)	4 (0.9)	6 (1.4)	11 (2.6)	6 (1.5)	8 (1.9)	12 (3.5)	7 (2.4)	5 (1.9)
	Pseudomonas spp.	8 (11)	18 (8.1)	32 (10.6)	42 (10.8)	46 (10.4)	59 (13.5)	35 (8.1)	33 (8.3)	36 (8.7)	19 (5.6)	21 (7.2)	12 (4.5)
	Salmonella spp.	0 (0)	0 (0)	1 (0.3)	7 (1.8)	5 (1.1)	5 (1.1)	9 (2.1)	11 (2.8)	8 (1.9)	8 (2.3)	5 (1.7)	2 (0.8)
	Serratia spp.	0 (0)	0 (0)	1 (0.3)	11 (2.8)	15 (3.4)	21 (4.8)	31 (7.2)	12 (3)	19 (4.6)	14 (4.1)	3 (1)	6 (2.3)
	Stenotrophomonas spp.	1 (1.4)	7 (3.1)	9 (3)	13 (3.3)	7 (1.6)	14 (3.2)	9 (2.1)	13 (3.3)	9 (2.2)	11 (3.2)	12 (4.1)	10 (3.8)
	Others	3 (4.1)	15 (6.7)	36 (11.9)	17 (4.4)	15 (3.4)	25 (5.7)	25 (5.8)	14 (3.5)	10 (2.4)	11 (3.2)	10 (3.4)	12 (4.5)
Fungi	Candida spp.	10 (13.7)	28 (12.6)	27 (8.9)	38 (9.8)	53 (12)	33 (7.6)	40 (9.3)	45 (11.3)	43 (10.4)	27 (7.9)	15 (5.1)	11 (4.1)
Total		73	223	303	389	442	437	431	400	415	341	292	266

Table 3: Frequencies of isolated microorganism from critical care units (CCU) during twelve years (2004-2015)

Critical Care Microorganism		2004 N (%)	2005 N (%)	2006 N (%)	2007 N (%)	2008 N (%)	2009 N (%)	2010 N (%)	2011 N (%)	2012 N (%)	2013 N (%)	2014 N (%)	2015 N (%)
Gram positive bacteria	<i>S. aureus/MSSA</i>	12(30)	19 (21.8)	22 (18.3)	24 (17.8)	27 (17.1)	13 (11.9)	20 (15.9)	16 (13.1)	7 (12.7)	17 (13.8)	23 (13.9)	13 (10.2)
	Streptococci spp.	3 (7.5)	8 (9.2)	13 (10.8)	15 (11.1)	8 (5.1)	8 (7.3)	6 (4.8)	4 (3.3)	3 (5.5)	2 (1.6)	3 (1.8)	4 (3.1)
	Enterococcus spp.	3 (7.5)	9 (10.3)	12 (10)	12 (8.9)	7 (4.4)	3 (2.8)	5 (4)	6 (4.9)	3 (5.5)	2 (1.6)	18 (10.9)	7 (5.5)
Gram negative bacteria	Acinetobacter spp.	1 (2.5)	13 (14.9)	8 (6.7)	14 (10.4)	30 (19)	19 (17.4)	20 (15.9)	18 (14.8)	10 (18.2)	23 (18.7)	40 (24.2)	31 (24.2)
	<i>E. coli</i>	6 (15)	7 (8)	11 (9.2)	4 (3)	11 (7)	6 (5.5)	8 (6.3)	14 (11.5)	6 (10.9)	12 (9.8)	9 (5.5)	10 (7.8)
	Enterobacter spp.	0 (0)	1 (1.1)	1 (0.8)	3 (2.2)	7 (4.4)	4 (3.7)	6 (4.8)	7 (5.7)	1 (1.8)	10 (8.1)	7 (4.2)	6 (4.7)
	Klebsiella spp.	3 (7.5)	4 (4.6)	16 (13.3)	23 (17)	12 (7.6)	8 (7.3)	18 (14.3)	26 (21.3)	9 (16.4)	22 (17.9)	25 (15.2)	35 (27.3)
	Proteus spp.	1 (2.5)	0 (0)	0 (0)	2 (1.5)	9 (5.7)	8 (7.3)	16 (12.7)	8 (6.6)	2 (3.6)	4 (3.3)	1 (0.6)	1 (0.8)
	Pseudomonas spp.	3 (7.5)	11 (12.6)	15 (12.5)	14 (10.4)	23 (14.6)	11 (10.1)	4 (3.2)	14 (11.5)	1 (1.8)	16 (13)	5 (3)	7 (5.5)
	Salmonella spp.	0 (0)	0 (0)	1 (0.8)	0 (0)	0 (0)	0 (0)	1 (0.8)	1 (0.8)	0 (0)	0 (0)	1 (0.6)	0 (0)
	Serratia spp.	0 (0)	0 (0)	0 (0)	7 (5.2)	6 (3.8)	12 (11)	7 (5.6)	0 (0)	6 (10.9)	2 (1.6)	6 (3.6)	1 (0.8)
	Stenotrophomonas spp.	2 (5)	4 (4.6)	3 (2.5)	3 (2.2)	1 (0.6)	3 (2.8)	1 (0.8)	0 (0)	1 (1.8)	1 (0.8)	5 (3)	0 (0)
Others	1 (2.5)	6 (6.9)	10 (8.3)	4 (3)	3 (1.9)	6 (5.5)	2 (1.6)	1 (0.8)	1 (1.8)	1 (0.8)	2 (1.2)	1 (0.8)	
Fungi	Candida spp.	5 (12.5)	5 (5.7)	8 (6.7)	10 (7.4)	14 (8.9)	8 (7.3)	12 (9.5)	7 (5.7)	5 (9.1)	11 (8.9)	20 (12.1)	12 (9.4)
Total		40	87	120	135	158	109	126	122	55	123	165	128

