ANALYSIS

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# Contamination of patients' bedside tables in a tertiary care center in Riyadh, Saudi Arabia

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## ABSTRACT

*Background:* Nosocomial infections are acquired during hospitalization which was not present at admission. The microorganisms causing these infections usually present under many conditions. Surfaces with a higher prevalence of contamination include daily-use equipment and items. In this study, we aimed to determine the bacterial contamination of patients' bedside tables at King

Abdul-Aziz Medical City. *Methods:* A cross-sectional study was conducted by collecting samples from patients' bedside tables at King Abdul-Aziz Medical City. Swabs were taken from the allocated tables randomly. Then, the samples were sent to the lab for culturing to determine the presence or absence of contamination. *Results:* Of the 226 patients' bedside samples, 203(90.22%) showed bacterial growth. Most of the isolated bacteria were gram-positive (97.72%), while gram-negative was found in 1.66% and fungi in 0.62% of the samples. The most common organism to be cultured was *Staphylococcus* negative coagulase, which was isolated 173 times (67.5[1] %), followed by *Corynebacterium* species (49.1%). However, the least organisms to be isolated were *Ochrobactrum anthropi*, *Proteus species*, and *Rhizobium radiobacter*, each isolated one time (0.4%). Most of the positive samples were taken from medical wards, followed by surgical and OB/GYN wards. Also, the medical wards carried most of the gram-negative organisms isolated in our study. *Conclusion:* The majority of patient's bedside tables were contaminated mostly with environmental bacteria. Fungus and gram-negative bacteria were rarely detected. Contaminated bedside tables could be a source of transmission of infection.

**Keywords:** Contamination, Nosocomial Infection, Bedside Tables

## 1. INTRODUCTION

Nosocomial infections or hospital-acquired infections (HAIs) are infections that are acquired during patients' hospitalization which were not present or incubated at time of admission. According to the World Health Organization (WHO), any infections occur in patients within 48 hours after admission are considered HAIs (WHO, 2016). These infections represent a significant burden on patients and healthcare facilities, leading to high numbers of morbidity and mortality around the world. According to The Center for Disease Control and Prevention (CDC), about two million patients suffer from HAIs every year, and 100,000 of them died in the United States (CDC, 2016). Locally, it has been estimated that the prevalence of HAIs in King Abdulaziz Medical City - Riyadh (KAMC) reached up to 8% of patients in May 2003, and the majority of them were above the age of 50 (Balkhy et al., 2006). Not only do HAIs affect patients, yet they impose significant economical issues on the healthcare systems (Haas et al., 2006; Stone et al. 2005).

The microorganisms causing HAIs are usually present under many conditions such as moist and dry environments. These conditions can be found in many surfaces used in everyday hospital settings. Recently, there is an increase number of evidence suggesting that these highly touched surfaces may act as reservoirs for some of the pathogens that can cause HAIs. These microorganisms are transmitted either directly or indirectly by the hands of healthcare workers, leading to healthcare outbreaks as reported by most of infection control protocols worldwide (Rhame et al., 1998). Not only HAIs can be spread inside the hospital, but also they can be further transmitted to the outside community since most of the highly touched surfaces are not just limited to healthcare workers or patients but also used by visitors or workers from outside leading to the spread of cross-infections and epidemics. Examples of these surfaces like door-knobs push plates, bed rails, faucet handles, and the poles supporting intravenous fluid supplies. Even with strict protocol and practice of routine cleaning and precautionary measures in most hospitals, effective environmental decontamination methods are still in demand (Yung Jolene et al., 2013; Kenawy et al., 2007).

In this study, we focused on measuring the contamination of patients' bedside tables, since there are no enough studies conducted regarding such surface. Patients' bedside tables are movable objects that can be easily suited either beside the patients or over their beds. It is used quite frequently providing support for everyday activities such as eating or drinking, making them one of the most highly touched surfaces. This study aims to measure the contamination of bedside tables in a tertiary care center with high inpatient load and variable medical specialties, and, if found, identify the microorganisms colonizing those tables.

## 2. METHODOLOGY

### Ethical committee

Our study has been accepted and approved by King Abdullah International Medical Research Center (IRBC/1065/16).

