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OCCURRENCE OF *STAPHYLOCOCCUS AUREUS*, *ESCHERICHIA COLI* AND *KLEBSIELLA PNEUMONIAE* ON INANIMATE SURFACES OF PUBLIC RESTROOMS AT BOA VIAGEM BEACHFRONT, RECIFE/PERNAMBUCO

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ABSTRACT

Public restrooms on the busy Boa Viagem beachfront in Recife, Brazil, are potential reservoirs for pathogenic bacteria, posing a significant public health risk due to high user turnover and humidity. This study aimed to isolate and identify *Staphylococcus aureus, Escherichia coli* and *Klebsiella pneumoniae* from samples collected on surfaces of public restrooms at Boa Viagem beachfront, as well as to evaluate the antimicrobial resistance profile of these isolates. Samples were collected from three restrooms using sterile swabs. Bacteria were I solated and identified through culturing, Gram staining, and biochemical tests. Antimicrobial susceptibility was determined using the Kirby-Bauer disk diffusion method, and the Multiple Antibiotic Resistance (MAR) index was calculated. The overall bacterial contamination prevalence was 50% (18/36). *S. aureus* was the most frequent (50%), followed by *E. coli* (27.8%) and *Klebsiella* spp. (11.1%). Faucets were the most contaminated surfaces. Alarmingly, 100% of *S. aureus* isolates were Methicillin-Resistant *Staphylococcus* aureus (MRSA), and the Gram-negative isolates exhibited Extended-Spectrum Beta-Lactamase (ESBL) and suspected *Klebsiella pneumoniae* Carbapenemase (KPC) production phenotypes. All isolates were multidrug-resistant (MDR) with high MAR indices. High-touch surfaces in these public restrooms are reservoirs for clinically relevant MDR pathogens. The findings underscore an urgent need for stringent cleaning protocols and public hand hygiene

Keywords: Microbial contamination; Public restrooms; Antimicrobial resistance; Public health.

INTRODUCTION

Public restrooms are shared spaces of great importance for maintaining hygiene conditions in high-traffic areas. However, surfaces frequently touched by numerous individuals are highly prone to microbial contamination due to high user turnover, variability in hygiene practices, and the characteristic humidity of these environments (Queiroz et al., 2013; Mendes; Oliveira Júnior; Siqueira, 2022).

Boa Viagem beachfront, located in the city of Recife, Pernambuco, Brazil stretches for approximately 7.5 kilometers and receives a significant daily flow of visitors, establishing itself as one of the longest and busiest urban beaches in the country, according to data from the Recife City Hall (Prefeitura da Cidade de Recife. 2023). The intense use of public restrooms in this beach environment heightens the potential for microbiological contamination hotspots, representing a substantial risk to public health (Flores, et al., 2011; Medeiros et al., 2012).

Inherently, these locations present unsanitary conditions, and repeated contact with surfaces such as faucets, flush valves, and doorknobs facilitates the transfer of microorganisms between individuals and inert surfaces, which, in turn, can serve as a vehicle for transmission, subsequently exposing new users (Medeiros et al, 2012).

Monitoring high-traffic community environments, such as public restrooms, is extremely relevant due to the particularities of human behavior and the frequent inadequacy of hygiene practices. Neglecting hand hygiene after using these spaces is a determining factor in the spread of resistant microorganisms (Aiello et al., 2008). It is recognized that evidence-based interventions, including the regular cleaning and disinfection of surfaces, combined with educational campaigns on hand hygiene and the rational use of antimicrobials, demonstrate effectiveness in reducing microbiological contamination and preventing the spread of resistance in various contexts (CDC, 2008).

According to the WHO, antimicrobial resistance is one of the top ten global public health threats (WHO, 2023), with records of a significant increase in resistance of Gram-negative bacteria to commonly used antimicrobials (WHO, 2017; 2021). This scenario is particularly alarming, as it reduces effective therapeutic options, increasing morbidity and mortality rates associated with infections. Although traditionally more associated with hospital environments, this problem extends to community settings, such as public restrooms, where natural selection and selective pressure favor the survival and dissemination of resistance determinants (Livermore, 2003).