Among GPBs, *MSSA* was the most commonly encountered microbe followed by Streptococci spp. and *Enterococcus* spp. from the positive cultures of general wards. Therefore, *MSSA* can be regarded as the major etiologic agent for GPB in general wards. The major causative agents of GNB in general wards included *Acinetobacter* spp., *E. coli*, *Klebsiella* spp., and *Pseudomonas* spp. (yearly percentages and reports of highly prevalent bacteria are highlighted in Table 2).

In the case of CCU, as far as GNBs are concerned, *MSSA* was the most commonly isolated microorganism. However, over the course of the study, the prevalence of GNBs started to mount, with *Acinetobacter* spp. being the most prevalent microbe to cause BSIs. The other GNBs recovered from the positive blood cultures were *Klebsiella* spp., *Pseudomonas* spp. and *E. coli* (Table 3). The data suggests that the major contributors of BSIs from the CCU include *Acinetobacter* spp. and *Klebsiella* spp., which appear most in the GNBs from the CCU.

DISCUSSION

The results from the twelve-year study show an increase in total number of blood culture samples due to an increase in the numbers of residents in and visitors to Makkah, while the decline in 2014 was due to the transfer of pediatric and obstetrics & gynecology departments to another specialist hospital at the end of 2013. However, blood culture tests received from the CCU rose in 2014, because of the opening of new CCU wards that year. From general wards, the percentage of CNS-contaminated blood cultures was 7.4% while 3.4% were other contaminants, giving a total contamination percentage of 10.8%, and in the CCU there was a total of 16.8% contamination (CNS 12.3% and 4.5% others). Both are far higher than the rates recommended by Snyder et al. (2012) of under 3%, with reported contamination rates of between 0.6% to 12.5% for blood cultures. The high contamination rates need to be properly addressed. Overall, the microbial prevalence in general wards and the CCU increased. These findings are quite similar to a Brazilian study that similar trends for GNBs and GPBs in nosocomial BSIs in 16 Brazilian hospitals over 3 years.⁶ On the other hand, another study on nosocomial BSIs in 49 US hospitals over a 7-year period presented that Gram-positive organisms caused 65% of these BSIs, Gram-negative organisms caused 25%, and fungi caused 9.5%.⁷ The most-common organisms causing BSIs were CNS (31%), *S. aureus* (20%), enterococci (9%), and *Candida* species (9%). The differences in results from this report may be due to variations in geography and population (residents and visitors).

MSSA bacteremia was the most prevalent in total blood culture samples. *MSSA* bacteremia (SAB) is one of the most prevalent and difficult to treat infections and

is associated with significant morbidity and mortality.⁸ *MSSA* is the most common cause of nosocomial bacteremia in North America (26.0% prevalence) and Latin America (21.6% prevalence) and the second-most common cause of nosocomial bacteremia in Europe (19.5% prevalence).⁹ Furthermore, *MSSA* was found to be the most common cause of early-onset bacteremia and nosocomial bacteremia US and Taiwanese hospitals.^{10, 11} The prevalence reports from the American and European regions are higher than our average *MSSA* prevalence of 16%, which is roughly equal to a report of 18% in an Indian tertiary care hospital.¹² Still, this percentage is a significant threat given the challenges that may arise from this microorganism with its proven global association with resistance.

The average prevalence pattern from our study revealed *S. aureus*, *E. coli*, *Klebsiella* spp, and *Acinetobacter* spp (17.32%, 10.42%, 10.19% & 9.10% respectively) to be the main four isolated pathogens from the general wards, while for the CCU, *Acinetobacter* spp (16.59%) was the most prevalent organisms followed by *MSSA* (15.57%) and *Klebsiella* spp (14.69%). These results are quite similar to a study by Marra et al.⁶ that reported 14% *S. aureus*, 12% *Klebsiella* spp. and 11.4% *Acinetobacter* spp. *A. baumannii* is emerging as an important nosocomial pathogen worldwide, especially in CCUs.¹³ In recent years, it has been designated a 'red alert' human pathogen and has caused considerable concern in the medical community.¹⁴ Furthermore, a recent meta-analysis suggested that prior central venous or urinary catheterization, mechanical ventilation, and nasogastric tube use are associated with a higher risk of *A. baumannii* nosocomial bacteremia in CCUs.¹⁵ The prevalence and rise of *Acinetobacter* spp. highlighted in the present study is an important aspect that requires proper address.