### Design

This study was a cross-sectional study conducted at KAMC-Riyadh in 2018. The bed capacity at KAMC has increased to more than 540 beds, and 132 beds for emergency cases. There are approximately 1000 bedside tables. By using Raosoft sample size calculator and after applying our exclusion criteria, the population size is 540, 5% as a margin of error with 95% confidence interval, and 50% as the response distribution, the calculated sample size is 226. Variables were analyzed by Chi square test. P values <0.05 were considered significant.

**Data Collection and Integrity**

Non-probability convenience sampling was used. All of 226 samples were collected by a single data collector to ensure consistency of the swabbing technique. Each morning the principal investigator would assign the data collector to a different ward. A swab from the right lower 2 borders from the side of each table was taken. Samples were taken by using sterile cotton swab moistened with sterile normal saline. Simultaneously, the rest of the assigned students were filling the data collecting sheets. The collected samples and data collection forms were matched through serial numbers. Ten samples were collected per day. Then, the swabs were taken to the lab, and assigned lab technicians cultured the samples on blood agar media for 48 hours. One or more colony forming units (CFUs) per swab was considered as a positive result. Positive cultures were analyzed using Gram stain, Coagulase, and Catalase reactions.

**Inclusion and Exclusion Criteria**

All tables were included from medical and surgical wards, emergency (ER), and obstetric and gynecological (OB/GYN). However, we excluded regular Intensive care units (ICU), pediatric wards, pediatric and neonatal ICU, and all isolated rooms including respiratory and contact isolation were also excluded.

After obtaining culture results, data from the lab were entered into Microsoft Excel then exported to SPSS version 21 for analysis. Categorical variables were described as frequencies and percentages.

## 3. RESULTS

Total bed capacity at KAMC was approximately 1000 beds. After applying our exclusion criteria, we were able to collect swabs from 226 bedside tables. Of all bedside tables retrieved for sampling, 203 tables (90.22%) had a positive growth result with at least one species of bacteria. Table 1 represents a comparison of cultured organisms from the contaminated bedside tables. Of all positive samples, most of the isolated bacteria were gram-positive (n=471; 97.72%). The most predominant cultured organism was *Staphylococcus* negative coagulase (CoNS) (n = 173; 67.5%), followed by *Corynebacterium* species (n=111; 49.1%). With the exception of (CoNS), the incidence of contamination by gram-positive bacteria was as follows: *Bacillus* species (n=88; 38.9%), Diphteroids (n= 45; 19.9), *Micrococcus* species (n=36; 15.9%), Alpha hemolytic *streptococcus* (n=15; 6.6%) and *Staphylococcus aureus* (n=2; 0.9%). Moreover, the incidence of contamination by gram-negative bacteria represented 1.66% of all positive growth samples, including *Klebsiella pnemoniea* (n=2; 0.9%), *Morexella osloensis* (n=1; 0.4%), *Proteus mirbilis* (n=1; 0.4%), *Acinetobacter baumanni* (n=1; 0.4%), *Rhizobium radiobacter* (n=1; 0.4%), *Proteus* species (n=1; 0.4%) and *Ochrobactrum anthropi* (n=1; 0.4%). Bedside tables contaminated with fungi (n=3; 0.62%) included: *Aspergillus niger* (n=2; 0.9%) and *Curvularis* species (n=1; 0.4%)

**Table 1** The number and frequency of different microorganisms identified (N=226)

| Organism | Positive sample | |
|---|---|---|
| | N | % |
| *Staphylococcus* negative *coagulase* | 173 | 76.5 |
| *Corynebacterium* species | 111 | 49.1 |
| *Bacillus* species | 88 | 38.9 |
| Diphteroids | 45 | 19.9 |
| *Micrococcus* species | 36 | 15.9 |
| Alpha hemolytic *streptococcus* | 15 | 6.6 |
| *Aspergillus niger* | 2 | 0.9 |
| *Klebsiella pneumoniea* | 2 | 0.9 |
| *Staphylococcus aureus* | 2 | 0.9 |
| *Moraxella osloensis* | 1 | 0.4 |
| *Curvularis* species | 1 | 0.4 |
| *Proteus mirabilis* | 1 | 0.4 |
| *Acinetobacter baumanni* | 1 | 0.4 |
| *Rhizobium radiobacter* | 1 | 0.4 |
| *Proteus* species | 1 | 0.4 |
| *Ochrobactrum anthropi* | 1 | 0.4 |