Therefore, the implementation of such measures becomes imperative to mitigate risks and promote public health in these shared spaces. Given this context, the present study aimed to isolate and identify *Staphylococcus aureus*, *Escherichia coli and Klebsiella pneumoniae* from samples collected on surfaces of public restrooms at Boa Viagem beachfront, as well as to evaluate the antimicrobial resistance profile of these isolates.

MATERIALS AND METHODS

STUDY DESIGN

This is a descriptive, cross-sectional, and experimental study in which three public restrooms, randomly selected and located along the Boa Viagem beachfront in Recife/Pernambuco/Brazil, were analyzed. The restrooms encompassed different points with high user traffic. Samples were collected in duplicate from each of three high-touch surfaces: door handles (main access point - one per restroom), flush valves/levers (hand-contact area - three per restroom), and sink faucets (humid surface with biofilm risk - two per restroom). Each restroom was identified as Restroom 1 (B1), Restroom 2 (B2), and Restroom 3 (B3), covering both female (F) and male (M) sections.

SAMPLE PROCESSING AND ANALYSIS

Collection was performed in duplicate per point using sterile swabs moistened with buffered saline solution (0.85% NaCl). The swabs were stored and transported to the Microbiology and Parasitology Laboratory of the Centro Universitário Maurício de Nassau (UNINASSAU - Boa Viagem) for subsequent analysis. In the laboratory, the swabs were added to test tubes containing Brain Heart Infusion (BHI) broth and incubated in a bacteriological incubator for 24 hours at 36ºC±1ºC. Afterwards, exhaustion streaking was performed onto Eosin Methylene Blue (EMB) agar, MacConkey agar, Chromogenic Coliform agar, Mannitol Salt agar, and Cystine-Lactose-Electrolyte-Deficient (CLED) agar, followed by incubation at 36ºC±1ºC for 24 hours (Silva Júnior, et al., 2020).

Isolated bacterial colonies underwent macro- and microscopic characterization, including assessment of morphology (color, edges, elevation, and diameter), Gram staining, and conventional biochemical tests: catalase test, coagulase test, fermentation tests on Triple Sugar Iron (TSI) agar, indole test for tryptophanase detection, Voges-Proskauer (VP) reaction, and amino acid decarboxylation tests (lysine, ornithine, arginine). All tests included positive controls (*E. coli* ATCC 25922, S. *aureus* ATCC 25923) and negative controls (sterile medium), performed in triplicate to ensure reproducibility (Silva Júnior, et al., 2020).

DETERMINATION OF THE RESISTANCE PROFILE

The analysis of the antimicrobial resistance profile followed the disk diffusion (Kirby-Bauer) method on Mueller Hinton agar, according to the guidelines of the Brazilian Committee on Antimicrobial Susceptibility Testing (BrCAST, 2023). Bacterial suspensions were standardized in sterile saline solution (0.85% NaCl) to achieve turbidity equivalent to the 0.5 McFarland standard (1.5 × 108 CFU/mL). The following antibiotics were tested for Gram-negative bacteria: carbapenems (imipenem, meropenem), aminoglycosides (gentamicin, amikacin), fluoroquinolones (ciprofloxacin), macrolides (azithromycin), monobactam (aztreonam), cephalosporins (cefotaxime, cefepime, ceftazidime, ceftriaxone), beta-lactam/beta-lactamase inhibitors (amoxicillin/clavulanic acid, piperacillin/tazobactam), and phenicol (chloramphenicol). For Gram-positive bacteria: penicillins (oxacillin), glycopeptides (vancomycin, daptomycin), oxazolidinones (linezolid), cephalosporins (ceftriaxone, cefoxitin), macrolides (erythromycin), lincosamides (clindamycin), and tetracyclines (tetracycline).

