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REVIEWS

Characterization of Bacterial Strains and Their Resistance Status in the Hospital Environment: Systematic Review

Diego Alejandro ESTRADA RIOS[1], Isabela MUÑOZ ARIAS[1], Alvaro Javier CASTELLANOS GARCÍA[1], Monica CHAVEZ VIVAS[2*]

Abstract

Background: Clinical environments are considered reservoirs of antibiotic-resistant microorganisms that lead to the constant progression of nosocomial infections. The objective of this systematic review is to provide an epidemiological description of the role of the hospital environment as a reservoir of antibiotic-resistant bacteria and antibiotic-resistance genes.
Materials and Method: A systematic review based on the PRISMA guide was carried out, from the Science Direct, Redalyc, Scopus, Hinari, Scielo, Dialnet, PLOS, ProQuest, Taylor, Lilacs and PubMed databases with original studies conducted between January 2013-July 2024.
Results: A total of 1751 studies were identified, but only 60 studies were considered eligible for inclusión. The most common hospital environment sample sources were inanimate surfaces and medical devices and implements. extended-spectrum β-lactamases-producing Enterobacteriaceae, Methicillin-resistant *Staphylococcus aureus* and carbapenemase-producing non-fermenting bacilli as the main organisms found in the hospital environment mediated mainly by *bla* genes. Multidrug-resistant organisms were identified as the most abundant type in most samples, largely due to the ubiquity of efflux pumps (*acr*, *mex*, *mdt* and *emr*).
Conclusion: Our systematic review reveals the hospital environment is an ecological niche with predominance of few clones with a high degree of multi-resistance to antibiotics that contributes to generate new clones that spread through inanimate surfaces and equipment.
Keywords. Antibiotic-resistant bacteria, resistance genes, hospitals, environment, medical, devices, equipment contamination, systematic review.

[1]Medicine Program, Faculty of Health Sciences, Universidad Libre, seccional Cali-Colombia, Colombia
[2]Health Sciences Faculty, Universidad Libre, GIMMEIN research group, Colombia

***Corresponding author:**
Monica Chavez VIVAS, Universidad Libre – Seccional Cali, Campus Valle de Lili, Carrera 109. No. 22-00, Colombia
E-mail: monica.chavezv@unilibre.edu.co, monikchavez@gmail.com

INTRODUCTION

Clinical environments are reservoirs of potentially pathogenic microorganisms. These environments comprise inanimate surfaces objects and medical devices, as well as different fomites related to the patient's environment that produce significant bacterial contamination and contributes to the constant progression of Healthcare-Associated Infections (HAI).[1-3]

Among the most frequently reported pathogenic bacteria in HAIs are: *Staphylococcus aureus*, *Enterococcus spp*, *Escherichia Coli*, Coagulase-negative *Staphylococci* (CoNS), *Klebsiella spp*, *Pseudomonas aeruginosa, Enterobacter spp* y *Acinetobacter baumannii*.[4] These microorganisms can survive on inanimate surfaces for days, weeks, and even months, increasing the likelihood of transmission to patients.[2]

The problem that generates these infections is complicated by the presence of antibiotic-resistant bacteria, especially those with multiple drug resistance (MDR), which is a significant risk to human health.[4-6]

The term MDR refers to those bacteria that are simultaneously resistant to three or more classes of antibiotics that are commonly used in clinical practice.[4] multidrug-resistant organisms (MDROs) include methicillin-resistant *S. aureus* (MRSA)[7], vancomycin-resistant *Enterococcus* (VRE)[8], carbapenem-resistant Enterobacterales (CRE)[9], Extended-spectrum β-lactamases (ESBL)[10], carbapenem-resistant *A. baumannii* (CRAB)[11], multi-drug/pan-drug-resistant *P. aeruginosa* (MDR/PDR-PA)[12] and *Clostridium difficile*.[13]

The presence of MDR-bacteria in the hospital environment represents a great burden on health services because the lack of an effective therapy to treat this type of bacteria has significantly increased mortality due to HAI.[1,2] The objective of this systematic review is to provide an epidemiological description of the role of the hospital environment as a reservoir of antibiotic-resistant and MDR-bacteria, as well as antibiotic-resistance genes, in order to highlight the urgent need for further epidemiological research and studies that lead to the creation of programs and protocols for preventing the transmission of antibiotic-resistant and multi-resistant bacteria in all regions of the world with the development of effective strategies to mitigate the impact of HAIs on the healthcare system.

MATERIALS AND METHODS

Study protocol.
This review was conducted following the Preferred Reporting Items for Systematic Reviews and Meta-analysis (PRISMA) reporting guidelines for reporting record identification, title and abstract screening, as well as assessing full text eligibility for final inclusion ensuring inclusion of relevant information/studies in this systematic review.[14] The PRISMA checklist was also strictly followed in conducting this systematic review.

Database.
Systematic searching of various electronic databases such Science Direct (Elsevier), Redalyc, Scopus, Hinari, Scielo, Dialnet, PLOS, ProQuest, Taylor, Lilacs and PubMed was conducted to retrieve relevant published articles. Online library repositories of different institutions were also searched. Relevant MeSH terms and keywords were used to retrieve all relevant articles from the above-listed databases. The keywords and MeSH terms used were: "antibiotic resistance", "antimicrobial resistant strains", "Multidrug-resistant", "antibiotic susceptibility", "antimicrobial sensitivity", "drug resistance, bacterial", "resistance genes", "antibiotics", "Hospitals", "Environment", "Medical, devices", "Equipment Contamination" and "fomites".

