# Multidrug Resistant Organisms in the Intensive Care Unit of a Tertiary Care Hospital in Jamaica

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## ABSTRACT

**Objective:** The aim of this study was to determine the presence of multidrug resistant (MDR) pathogenic bacteria in the environment of the Intensive Care Units (ICUs) a tertiary care hospital in Jamaica. This was done to find out if organisms previously associated with outbreaks are present and to make recommendations as appropriate, for infection prevention and control measures.

**Methods:** Two hundred environmental swabs taken from specific areas such as sinks, doors, cupboard handles, drip stands and bed railings were taken from the ICU of a tertiary care hospital in Jamaica. Conventional methods such as microscopy and culture techniques according to the guidelines set out by the Clinical Laboratory Standards Institute (CLSI) were used to identify them. After identification the antibiotic susceptibility tests were done using primarily the Kirby-Bauer Disk Diffusion method and the individual patterns of susceptibility noted.

**Results:** Of the 200 samples collected from the ICU, 25 MDR were identified: eight per cent (2 organisms) were Methicillin Resistant Staphylococcus (MRSA) and the remaining 92% (23 organisms) were MDR Gram negative organisms.

**Conclusion:** Multidrug resistant pathogenic organisms were detected in the ICU milieu, indicating the potential for transmission to critically ill patients. The identification of these pathogens highlights the need for reinforcement of infection control strategies to eliminate this potential reservoir of infectious MDR organisms.

**Keywords:** Environment, multidrug resistant, organisms

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## INTRODUCTION

The world in which we live consists of diverse micro-organisms which exhibit a symbiotic mutualistic relationship although some may be pathogenic (1–2). Some are beneficial and are a part of the normal flora, however, when pathogenic they can become multidrug resistant (MDR) and cause significant morbidity and mortality. A MDR organism for the purpose of this study (MDRO) is defined as one which is resistant to one or more drugs in three or more antimicrobial classes (3). The emergence of bacteria-mediated diseases caused by multidrug resistant organisms (MDROs) is an immediate and emerging problem (4).

The Intensive Care Units (ICU) is often one of the places that most MDR organisms appear for many reasons including the fact that the patients admitted there are usually critical and possibly immunocompromised (5). Many are treated with multiple antibiotics, increasing the possibility of selection for MDR pathogens (5). Also, in most developing countries the ICUs have inadequate staff to patient ratio, lack of equipment and large pool of infectious patients; these all increase the nosocomial infection risk (6). Other causes for the development of MDROs include the use of antibiotics in the food and veterinary industries, in which antibiotics were prophylactically against certain fish pathogens by giving them in the form of injections, food or baths, which weakens the marine animals' immune system (7). This resulted in a possible transfer to human beings and terrestrial animals. Human pathogen, *E coli* and fish pathogen, *Aeromonas* spp, display close linkage in the determinants used for antibiotic resistance (7). Similar characteristics are also seen in animal husbandry and agricultural industry (genetically modified produce) industries. The lack of knowledge and unnecessary antibiotic usage hastens us towards the post-antibiotic *era* where common infections which were previously able to be managed by simple antibiotics, could once again become lethal to patients (8).

The post-antibiotic *era* which has already started, raises concerns of severely limited therapeutic options as a result of newly developed antibiotics being at its minimum (9). This effect is particularly seen when there are multidrug resistant (MDR) pathogens, such as *Acinetobacter* spp. within the intensive care unit environment, which poses great threats of causing infections in patients as well as challenges for healthcare professionals in the management of these pathogens should they cause infections (10). Patients infected with MDROs (which are often found in the intensive care unit) require special attention since treatment becomes more difficult, as options for antimicrobial therapy is limited (11).

Among the Gram positive bacteria one of the more notable multiply drug resistant organisms described is methicillin resistant *Staphylococcus aureus* (MRSA). Methicillin resistant *Staphylococcus aureus* may be hospital acquired (HA MRSA) or community acquired [CA MRSA] (12). Hospital acquired MRSA is typically resistant to multiple antibiotics, while CA MRSA may be susceptible to a wide range of antibiotics but remain resistant to most of the B-lactam antibiotics (13). Methicillin resistant *Staphylococcus aureus* has many routes of transmission including fomite contact or the hands of colonized healthcare workers. The Gram negative bacilli (GNB) *Pseudomonas aeruginosa, Acinetobacter baumannii, Klebsiella pnuemoniae,* and *Stentrophomonas maltophilia* can also be become MDR, thus, limiting therapeutic options (14). They have become increasingly resistant to agents from various pharmaceutical classes. For example, according to the US Nosocomial Infection Surveillance System, *P aeruginosa* isolates taken from the ICU had a resistance rate of 52% to ciprofloxacin, 38% to imipenem, 31% for piperacillin and tazobactam and 24% to ceftazidime (14). Previous studies involving multidrug resistance in Jamaica show that Gram negative bacteria seem more common in hospital acquired infections especially in the ICU at the University Hospital of the