Further analysis showed that 192 (84.95%) samples had gram-positive growth only and no samples with gram-negative growth only. The remaining 11 samples (4.86%) had mixed organisms' growth. Figure 1 represents the distribution of mixed organisms identified. Out of the mixed growth samples (n=11), CoNS was the most common gram-positive organism identified followed by Corynebacterium, bacillus, Micrococcus and Diphteroids. Gram-negative identified within the mixed growth samples were *Klebsiella pneumonie*, *Proteus mirabilis*, *Moraxella osloenosis*, *Acinetobacter baumanii*, *Rhizobium radiobacter* and *Ochrobactrum anthropi*. In addition, fungi identified within the mixed growth samples were *Aspergillus niger* and *Curvularis* species.

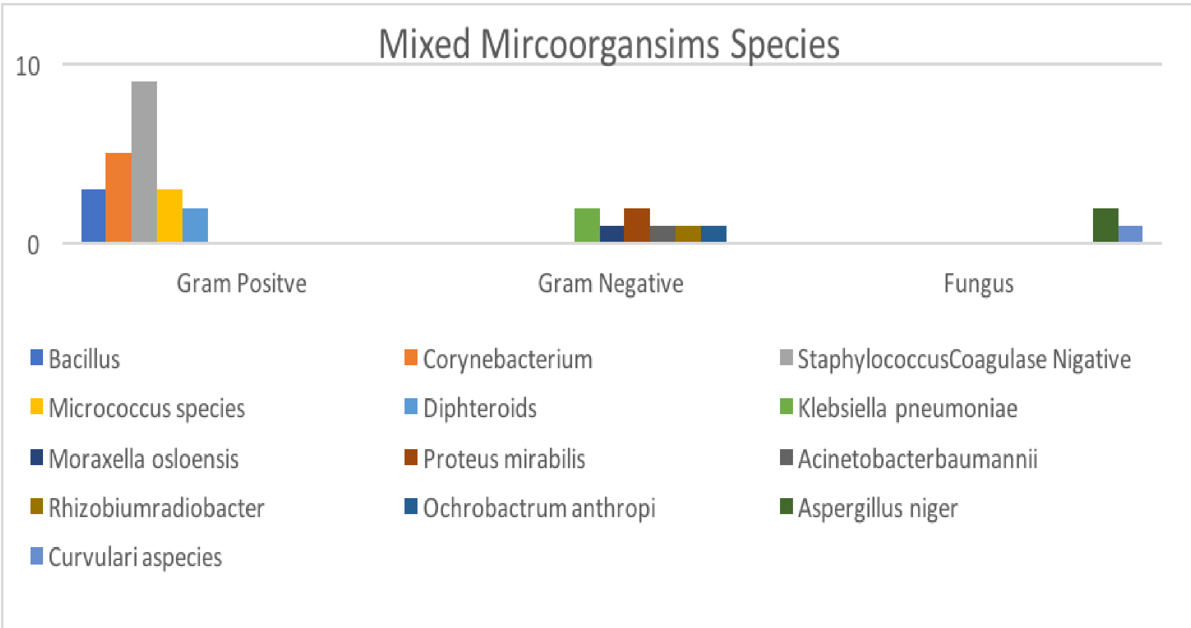


**Figure 1** Mixed microorganisms species identified from positive growth samples

Figure 2 shows a comparison between four main different wards raging from medicine, surgery, OB/GYN, and ER wards. The sampling rate of the tables was 91 (40.26%) for medical wards, 57 (25.22%) for surgical wards, (57 25.22%) for OB/GYNand 21(9.29%) for ER bedside tables. These distributions highlighted the significant number of microorganisms isolated from medical wards followed by surgical, OB/GYN and ER wards.