Eligibility criteria.
Articles included in this review met the following criteria: 1) the search strategy was restricted to English and Spanish; 2) We analyzed data from the most complete data set, if multiple publications reporting findings of the same study in preliminary abstracts and articles were retrieved; 3) information describing the prevalence of antibiotic-resistant bacteria (ARB) and antibiotic-resistance genes (ARG) isolated from the hospital environment, medical equipment or devices and from fomites that have been in contact with patients; 4) studies reported in a 10-year time span from 1st January 2013 and 31st July 2024. Review articles, systematic review, meta-analyses, editorials, policy statements, and those with data collection commencing prior to 2012 were excluded.

Data extraction.
The articles were analyzed to extract information on antibiotic-resistant bacteria in the hospital environment as well as the presence of ARGs. Screening process and the quality of the full articles were independently reviewed by two authors (IMA, AJC), and double checked by DAE. The authors first reviewed the titles and abstracts of the articles in detail, also collected the

full texts of the studies and MCV assessed their eligibility for final inclusion.

Data were extracted and stored using a Microsoft 365 spreadsheet with information that included the environmental source, place of study, type of bacteria, ARB and ARG reported, the techniques used to identify and characterize ARB and ARG (Table S1, Supplementary Material).

After extraction, data were reviewed and compared by MCV, and any disagreements were resolved by a consensus among the investigators. A full list of the data elements extracted from each study are reported elsewhere (see supplementary material).

RESULTS AND DISCUSSION

Study characteristics.

A total of 1751 records were identified through an online search of electronic databases. Of these, 60 studies fulfilled the eligibility criteria and were included in this systematic review,[6-65] which gave a report about the topic of ARB and ARG detected in the hospital environment (Figure 1). The largest number of retrieved documents in our sample were studies usually conducted in either Europe or the Africa (16 articles each). However, more studies took place in southern Europe.

Thirty-two articles have data on Gram-positive and Gram-negative bacteria[4,6,15-44], 19 were based only on Gram-negative bacteria [9-12,45-59], and 9 were from Gram positive bacteria.[7,8,13,60-65]

The type of sample used by the studies in this systematic review are presented in figure 2. The most common sample used for studies were inanimate surfaces (29 articles). These surfaces were represented by floors, walls, doorknobs, door handles, window handles, room light switch plates, switches, lamp, tables, work table, tray tabletops, tabletops, ward furniture and chairs. Medical devices and implements (stethoscopes, thermometers, clinician

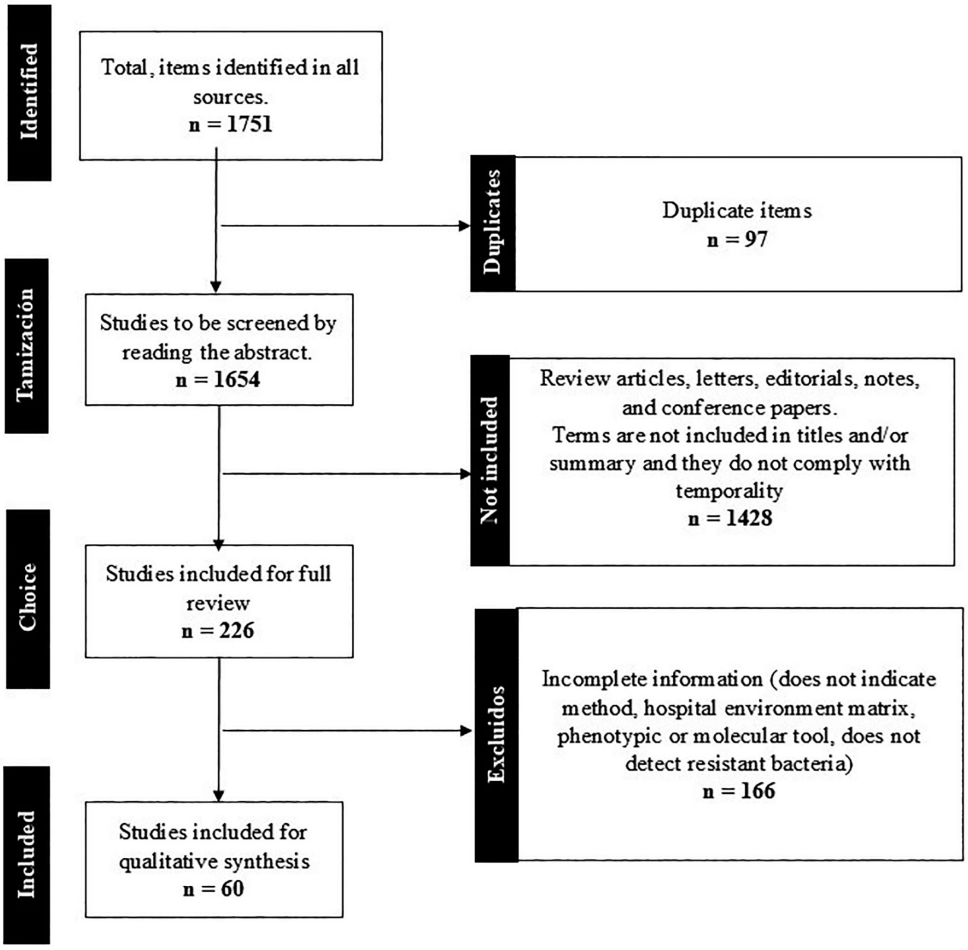

Figure 1. Flow chart of literature search and study selection based on PRISMA guidelines