West Indies (UHWI), a tertiary care hospital in Jamaica (5). The extended spectrum beta-lactamase (ESBL) and AmpC B-lactamase producing strains of Enterobacteriaceae are often implicated in ICU nosocomial infections, and inactivate several classes of antibiotics, including the extended spectrum cephalosporins, ceftazidime and ceftriaxone (15). Bacteria such as *Pseudomonas aeruginosa*, *Acinetobacter*, *Klebsiella* and *Enterobacter* species at the UHWI, are among those found to be MDR. The two main bacteria causing MDR infections in the United States of America are *Pseudomonas aeruginosa* and *Acinetobacter* spp. (3). Similar results were reported in Jamaica by Thoms-Rodriguez *et al* (16). According to a recent study 26% of MDR *P aeruginosa* isolates and 24% of Acinetobacter spp. isolates were discovered in the ICU in UHWI and were the commonest Gram negative bacilli seen. According to Alexiou *et al* (2012), patients with infections had certain risk factors including hospital and ICU treatment and had more deaths in comparison to other hospitalized patient groups (17).

The aim of this research is to determine whether pathogenic MDROs are present in the ICUs at a tertiary care hospital in Jamaica. This was done after a recent study showed that majority of infections occurring due to *Acinetobacter* and *Pseudomonas aeruginosa* in the ICU were clonally related. We sought to determine whether there was a strain of these pathogens endemic in the environment and to characterize these potential pathogens.

## SUBJECTS AND METHODS

Two hundred environmental swabs were collected from various locations in a Jamaican tertiary care hospital's ICU over two weeks in two batches. The samples were taken from dry surfaces with swabs moistened with sterile distilled water pre-sampling then transported in Stuarts transport

medium and stored at 4 ˚C for approximately 18 hours. Each sample was plated on sheep blood agar (TSA with 5% Sheep Blood) and MacConkey agar and grown at 37 ˚C aerobically for 18–24 or 48 hours. Conventional techniques according to Clinical Laboratory Standards Institute (CSLI) standards were used to identify specific organism. Susceptibility tests were done using the Kirby-Bauer Disk Diffusion methods and E-tests. The antibiotics used for susceptibility testing for all Gram negative bacilli (GNB) with the exception of *P aeruginosa* included ampicillin (AMP), cotrimoxazole (SXT), amoxicillin-clavulanate (AMC), gentamicin (CN) and cefuroxime (CXM). Those for *P aeruginosa* included ciprofloxacin (CIP), meropenem (MEM), gentamicin (CN), piperacillin – tazobactam (TZP), ceftazidime (CAZ) and amikacin (AK). Vancomycin (VA) and oxacillin (OX) were used to test Gram positive cocci (GPC).

**RESULTS**

Of the 200 samples obtained from the intensive care units, 26 were negative for bacterial growth after 48 hours of incubation aerobically and anaerobically at 37 ˚C on Sheep Blood or MacConkey's agar, while the remaining 174 samples were positive (104 had Gram positive bacilli (GPB); 113 GPC; 45 GNB). More than one type of bacteria was identified for some samples.

The GPBs isolated were characteristic of diphtheroids. From the 113 samples that had GPCs, a total of 145 such isolates were obtained and included a mixture of *Staphylococcus* spp. (*Staphylococcus aureus* and Coagulase Negative *Staphylococcus aureus), Streptococcus* spp. and *Enterococcus* spp. Of the 145 isolated GPCs, only two were methicillin-resistant *Staphylococcus aureus* and both susceptible to vancomycin.