The interpretation of inhibition zones (diameter in mm) followed the BrCAST 2023 breakpoints, classifying the strains as resistant (R), standard dose susceptible (S), or susceptible with increased exposure (I). MDR was determined by the Multiple Antibiotic Resistance (MAR) index, calculated by the ratio of the number of antimicrobials to which resistance was observed (A) to the total number tested (B), considering MDR when MAR ≥ 0.2 (Krumperman, 1983).

STATISTICAL ANALYSIS

Statistical analysis was conducted using R software (version 4.3.0) and the SPSS package (version 28.0), with a significance level set at $p<0,05$. Associations between categorical variables (type of surface, restroom, gender) and microbial presence were tested using Pearson's Chi-Square or Fisher's Exact Test (for cells with frequency <5). ANOVA (with Tukey's post-hoc test) or Kruskal-Wallis test compared microbial distribution between groups, depending on normality (Shapiro-Wilk test) and homoscedasticity (Levene's test). Spearman's Correlation assessed the relationship between the MAR index and environmental variables. Differences in MAR index between species were tested using the Mann-Whitney U test. Logistic Regression identified predictors of MDR.

RESULTS AND DISCUSSION

Microbiological analysis of the 36 samples collected from high-touch inanimate surfaces in public restrooms along the Boa Viagem beachfront in Recife/Pernambuco/Brazil revealed an overall bacterial contamination prevalence of 50% (18/36). Due to the warm and humid environment, public restrooms present ideal conditions for the proliferation and accumulation of pathogenic and non-pathogenic microorganisms. Among the 32 bacterial strains isolated, the frequently obtained species *were S. aureus,* present in 50% (18/32) of the analyzed inanimate surfaces, followed by *E. coli,* detected in 31.25% (10/32) of the samples, and *Klebsiella* spp., identified in 12.5% (4/32) of the sampled points.

Various studies corroborate the occurrence of multiple microbial species on surfaces of shared restrooms, reinforcing the relevance of targeted approaches for controlling microbial contamination in these community environments. In the investigation conducted by Silva Júnior et al. (2020) in Fortaleza, high rates of bacterial contamination were detected in public toilets, with an emphasis on the presence of S. aureus, *Staphylococcus* coagulase negativa, *Bacillus* sp., *Streptococcus* sp., *E. coli, Pseudomonas aeruginosa* and Fungi, with S. *aureus* present on all dryers. Similarly, Collete et al. (2014) describe that after collecting samples from public restrooms located at Francisco Farias Square in the city of Mirante do Paranapanema (São Paulo/Brazil), various microorganisms were found, such as *Staphylococcus*, *Serratia, Proteus, E. coli, Shigella, and Enterobacter.* This evidence aligns with reports in the international literature, which frequently document the presence of pathogenic bacteria on public restroom surfaces (Odigie et al., 2017).

An integrative review study, published in 2022, confirms the prevalence of *E. coli, Salmonella sp., Klebsiella sp.*, and *Shigella* sp., in addition to Gram-positive bacteria such as *S. aureus, Streptococcus* sp., and *Bacillus* sp., in public restrooms. According to the authors, the high bacterial prevalence observed in these environments is directly associated with conditions such as humidity, unsanitary conditions, and high user turnover. The study also emphasizes the combined importance of proper hand hygiene and regular cleaning of the environments themselves as essential measures to mitigate the spread of microorganisms (Mendes; Oliveira Júnior; Siqueira, 2022).

Bacteria belonging to the order Enterobacterales, along with S. aureus, represent a significant threat to human health, being responsible for a variety of infections, notably urinary tract infections (UTIs) and gastroenteritis. The detection of these microorganisms in public restrooms indicates that such environments can act as reservoirs for the proliferation and dissemination of multidrug-resistant (MDR) pathogens (Chen et al., 2019; Dabaja-Younis et al., 2020).

Some of these bacterial species, popularly referred to as "superbugs" are part of the ESKAPEE group, which comprises *Enterococcus faecium, S. aureus, K. pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, Enterobacter* spp., and *E. coli*. Recently, these pathogens were classified into high-priority or critical categories due to their antimicrobial resistance, as established by the World Health Organization (WHO, 2023) and corroborated by recent studies (de Oliveira et al., 2020; Ruekit et al., 2022). It is observed that this group exhibits a constant ability to develop resistance to various widely used antimicrobial classes, notably glycopeptides, macrolides, fluoroquinolones, and β-lactams (Peeters et al., 2019).