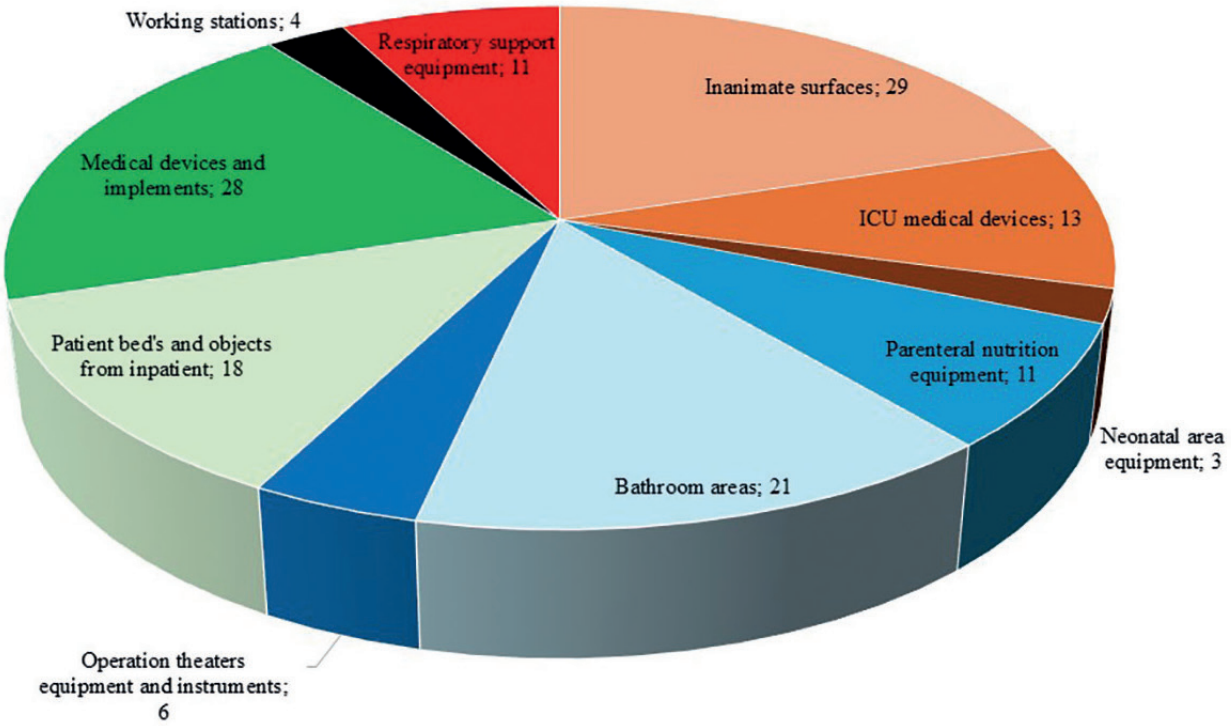

Figure 2. Distribution of the number of samples included in the studies reviewed.

gowns, medical devices, sphygmomanometer, cardiac monitors, pulse oximeters, bronchoscope cabinet/electrocardiography machines, call button, heating pad, urinal, blood pressure cuf, wash basin, heel protector) were also commonly analyzed in the studies (28 articles).

Most of the studies performed an identification of the bacterial organism to species level based on specific conventional biochemical tests (53.3%)[4,6,9,13,16,23,25,26,30-34,38,39,41-43,49,50,52,57,58,60,65], and 40% using automated systems including Vitek 2[10,15,24,28,33,37,44,53,54,56,59,] matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALD-TOF MS)[11,28,31,35,44,46,48,51,56] and API-20E.[40,45,46,63]

Ten studies (16.7%) carried out identification based on sequencing.[28,34,36,44,47,48,51,59,61,64] Molecular typing methods were reported in 23.3% of the studies, including pulsed-field gel electrophoresis (PFGE)[8,42,45,46,56,58,59,65], multilocus sequence testing (MLST)[8,46,47,52,56], and repetitive sequence-based polymerase chain reaction assay (rep-PCR).[56,62]

Almost 60% of studies used the Kirby-Bauer disk diffusion technique to assess antimicrobial susceptibility, following the reference cut-off point guidelines according to the Clinical and Laboratory Standard Institute (CLSI) (58.3%), the European Committee on Antimicrobial Susceptibility Testing (EUCAST) (6.6%) or the Antibiogram Committee of the French Society of Microbiology (5%) (Table S1, Supplementary Materials).

Pathogens reported in different samples from the hospital environment

Several bacteria were detected from the studies analyzed in this systematic review. Gram-positive bacteria represented by *S. aureus* (31/60, 51.7%) and CoNS (22/60, 36.7%). Among the Gram-negative bacteria, non-fermenting bacilli were prominent, including *Pseudomonas spp.* in 26 (43.3%) and *Acinetobacter spp.* in 25 studies (41.7%) (figure 3A). These organisms are among the bacteria most commonly reported to cause different HAIs, such as central line-associated bloodstream infections, catheter-associated urinary tract infections, ventilator-associated pneumonia, and surgical site infection.[2]

In the hospital environment, medical devices and inanimate surfaces were reported as the most contaminated. *Acinetobacter spp* and *S. aureus* were reported in 15 studies (25%) each as the main contaminants of medical devices and inanimate surfaces, respectively (figure 3B).