From the 45 GNBs, the following were isolated: *Enterobacter* spp, *Klebsiella* spp, *Pseudomonas* spp, *Acinetobacter* spp, *Alcaligenes* spp, *Serratia* spp, *Escherichia* spp and *Stentotrophomonas* spp. Of the 45 GNB isolated, 25 were MDROs. There were six major groups of MDROs isolated from the ICUs samples: *Enterobacteriaceae* (*Serratia* spp), *Pseudomonadaceae* (*Pseudomonas aeruginosa*), *Alcaligenaceae* (*Alcaligenes*), *Xanthomonadaceae* (*Stentotrophomonas maltophilia*), and *Staphylococcaceae*. A summary of the number and types of organisms obtained and those pathogens that were found in the ICU environment is shown in (Fig. 1).

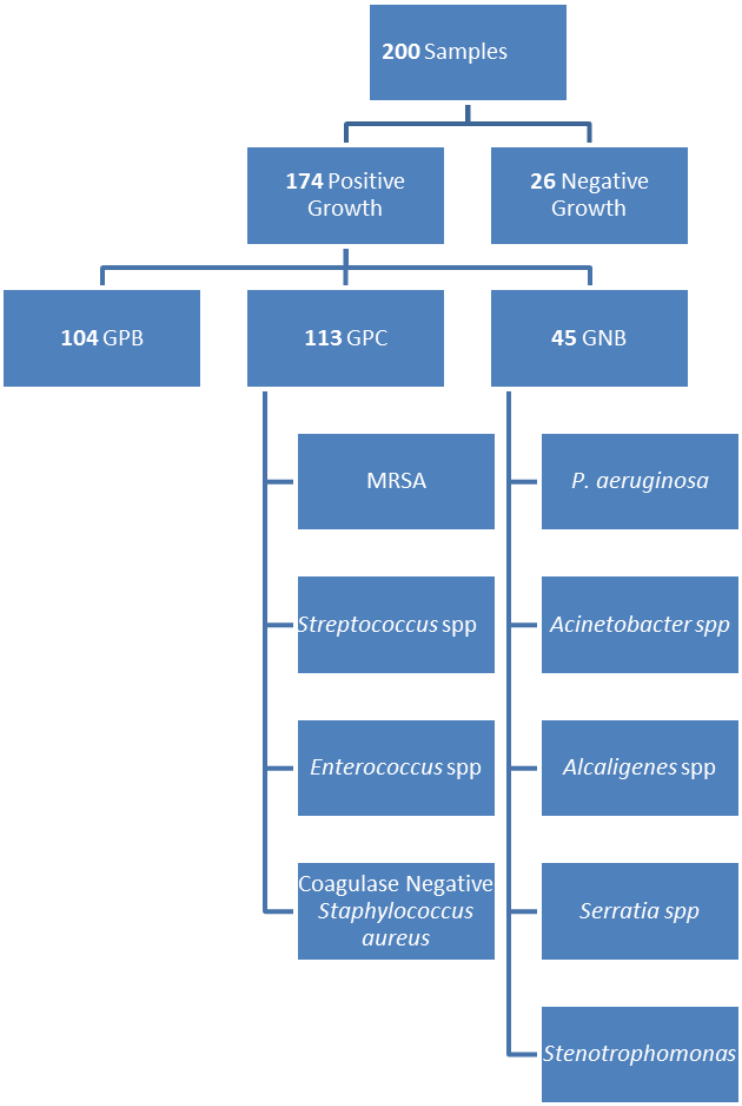


Fig. 1: Number and types of organisms and/or MDR pathogens found in the ICU environment.

Antimicrobial susceptibility test results for Gram negative bacilli showed varying susceptibility to the antibiotics tested (Fig. 2).