Over the past two decades, *E. faecalis* and *E. faecium* have become increasingly important pathogens especially as hospital-acquired infections. Enterococcus spp. is rated as the third leading cause of hospital-acquired bacteremia in the US and accounts for 9.4% of the bacteremias.⁷ Consistent with this, an Italian multi-centre study reported Enterococci in 11.4% of all bacteremias during a one-year survey.¹⁶ Similarly, Danish surveillance data demonstrated rising incidences of *E. faecalis* and *E. faecium* bacteremia.¹⁷ In the present study, Enterococci prevalence in total and CCU samples (4.51% & 3.87% respectively) were lower than the earlier reports, though the prevalence increased throughout the study period. This trend confirms the statement of Nielsen et al. that regardless of place of acquisition, the proportion of bacteremia caused by enterococci increase.¹⁸

An interesting finding of the present study was an increasing presence of *Candida* spp. in culture isolates originating from the CCU unit as well as general wards. *Candida* spp. was among the main etiologic agents in blood culture samples of general wards (9.22%) as well as the CCU (8.55%). Although *Candida* spp.-related BSIs showed a decreasing trend over the twelve years on the general wards, the situation was reversed in isolates from the CCU where an increasing trend was observed. Similar situation is observed in Taiwanese studies that concludes a significant increase in BSIs from *Candida* spp.¹¹

In the CCU, although GPBs and GNBs were almost the same in the first year of study, the trend changed in the following years with a progressive increase in GNBs over eleven years.¹⁹ However, our findings differ from a one-year study by Khan (2012) performed on Saudi Arabian hospitals that gave a GPB/GNB percentage ratio of 85% to 15%.²⁰ This difference may be attributed to the short period in Khan's study. Furthermore, the present study indicates that *A. baumannii*, *K. pneumoniae*, *P. aeruginosa* and *E. coli* are the most frequently isolated Gram-negative bacteria from the CCU, which is in agreement with similar studies in Turkey and Iran^{21, 22} and in hospitals in Makkah.¹

It seems that geographical distribution greatly affects prevalence of certain microorganisms. In a four-year Italian study²³, CNS was the leading organism (18.3%), followed by *E. coli* (11.2%), *MSSA* (7.4%), *E. faecalis* (5.4%), *P. aeruginosa* (4.3%), *Klebsiella* spp. (3.4%), *E. faecium* (2.5%), and *C. albicans* (2.5%). In a separate study of 13 hospitals in Korea²⁴, the ten most prevalent bacteria included CNS (28.7%), *E. coli* (16.2%), *MSSA* (9.3%), *K. pneumoniae* (8.7%), *Enterococcus* spp. (5.3%), *Streptococci* spp. (4.3%), *A. baumannii* (3.8%), *P. aeruginosa* (2.9%), and *Enterobacter* spp. (2.1%). Similarly, a 9-year study on bacteremia in Denmark¹⁸ revealed *E. coli* (28.3%), *MSSA* (12.3%), CNS (10.0%) and *S. pneumoniae* (9.1%) to be the most common causative microorganisms. More recently, it is found that 61.8% G-ve organisms, 33.6% G+ve organisms and 4.6% fungi to be the causes of BSIs, with *E. coli* (25.5%), CNS (14.1%) and *K. pneumoniae* (11.2%) the top three etiologic agents isolated from general wards.²⁵ However, in the case of the CCU, CNS (22.8%) and *Acinetobacter* spp. (13.4%) were reported. Also a recent study in Egypt²⁶, reported 20.8% *Staph. aureus* neonatal BSIs, 28.6% ENG, 16.5% *Candida* spp. And 14.2% CNS. This fluctuating data shows the need for consistent monitoring of microbes both retrospectively as well as prospectively at hospitals and especially at CCUs in order to realize the actual picture and corresponding threat to healthcare settings.

CONCLUSION

In conclusion, this study highlights the epidemiological picture of microorganisms in blood cultures received in Al-Noor Specialist Hospital and to a large extent in the Makkah region, Saudi Arabia. The results of this study are of significant use to clinicians dealing with patients with infectious diseases to predict microorganisms with which to start their empirical treatment. The findings are also of key significance to epidemiologists and health policymakers in order to forecast the microbial trends, thus chalking out reforms to better cope with infections and frame control practices in hospitals in general and specifically in CCU. Such studies are also pivotal in monitoring the ratio of microbial contamination and putting more effort into adherence to infection control measures.

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Conflicts Of Interest

The authors declare that there is no conflict of interest regarding authorship and publication of this paper.

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