However, the proportion of bacteria reported varied

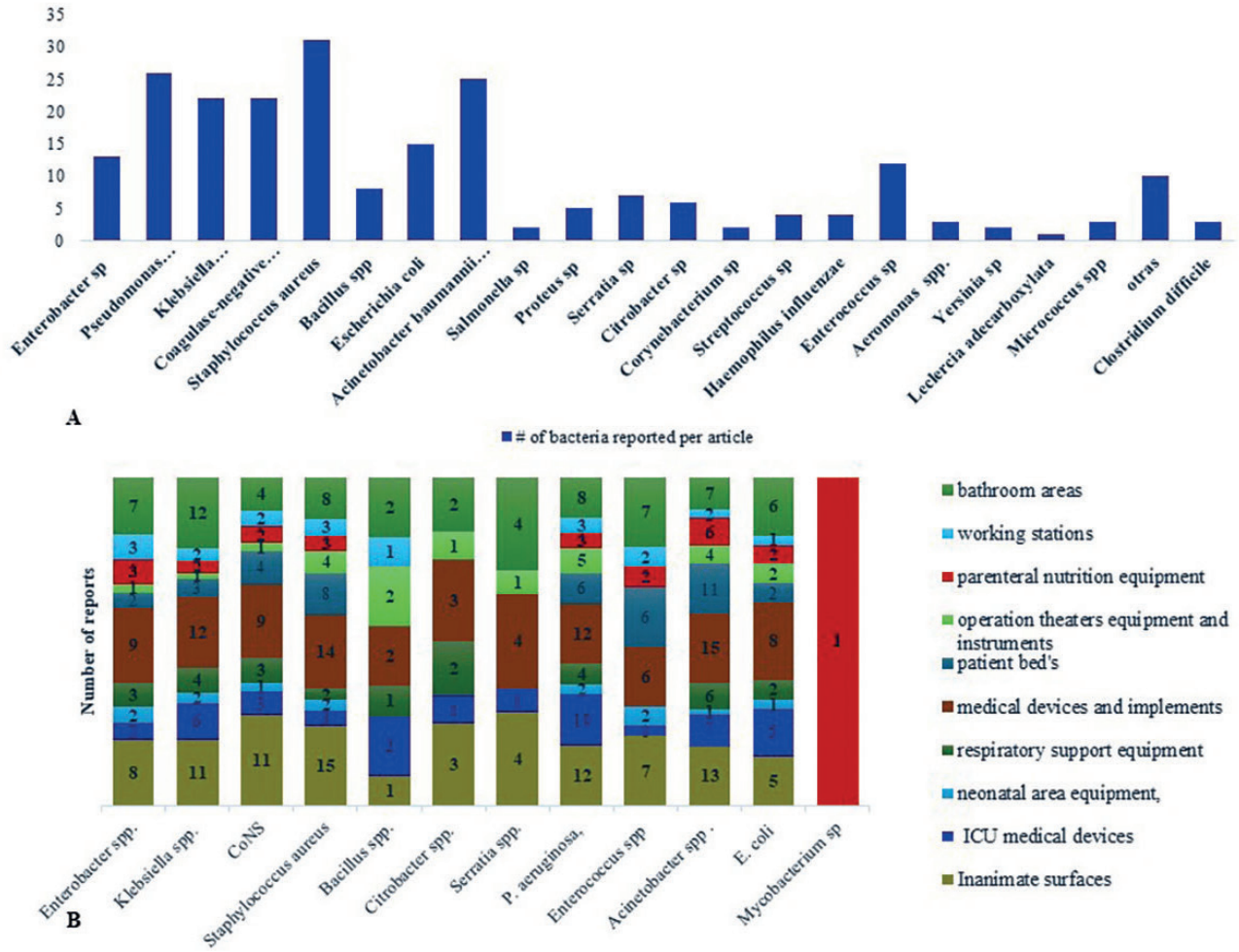

Figure 3. Distribution of bacteria according to: A. reported in the reviewed studies, and B. the type of sample evaluated.

considerably in some studies. The bacteria that contaminated inanimate surfaces and medical devices in Cameroon hospitals were *Enterobacter cloacae* (53.3%), followed by *P. aeruginosa* (22.6%) and *Klebsiella pneumoniae* (6.6%).[15] In hospitals in northwestern Ethiopia, CoNS, *S. aureus* and *K. pneumoniae* accounted for 52.8%, 47.2% and 43.2% respectively,[16] and in a hospital located in Mato Grosso, Brazil, CoNS (43.8%) and *A. baumanni* complex (21.9%) were the most prevalent.[37] While *S. aureus* was the most common bacterial isolate (44/219) from various sites like surface of biometric attendance devices, elevator buttons, door handles, staircase railings, telephone sets and water taps in a tertiary care hospital of Pokhara, Nepal.[26]

Pochtovyi et al. combined molecular methods based on quantitative PCR (qPCR) and Next Generation Sequencing (NGS) demonstrating DNA of pathogenic bacteria, *K. pneumoniae*, *P. aeruginosa*, *S. aureus* and CoNS on various inanimate surfaces. They pointed out the risks of insufficient regular disinfection of hospital surfaces and emphasized that control of nosocomial disease transmission relies on timely decontamination measures.[34]

Inanimate surfaces and commonly touched medical equipment are important reservoirs of potentially pathogenic bacteria that could predispose seriously ill patients to acquire HAIs.[17] Longtin et al. found in their study that the level of stethoscope contamination was substantial after a single physical examination and comparable to contamination of parts of the physician's dominant hand.[62]

Differential contamination on surfaces was also reported. Nkuwi et al. found that patient bed surfaces were the most contaminated by *S. aureus* (43.7%), while surgical carts were the least contaminated (7.7%), indicating the need to deepen decontamination practices that

lead to reducing the bacterial load, cleaning high-contact surfaces five times a day and providing soap at handwashing stations.[7]

In a survey of five hospitals in Cleveland, USA, the authors found that patient room floors were frequently contaminated with pathogens and that high-touch objects, such as blood pressure cuffs and call buttons, were frequently in contact with the floor and from there often resulted in transmission of pathogens to hands.[13]

The concept of environmental bacterial reservoir is a reality that requires strict compliance with current guidelines and recommendations for hand hygiene, cleaning, and disinfection of surfaces in hospitals.[6] Therefore, it is stressed that large-scale hospital infection prevention and surveillance systems must be permanently activated, as well as the periodic disinfection of objects as several authors suggest.[16,19,24,34]

Prevalence and profiles of antimicrobial resistance in bacteria isolated in the hospital environment

African countries recorded the highest number of ARB, especially to penicillins (18/60, 30%) and cephalosporins (12/60, 20%) (Figure 4 and Figure S1, Supplementary). Non-fermenting Gram-negative bacilli and *Enterobacteriaceae* with antibiotic-resistance were reported in 34 and 31 studies, respectively.