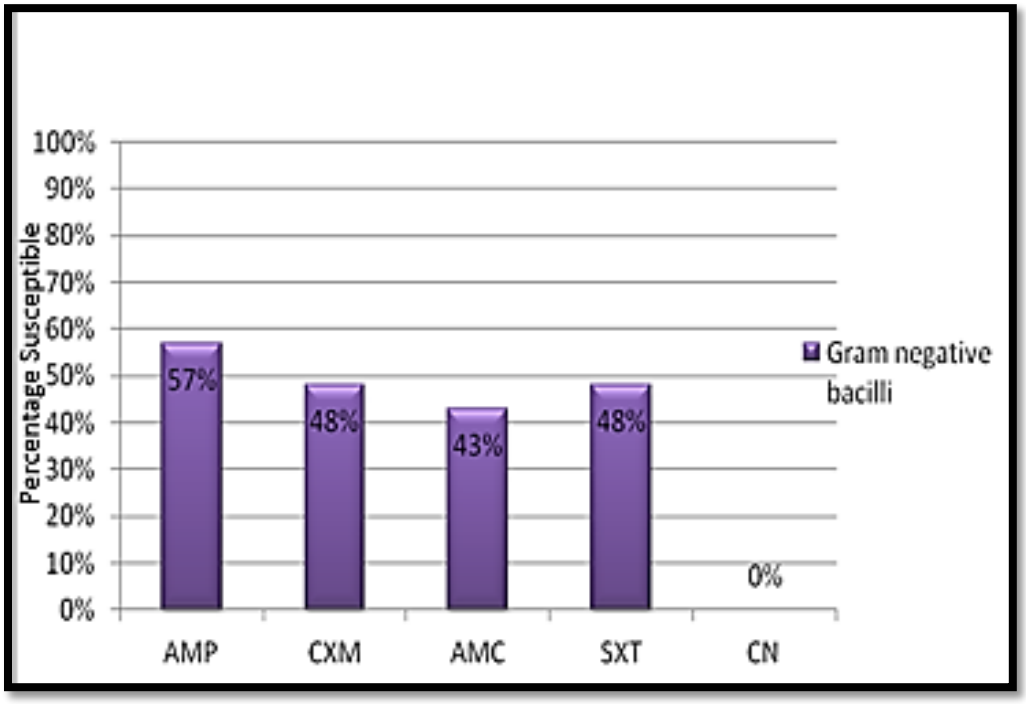


Fig. 2: Antibiogram for the Gram negative bacilli isolated. AMP, Ampicillin; CXM, Cefuroxime; AMC, Amoxicillin-Clavulanate; SXT, Cotrimoxazole; CN, Gentamicin

All of the GNBs were susceptible to CN. Forty-eight per cent were sensitive to CXM, AMC (43%) and SXT [48%] (Fig. 2) Due to the intrinsic resistance of *P aeruginosa* to various antibiotics, different sets of antibiotics are used for treatment and therefore, susceptibility testing. Antibiotic susceptibility testing. *P aeruginosa* showed 67% sensitivity to CN. Most *P aeruginosa* isolates were sensitive to MEM (83%) and CIP (67%). The sensitivity patterns were: AK (50%) and CAZ (33%).

The total number of multidrug resistant (MDR) organisms isolated from ICU-A was 11 and from ICU-B 14. However when the numbers of MDR GNBs and GPCs (MRSA) were

analyzed, with the exception of *P aeruginosa*, ICUA was found to have more of these organisms than ICUB. (Fig. 3). *Acinetobacter* spp. (45% *vs* 36%), *Alcaligenes* spp. (18% *vs* 14%), *Serratia* spp. (9% *vs* 0%), *S maltophilia* (9% *vs* 7%) and MRSA (9% *vs* 7%) were seen more in ICU-A than ICU-B (Fig.3). *Pseudomonas aeruginosa* on the other hand, was seen more in ICU-B, 36% in comparison to 9% in ICU-A. *Serratia* spp. was only isolated from ICU-A.