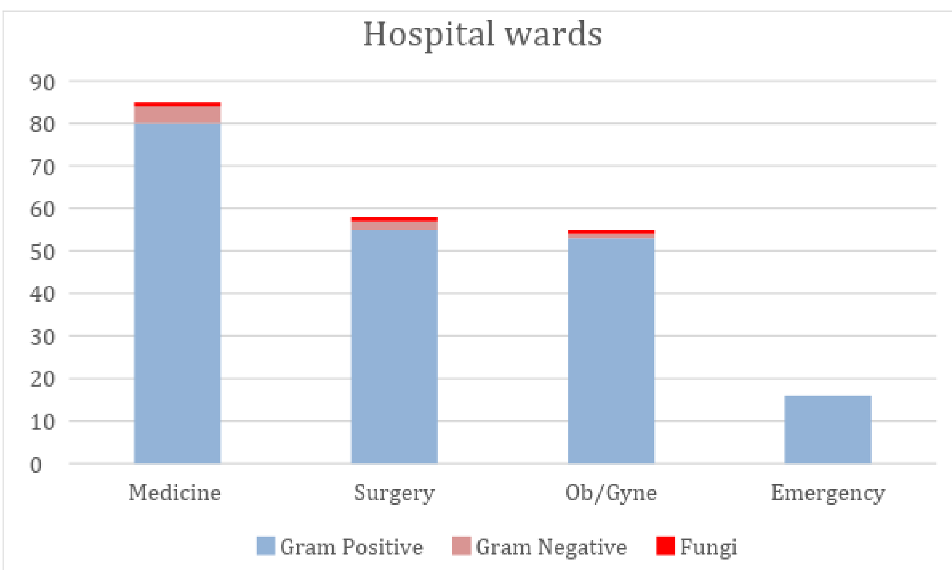


**Figure 2** Number of contaminated isolates according to the microorganisms distributed across major hospital wards.

In Figure 3, quantitative assessment of particular organisms isolated from each ward shows that, medical wards had the highest level of contamination, reaching the maximum for Diphteroids (44 unit/25cm2) followed by Alpha Hemolytic *streptococcus* (40 unit/25cm2) and minimum for *Curvularia* species (1unit/25cm2). While the lowest was in emergency rooms with the highest growth detected there was *Corynebacterium* species (16 unit/25cm2).