Odoyo et al. report that all isolates of *A. baumannii*, *Enterobacter* species, and *K. pneumoniae* recovered from high-touch surfaces in surgical, general, maternity, neonatal, outpatient and paediatric departments in Kenyan hospitals were non-susceptible to Piperacillin, Ceftriaxone and Cefepime.[22]

Gram-negative bacteria revealed the highest resistance levels to Ampicillin (97.5%), Ceftazidime (91.3%), Ceftriaxone (91.3%), and Aztreonam (90%) and Gram-positive bacteria had significantly high resistance levels to Penicillin (92.8%), Cefoxitin (83.5%), and Erythromycin (53.6%).[17] Specifically *P. aeruginosa*, *S. aureus*, and *S. pneumoniae* were

found to be highly resistant to Chloramphenicol (36%), Ciprofloxacin (91%), and Sulfamethoxazole (100%) on clinical surfaces and oxygen device accessories in the emergency unit of a tertiary health facility in Ghana.[21]

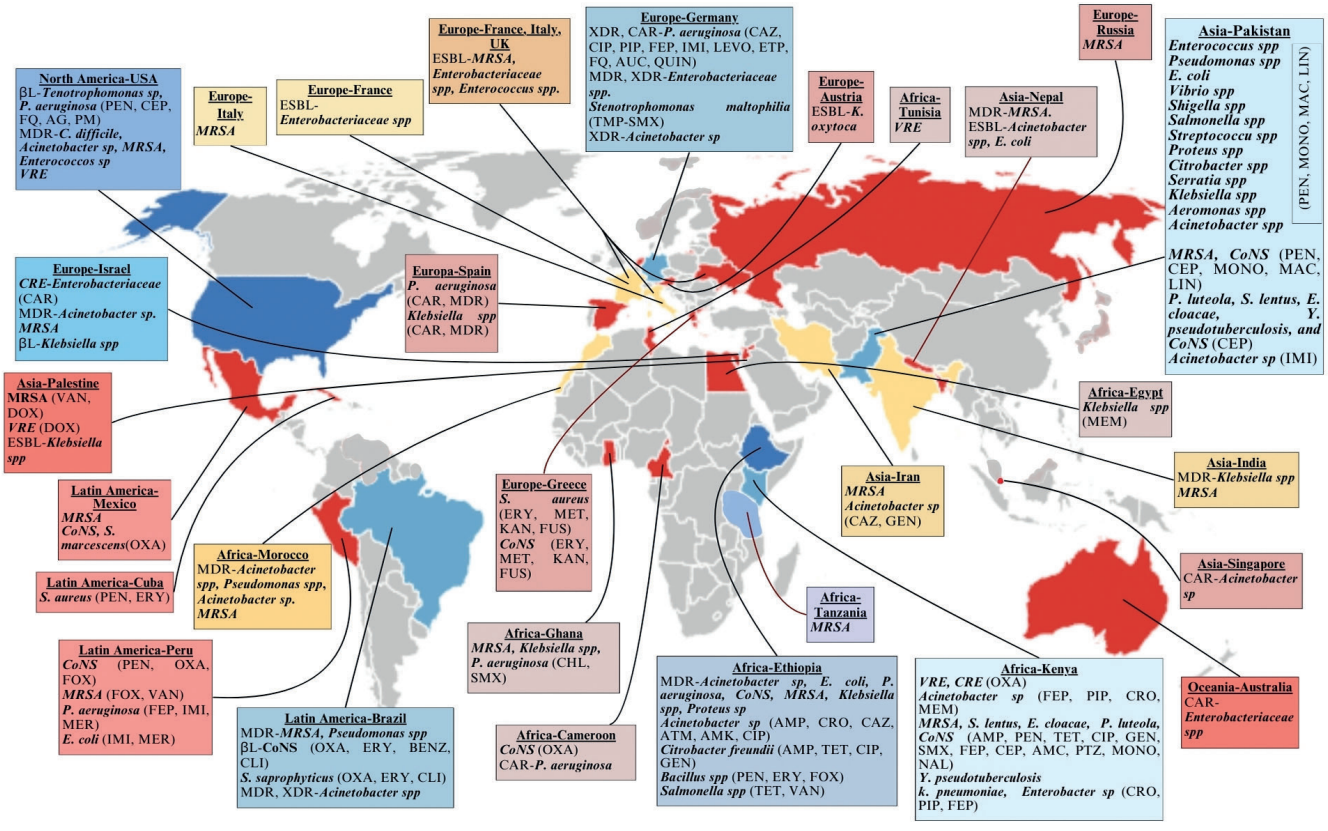

Figure 4. Antibiotic-resistant bacteria reported on hospital surfaces and on medical equipment and devices included in the study.