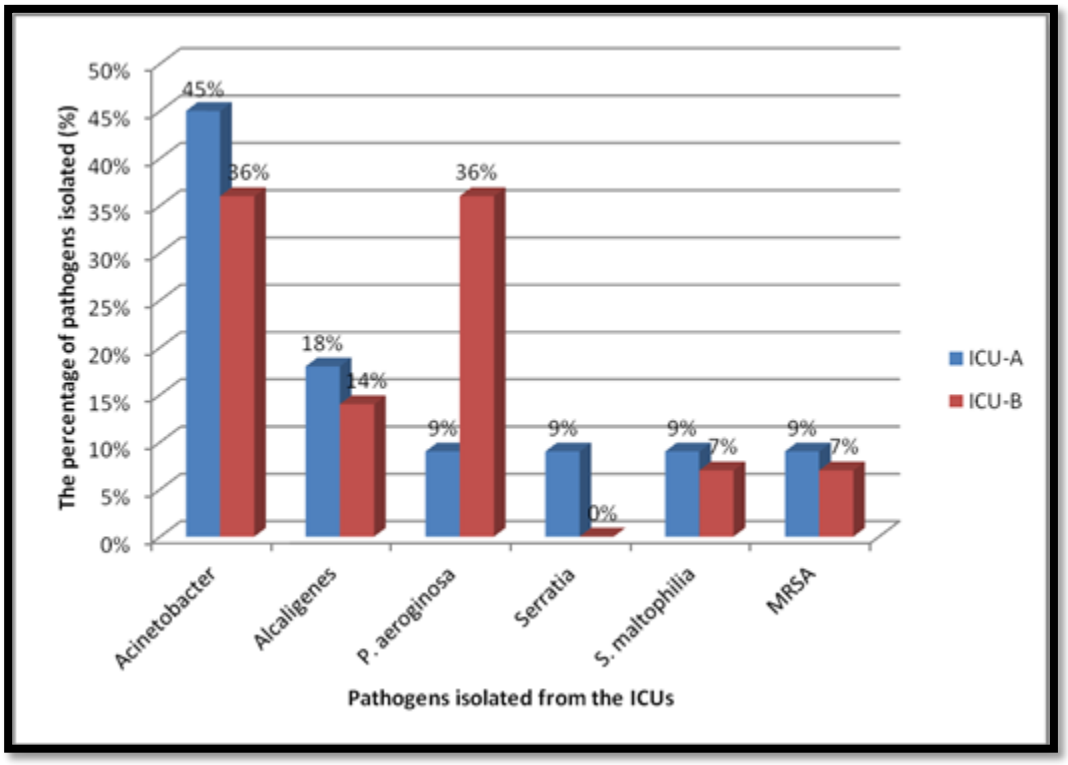


Fig. 3: Distribution of MDR organisms found in the different ICUs.

With the exception of *P aeruginosa* ICU-A had more pathogenic organisms in the environment than ICU-B.

The pathogens identified were distributed throughout the ICUs, with most organisms isolated from sinks (Fig. 4).