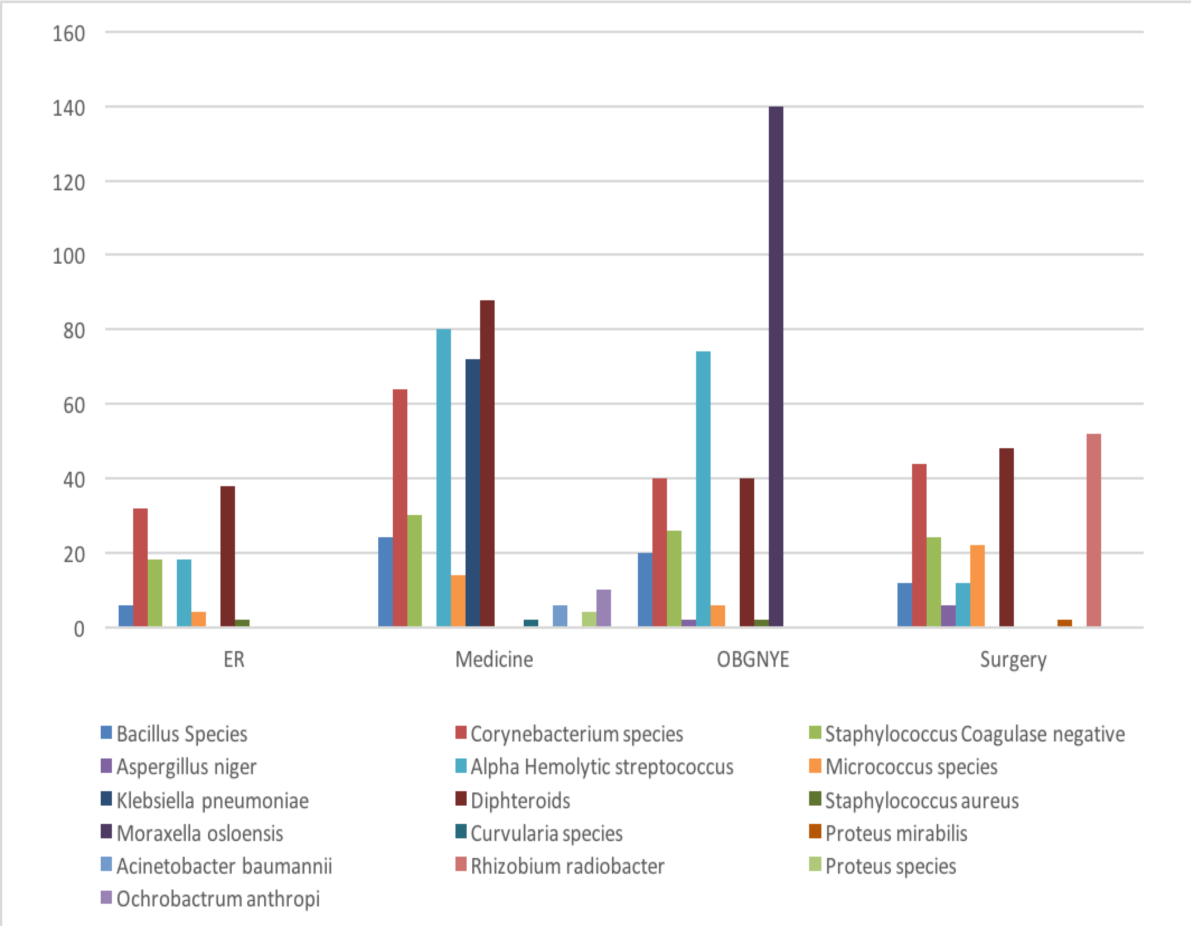


**Figure 3** The average concentration of particular species of organisms isolated from bed-side tables samples

## 4. DISCUSSION

Our results showed that the majority of the hospital bedside tables had a positive growth result with at least one positive species. Moreover, most of the isolated bacteria were gram-positive while gram-negative and fungi accounted for 1.66% and 0.62%, respectively. The most common isolated organisms were Coagulase-negative staphylococci (CoNS), Corynebacterium species (n=111; 49.1%). Furthermore, medical wards had the highest level of contamination, followed by surgical wards then OB/GYN, respectively. The lowest level of contamination detected was found in ER rooms. A study conducted by Chen et al. showed that general medical wards had the highest incidence of bacterial contamination, which is similar to our findings (Chen et al., 2014).

Our study found that Coagulase-negative *staphylococci* (CoNS) were the predominant species among all the isolated cultures. Similarly, multiple studies conducted among different types of frequently touched objects (i.e., Patients' medical charts, examination gloves, and mobile phones), reported that CoNS was the most commonly isolated organism (Chen et al., 2014; Diaz et al., 2008; Almeshal et al., 2017). Although other studies showed that the environmental methicillin-resistant *Staphylococcus aureus* (MRSA) is presented abundantly in multiple areas of the hospital and positive MRSA growth was not often detected among all bedside tables in different wards (Chen et al., 2014; Yuen et al., 2015). Our findings showed that only a very minimal detection of *Staphylococcus aureus*, while none of them were found to be MRSA. *Acinetobacter baumannii* is known to be responsible for hospitals' outbreaks worldwide, due to its rapid antibiotic resistance. Thus, it has a huge impact on public health (Mandell et al., 2015). *Acinetobacter baumannii* was isolated one time in our study which is less than what has been reported in another similar study. *Klebsiella pneumoniae* is another gram-negative organism that causes HAIs and has a significant clinical effect on the general public health (Gasink et al., 2009). In Chen et al. study *Klebsiella pneumoniae* was responsible for out of the total growth (Chen et al., 2014). However, our study showed only two positive growths of *Klebsiella pneumoniae*.