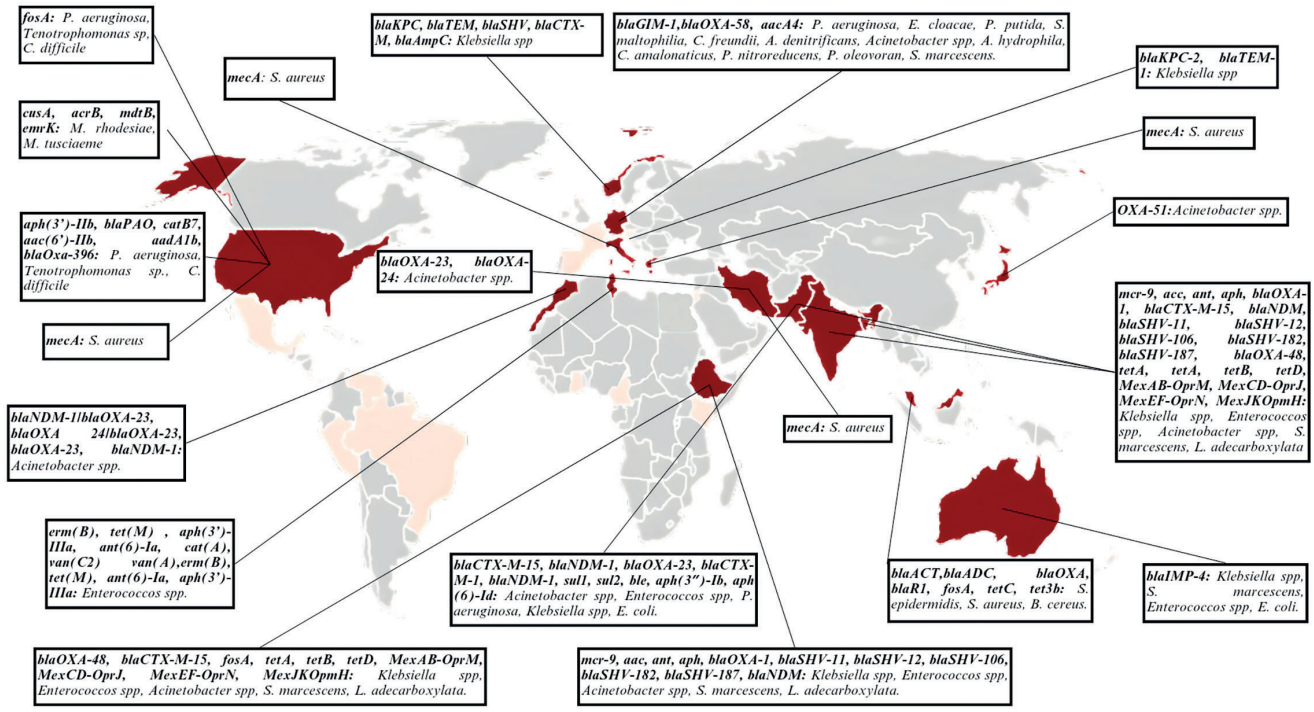

Figure 5. Antibiotic resistance genes reported in hospital environment included in the study.

The study conducted in the hospital environment of Ethiopia reported that linens were the most contaminated material (14.8%). Gram-positive bacteria showed significantly high levels of resistance to Penicillin (92.8%), Cefoxitin (83.5%) and Erythromycin (53.6%) and Gram-negative bacteria showed the highest levels of resistance to Ampicillin (97.5%), Ceftazidime (91.3%), Ceftriaxone (91.3%) and Aztreonam (90%). [17]

In all these studies, the authors point out that there is no regular disinfection and sanitation of hospital equipment and surfaces. Therefore, it is necessary for stakeholders to maintain continuous discussion and follow-up to develop the habit of regular disinfection and sanitation of hospital surfaces and equipment.

Several studies specifically reported ESBL-producing Enterobacteriaceae (22/60, 36.7%), MRSA (18/60, 30%) and carbapenemase-producing non-fermenting bacilli (15/60, 25%) as the main organisms found in the hospital environment.

There is a high risk for hospitalized patients to acquire these types of organisms through environmental exposure. In the assessment of carriage and environmental contamination by CRAB, the surrounding environment of all patients was reported to be contaminated with this bacterium. There was a positive correlation between the patient's colonization score and the environmental contamination score (Spearman rank-rank coefficient, r=0.63, p<0.001; r=0.4, p=0.04 for oral mucosa, r=0.7, p<0.001 for skin, and r = 0.46, p = 0.14 for rectum).[11] In rooms with patients colonized rectally with CRAB, 15.5% of environmental samples were positive for the bacteria.[57] Rosa et al. found that patients exposed to a hospital environment contaminated with CRAB had a 2.77-fold higher risk of contracting these bacteria than did unexposed patients (relative risk, 2.77 [95% confidence interval, 1.50-5.13]; P <0.002).[58]

In the same way, the study evaluating MRSA contamination of stethoscopes and physicians' hands found that the level of stethoscope contamination was substantial after a single physical examination and comparable to contamination of parts of the physician's hand. The researchers found that there was a stronger association with the level of contamination of fingertips (r=0.80; P<0.001).[52]

On the other hand, there is great concern in the hospital systems about the presence of MDROs due to the difficulty of treating the infections they cause and the possibility of triggering serious illnesses and death, constituting a serious threat to public health.[4,5]

The MDROs were reported in 28 (46.7%) studies.