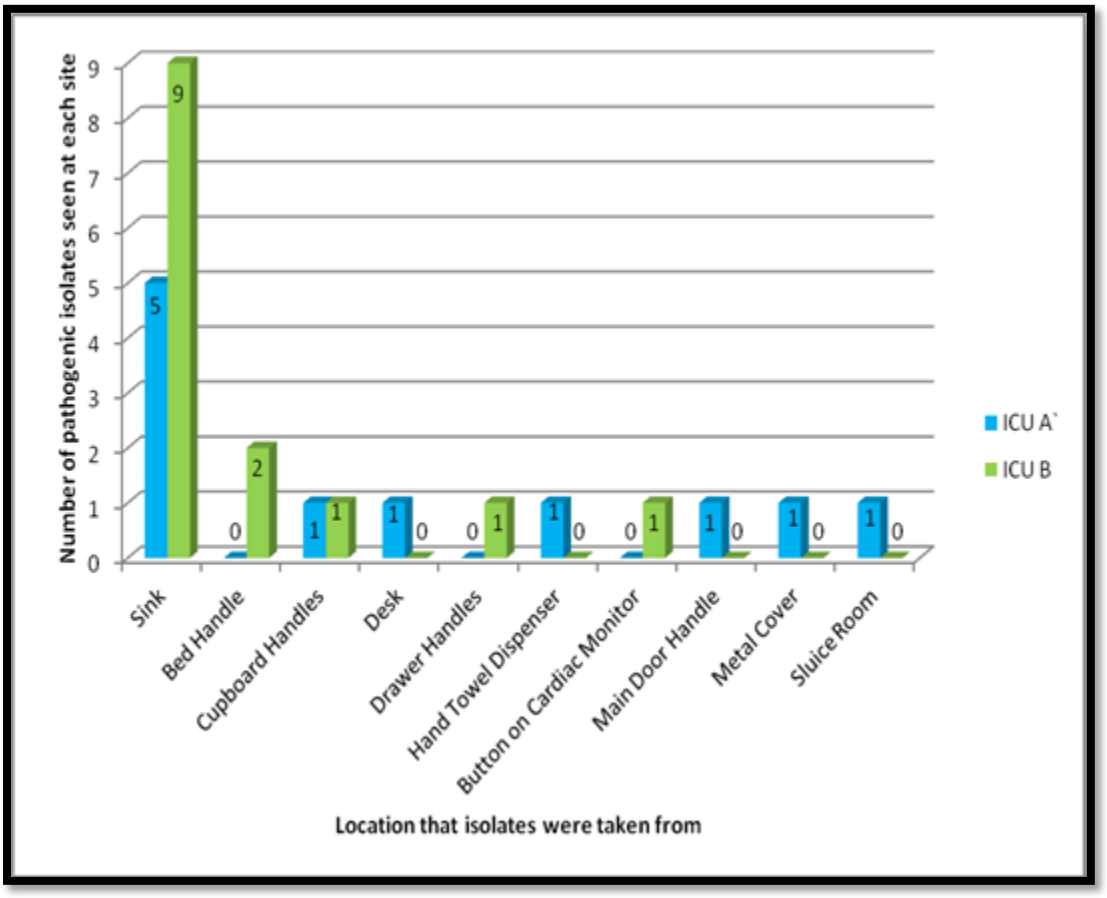


Fig. 4: Areas within the ICU where the isolates were detected.

## DISCUSSION

The results of the study showed that both potentially non-pathogenic (diphtheroids) and pathogenic organisms (MDRGNB and MDRGPC) were detected in the ICU environment. Micro-organisms were identified from areas touched or handled by staff and visitors of the ICU, the bed handles and containers of patients (*Pseudomonas aeruginosa* and a methicillin-resistant *Staphylococcus aureus*), and the majority from handwashing sinks which can be a source of recontamination of

the hands. The presence of pathogens in the sink could be a major source of infection for many reasons including the fact that the taps in the ICU lack aerators, which reduce the splashing effect of water back on to the hands or elsewhere. Previous studies showed outbreaks of *P aeruginosa* in a neurosurgery ICU possibly due to recontamination through the wash sinks (18). This is something that may be addressed with regular cleaning and the procurement of aerators to reduce splashing.

The ICU treats critically ill patients and as such is likely to be colonized with nosocomial pathogens although it is frequently cleaned (5). Despite this fact, of the 200 samples, 26 had no organisms present after incubation on either the Sheep Blood or MacConkey's agar plate aerobically at 37 $^{\circ}$C for 24 to 48 hours. This could have been due to frequent cleaning and decontamination of specific areas, or that the area swabbed was sanitized by personnel, thus, resulting in a negative bacterial growth. This action would have hindered the growth and existence of any micro-organism in that specific area. Proper sanitization techniques may have also been practiced in these areas by those transiting the ICU. The samples with no growth were mainly from cupboard handles, vents over beds and suction tubes. These areas had no pathogens or microbes and likely had highly commendable infection control measures which should be reinforced.

The detection of MRSA isolates in the ICU occurred during a recent admission of a MRSA infected patient there. The hospital environment is not likely to be the main source of MRSA infections at this tertiary care institution, as there have been no documented outbreaks of MRSA in the past five years and the prevalence rate of MRSA when examined in 2014 was 3% (19). Nevertheless, the presence of MRSA still poses a potential source of infection and it is important that proper cleaning is reinforced in order to ensure eradication of the organism from the environment.

The number of MDR isolates obtained from the hospital's two ICUs differed slightly. Intensive Care Units–A, however, had a higher percentage per type of individual pathogens than ICU-B. The reasons for this need to be further studied, however, it is possible that type of organisms seen may be related to the types of infections that admitted patients may have had.

Proper infection control in the healthcare sector is of great concern and is a key factor in preventing and eliminating nosocomial based infectious diseases, and may also reduce the ICU morbidity and mortality rates. Attention needs to be given to reinforcing regular cleaning and sanitization of the ICU environment to prevent the pathogens from becoming endemic there. The hydrogen peroxide vapor method of decontamination was found to be highly effective in sanitizing and eliminating certain pathogens from the environment as well as disinfection with bleach (20). The implementation of these strategies and others will provide a healthier, sanitary and well-kept environment within the hospital and will likely help to prevent, reduce and eliminate infections.

## CONCLUSION

Potentially pathogenic organisms as well as those not commonly associated with causing human disease were both found in the clinical and non-clinical surfaces in the ICU environment. The identification of pathogens on clinical surfaces highlights the need for reinforcement of infection control strategies to eliminate this potential reservoir of infectious MDR organisms.

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## Author Contributions

This research project was done as a partial requirement for D Lindsay's completion of the MSc in Medical Microbiology. She participated in all stages of the research process including the execution of the methodology, analysis and presentation of results. C Thoms-Rodriguez and AM Nicholson, supervised the candidate and participated in all stages of the research process as well. They helped to conceptualize the study, concretize the methodology, analyze the results and write, revise and approve the final version of the manuscript. S Maragh helped with the data analysis and the editing of the final draft of the paper for publication.

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