HAIs are known to cause an increase not only in morbidity and mortality but also inflict a significant financial burden on the healthcare system. Reduction of HAIs has been shown to be an effective cost-saving measure that can be achieved by optimized surveillance 13. Previous studies have found that patients are at risk of acquiring MRSA and vancomycin-resistant enterococci (VRE) from surfaces that are suboptimally cleaned (Huang et al., 2006; Hardy et al., 2006; Sexton et al., 2006; Martinez et al., 2003; White et al, 2008; Drees et al., 2008; Denton et al 2005). Also, in some hospital settings, improved environmental cleaning protocols had an essential role in limiting the transmission of methicillin-susceptible *Staphylococcus aureus* (Weber et al., 2007; Layton et al., 1993), MRSA (Boyce et al, 1997), glycopeptide-intermediate *Staphylococcus aureus* (de Lassence et al., 2006), and *Acinetobacter baumannii* (Wilks et al., 2006). A study conducted by Maragakis et al. found that bed rails, over-bed tables, intravenous pumps, and the bed surfaces on the medical-surgical floors that are considered high-touch surfaces (Maragakis et al., 2008). Several researches have recommended the use of quaternary ammonium compound (QAC)-based antimicrobial coating on high-touch surfaces (Talon et al., 1999; Rutala et al., 2001). Another study by Eckstein et al. has shown that routine disinfection cleaning of these surfaces, and regular interventions have a significant role in lowering HAIs (Eckstein et al., 2007).

Up to our knowledge, this study is the first study that gives a highlight of the bacterial contamination of patients' bedside tables in Saudi Arabia. However, as with most studies, this study had some limitations. First of all, it was conducted in a single tertiary care center, which may show different results when compared to another center due to different cleaning protocols used. Second, the sampled tables were movable objects, which make it difficult to identify the same item in case significant data was found. Also, all the high-risk wards such as ICU, pediatrics wards, and isolated rooms were excluded 3. In addition, bacteria are common to be colonized in various environments; therefore this colonization may have a clinical implication or a source of infections.

## 5. CONCLUSION

In conclusion, our final results have showed that bedside tables contained a high percentage of contamination. Among all of our findings, the majority of the sampled tables were mostly contaminated with environmental bacteria, whereas fungus and gram-negative bacteria were rarely detected. In comparison between all hospital departments, medical wards were the most with positive samples while emergency rooms were the least. Contaminated bedside tables could be a source of transmission of infections; therefore further studies are needed in this field.

**Declarations**

**Availability of data and material**

All data generated or analyzed during this study are included in this published article [and its supplementary information files].

**Competing interests**

The authors declare that they have no competing interests

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**Abbreviation**

| | |
|---|---|
| HAI = | Hospital-acquired Infections |
| WHO = | World Health Organization |
| CDC = | Disease Control and Prevention |
| KAMC= | King Abdulaziz Medical City |
| CFU = | Colony forming units |
| ER = | Emergency Room |
| OB/GYN= | Obstetric and Gynecological |
| ICU= | Intensive Care Units |
| CoNS= | Staphylococcus Negative Coagulase |
| MRSA= | Methicillin-resistant Staphylococcus aureus |
| QAC= | Quaternary Ammonium Compound |

**Authors' contributions**

TB,SS,SM,WA,AK and HG all co-conceptualized the study, undertook sample collection, prepared tables and figures, interpreted results and drafted the manuscript. AO, SJ undertook sample laboratory work, analyses and vetted the results. AM undertook the statistical analysis of the data. MB and AA co-conceptualized the study, undertook vetting of the results and critically reviewed the manuscript. All authors read and approved the manuscript.

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**Authors Role**

Tala Al Bassri - Her role was writing the proposal, collecting data, data analysis and writing the manuscript.
Sarah Al Sadun - Her role was writing the proposal, collecting data, data analysis and writing the manuscript.
Seba Al Mutairi - Her role was writing the proposal, collecting data, data analysis and writing the manuscript.
Atheer Al Khunein - Her role was writing the proposal, collecting data, data analysis and writing the manuscript.
Al Wateen Al Abdullah - Her role was writing the proposal, collecting data, data analysis and writing the manuscript.
Hadeel Ghazal - Her role was writing the proposal, collecting data, data analysis and writing the manuscript.
Dr. Mohammed Bosaeed - His role was reviewing the data and manuscript
Dr. Ahmed Al Harbi - His role was reviewing the data and manuscript
Dr. Afaf Moukaddem - Her role was data analysis
Ahmed Alowaji - His role was microbiology analysis of samples
Dr. Samerah Al Johani - Her role was microbiology analysis of samples
Dr. Adel Al Othman - His role was supervising the process of this research

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