The highest number of reports of this type of bacteria was found in studies from Africa (13/60, 21.7%). There were three reports of extensively drug resistant (XDR)-isolates in Pakistan, German and Brazilian hospitals with a prevalence of 73%, 54.4% and 42.9%, respectively, on ICU surfaces.[27,37,54]

The studies included in this review show that both hospital surfaces (19 reports) and medical equipment and supplies (18 reports) were contaminated with MDROs in the same proportion. MDR-Gram-positive bacteria prevalence was relatively lower (13/60, 21.7%) in the hospital environment that MDR-Gram-negative bacteria (18/60, 30%). However, in some studies this difference is greater. In the hospital environment of hospitals in Ethiopia, MDROs were observed in 36.1% of Gram-positive isolates and 78.4% of Gram-negative isolates that were present[16] and in *E. coli* (72.7%) and *S. aureus* (58.7%)[19]. Similarly, the study that evaluated the surfaces of several hospitals in Morocco determined that approximately 31.7% of the Gram-negative isolates were MDROs.[6]

Kindu et al. reported MDR and carbapenemase-producing *K. pneumoniae* at rates of 89.9% and 85.7%) respectively, on most types of surfaces in the hospital environment, especially from the baby bed sets and incubators.[9]

MDROs are among the most common organisms causing nosocomial infections in ICUs and are associated with increased mortality.[5] They are also extremely adaptable to the selective pressure caused by antimicrobial agents. Because of the need for intensive antimicrobial therapy in ICUs, selective pressure in this setting is considerably high. This is supported by the finding that antimicrobial therapy prior to an ICU stay increases the risk of colonization with MDROs.[4, 5] MDR-*P. aeruginosa* has been shown to cause outbreaks that are often associated with hospital surfaces as a continuing source of further spread.[12]

On the other hand, a prospective multicenter study conducted to characterize the nature of MDROs transmission between the environment and patients demonstrated that bacterial transfer events occurred early in admission in 18.5% of cases.[42] The authors note that further studies on prevention methods beyond the standard practice of room disinfection at the end of a patient's stay are needed to better prevent the acquisition of MDROs through the environment.

Some reports indicate that dried biofilms form on inanimate surfaces and medical devices and persist for a long period of time, making cleaning and disinfection of hospital environments difficult. Additionally, these biofilms have been shown to contain pathogens and MDROs that can be transmitted, posing a risk to patients.[36,54]

Contamination of hospital surfaces by MDROs is a real danger to public health. The concept of environmental bacterial reservoir is a reality that requires strict compliance with current guidelines and recommendations for hand hygiene, cleaning, and disinfection of surfaces in hospitals.

Resistance genes reported in the hospital environment.

In this systematic review, information on the distribution of ARG was compiled from 27 (45%) studies, in which seven studies (11.7%) performed wholegenome sequencing.[28,44,47,48,52,61,64] Three studies (5%) detects resistant genes via quantitative real-time PCR (qPCR).[35,56,62] In comparison, seventeen studies (28.3%) performed a conventional PCR assay for the investigation of ARG. The description of the types of ARG distributed in the regions is presented in Figure 5. The highest diversity of ARG was reported on hospital surfaces and medical devices from hospitals in Asia.[27,28,47-49,51,60,61]

Most of the ARG reported are those that confer resistance to β-lactam antibiotics (*bla*), aminoglycosides (*aph*) and tetracyclines (*tet*). Nine studies reported the presence of *bla* genes on both hospital surfaces and medical devices and implements[28,44,46-48,51,54-56], three studies reported them only on surfaces[27,52,59], and one study on medical devices and implements.[35]

Genes encoding ESBL-type enzymes (*bla*SHV, *bla*TEM, *bla*CTX-M) have been frequently detected in the hospital settings around the world.[27,28,35,48,52,56] However, the report of a variety of carbapenemase-producing genes such as *bla*OXA, *bla*NDM, *bla*KPC, *bla*IMP and *bla*GIM-1 is a distinctive feature in the articles included in this review.[27,28,35,44,46-49,51,52,54-56,59,61]

Particularly, the multicenter study involving six countries in Asia determined that 13.3% of hospital surface swabs were positive for *bla*CTX-M-15, 5.4% for *bla*NDM, and 1.2% for *bla*OXA-48-like.[48]

Isolates carrying *bla* genes were detected on ICU surfaces in hospitals in Pakistan, with the most prevalent being *bla*TEM (68%), *bla*SHV (66%), *bla*CTX-M (29%), *bla*NDM (18%) and *bla*OXA (16%). Among the species, *Aeromonas spp*. and *E. coli* were found to possess all five detected genes, while *Acinetobacter spp.*,

Salmonella spp. and *Klebsiella spp*. also harbored four of the five genes. The highest prevalence of *bla*NDM was found in *Acinetobacter spp*., which is a real threat as it causes resistance to carbapenems and Colistin, antibiotics reserved as a last resort against infections.[27]

In *A. baumannii* recovered from the surface of ICU beds in Iranian hospitals, 77.5% were carriers of OXA-23 and 5% of OXA-24.[49]

A differential pattern in the distribution of *bla* genes is also reported. For example, in Malaysian hospitals, the presence of different variants of *bla*OXA has been reported in the hospital settings, while *bla*SHV-27, which encodes ESBL in *K. pneumoniae*, was found in patient sinks and *bla*ADC-32, which confers resistance to cephalosporins in *A. baumannii*, was found on staff counters.[61]

The study of an outbreak caused by KPC-2-producing *Klebsiella oxytoca* in the Division of Hematology of a hospital in Austria determined that isolates obtained from sinks harbored the genes *bla*K-PC-2 and *bla*TEM-1 and handwashing sinks were considered a possible reservoir.[52] In the same way, carbapenem-resistant Enterobacteriaceae harbouring gene *bla*IMP-4 were detected in In ICU sink swab samples from Australian hospitals.[59]

Strains carrying *bla* genes, especially those that confer resistance to carbapenemases, have become a public health problem due to their associated multi-resistance, their implications in the hospital outbreaks and their tendency to spread rapidly throughout the world.

In MDR-A. *baumannii* isolates obtained from beds in two ICU in a Moroccan hospital, the coexistence of the genes *bla*NDM-1/*bla*OXA-23-like and *bla*OXA 24-like/*bla*OXA-23-like were detected.[46]

Dziri et al. investigated the hospital environment in a Tunisian hospital and recovered MDR-VRE in 33.3% carrying resistance genes: *erm*(B), *te*t(M), *aph*(3')-IIIa, *ant*(6)-Ia, *cat*(A) and *van*(C2), thus demonstrating that the hospital is a reservoir of ARG, which can potentially become particularly problematic.[8]

In addition, MDR was identified as the most abundant type in most samples, largely due to the ubiquity of MDR efflux pumps in prokaryotes, these genes corresponded to*: acr*, *por,mex, opr, mdt* and *emr*.

Antibiotic-resistance and especially MDR are maintained in the hospital environment largely by horizontal gene transfer (HGT), particularly mediated by plasmids and integrons.[8,54] Favored by biofilms that provide a biological niche for horizontal gene transfer between bacteria, facilitating cross-transmission of MDROs among patients, staff and the environment.

Patterns of dissemination of resistant bacteria in the hospital environment.

Inanimate surfaces and frequently touched medical equipment in operating rooms and ICUs are reservoirs of potentially pathogenic bacteria that could predispose critically ill patients to acute respiratory infections. Sebre et al. found that the proportions of the antimicrobial resistance profile of isolates are much higher in the clean inanimate environments studied.[17] The researchers suggest that bacterial environmental contamination could possibly be contributing to acute respiratory infections and the dissemination of MDR strains in the hospital environment, and therefore recommend conducting large-scale investigations to evaluate the clonal relationship between inanimate surface and clinical strains.

It is then proposed that the hospital environment is an ecological niche with predominance of few clones with a high degree of multi-resistance to antibiotics that contributes to generating new clones that spread through inanimate surfaces and equipment. In addition, they increase the possibility of generating outbreaks of nosocomial infections due to the cross-transmission of these pathogens between patients through contaminated hands and surfaces.[8,28,45,46-48,52,56,59]

The study that evaluated MDR-*E. faecium* in the hospital environment of Tunisian hospitals, found that most of them belonged to a single clone called sequence type (ST) 910 with characteristics similar to clone ST80 belonging to clonal complex (CC17), which is characterized by presenting ampicillin and vancomycin resistance, as well as by the presence of virulence determinants such as *hyl* (encoding a hyaluronidase-like protein) and a putative pathogenicity island that includes *esp* (enterococcal surface protein) and is responsible for severe nosocomial infections and hospital outbreaks.[8]

The study carried out with clinical and environmental isolates of MDR-*A. baumannii* grouped all isolates into two main groups (ST 195 and ST 1089) with a genetic similarity of 96.4%, indicating that the clonal dissemination of environmental isolates of *A. baumannii* would be related to that of clinical isolates recovered from colonized or infected patients.[46]

MRSA isolates recovered from the ICU environment were *spa* typed and found to comprise 11 spa types, including t7688, t7689, and t7789, which have

not been reported previously. The majority of isolates (43%) belonged to spa types t030 and t037, and isolates from patients and the environment were generally indistinguishable.[60] Similar results are reported with *P. aeruginosa*[44] and *K. pneumoniae* isolates.[45,52,59]

However, genomic analysis performed on MDROs recovered from ICU sinks in two hospitals in the United States and Pakistan revealed long-term colonization by *Pseudomonas spp*. and *Serratia marcescens* strains in multiple rooms and not limited to the outbreak setting[28]. Similarly, *K. pneumoniae* ST15 has been identified in the same hospital ward in Pakistan, Bangladesh, and Ethiopia on multiple occasions, suggesting clonal persistence in the same setting, and has been found to be identical to isolates causing neonatal sepsis in Pakistan over similar time periods, suggesting persistence of dominant clones at multiple time points.[48] Evaluation of a low-frequency, long-term hospital outbreak caused by KPC-producing *K. pneumoniae* ST258 determined clonal transmission to play a predominant role in maintaining this long-term outbreak.[56]

Contamination of hospital surfaces by MDR-bacteria is a real danger to public health. Therefore it has been proposed that hospitals can best reduce the bacterial loads by improving waste-handling protocols, cleaning high-touch surfaces five times a day and providing soap at the handwash stations as suggested by Odoyo et al.[23] For example, the reported outbreak of amikacin- and ciprofloxacin-resistant *A. baumannii* ST219 in the emergency ICU of Tokai University Hospital was due to colonization and spread through tap water. The outbreak was successfully controlled after replacement of the water system and implementation of daily cleaning of water taps and oral care using a dry method.[47]

The limitation of our study is that we do not have a larger number of data from Oceania; furthermore, most of the studies are from African and Asian countries, which might not be an adequate description of the entire world. In 60% of the studies, ARGs or ARBs were not determined. However, our study shows an exclusive preview of antibiotic-resistance in the world.

CONCLUSION

Our systematic review reveals that inanimate surfaces represented by floors, walls, doorknobs, switches, lamps, work tables, trays, table tops were most frequently reported to be contaminated, thus constituting important reservoirs of potentially pathogenic bacteria that could predispose seriously ill patients to acquire HAIs. ESBL-producing Enterobacteriaceae, MRSA, carbapenemase-producing non-fermenting bacilli and a marked presence of MDROs were most reported in the hospital environment around the world. The *bla* gene was the most reported among the isolates studied in all continente, and the *acr, mex, mdt* and *emr* genes encoding efflux pumps were reported in some studies, largely favoring the ubiquity of MDR in environmental samples.

The genetic structure of all these isolates shows a predominance of a few clones with MDR phenotype and the emergence of new clones that have efficiently adapted to the hospital environment with a great capacity to survive for a long time. These are the high-risk clones that must be carefully monitored with policies for their control and elimination according to the specific conditions of each hospital and country.

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