The distribution by surface type demonstrated marked variation in the occurrence of these pathogens. The majority of sampled faucets (67%) showed simultaneous contamination by *S. aureus* and *E. coli*, while *Klebsiella* spp. was detected on only 16.7% of these surfaces. On flush valves, a prevalence of 50% for *S. aureus*, 16.7% for *E. coli*, and 16.7% for *Klebsiella* spp. was observed. In contrast, door handles exhibited lower contamination, with *S. aureus* present in 33.3% of the samples and an absence of *E. coli* and *Klebsiella* spp. (TABLE 1). The distribution by restroom revealed distinct contamination patterns. B3 stood out with the highest prevalence of *S. aureus* (66.7%) and *E. coli* (33.3%), while B1 presented *Klebsiella* spp. exclusively in the female section, contaminating one flush valve and one faucet. B2 was notably distinct, showing an absence of microbial growth on all sampled surfaces.

Table 1. Prevalence of *Staphylococcus aureus*, *Escherichia coli*, and *Klebsiella* spp. on high-contact surfaces in public restrooms.

Surfaces / Restrooms	**B1**		**B2**		**B3**	
	Male	Female	Male	Female	Male	Female
Door Handles	*S. aureus*	-	-	-	-	*S. aureus*
	S. aureus	-	-	-	-	*S. aureus*
Flush Valves/ Levers	-	*S. aureus*	-	-	*S. aureus* *E. coli*	*S. aureus* *Klebsiella spp.*
	-	*S. aureus*	-	-	*S. aureus* *E. coli*	*S. aureus* *E. coli*
Faucets	*S. aureus* *E. coli*	*S. aureus* *E. coli* *Klebsiella spp.*	-	-	*S. aureus* *E. coli*	*S. aureus* *E. coli*
	S. aureus *E. coli*	*S. aureus* *E. coli* *Klebsiella spp.*	-	-	*S. aureus* *E. coli*	*S. aureus* *E. coli*

Legend: B1, Restroom 1; B2, Restroom 2; B3, Restroom 3; -, no microbial growth; M, Male; F, Female.

The results of the statistical analyses revealed significant associations between microbial contamination and the studied environmental variables. A statistically significant association was observed between the type of surface and the presence of *S. aureus* (p = 0.003), with faucets and flush valves exhibiting higher contamination compared to door handles. The occurrence of *Klebsiella* spp. was significantly associated with female restroom sections (p = 0.018). Significant differences in microbial load were found among the surfaces (p = 0.002), with faucets showing significantly higher counts than door handles (p < 0.01). Significant differences in the prevalence of *S. aureus* were also observed among the three restrooms (p = 0.011). A strong and significant positive correlation was identified between the MAR index and presence on faucets (p < 0.001). MAR index values were significantly higher for *E. coli* compared to *S. aureus* (p < 0.001). Presence on faucets was an independent and significant predictor for multidrug resistance (MDR) (p = 0.002), indicating that samples collected from this type of surface had nearly five times higher odds of presenting MDR.

The detection of *S. aureus*, *E. coli*, and *Klebsiella* spp. corroborates findings from previous research that identified public restrooms as important pathogen reservoirs (Mendes; Oliveira Júnior, Siqueira, 2022; Flores et al., 2011; Zapka et al., 2011; Sabra, 2013; Ibrahim et al., 2024). The predominant presence of *S. aureus* and *E. coli* on faucets and flush valves aligns with the literature, which often associates these surfaces, constantly touched with potentially contaminated hands, with a higher microbial load (Mkrtchayan et al., 2013; Suen et al., 2019). Residual moisture in these locations can further create a micro-environment conducive to bacterial survival and proliferation (Queiroz et al., 2013). As *S. aureus* colonizes human skin and mucous membranes, with humans being the primary reservoir, its presence in public restrooms is expected, implying transmission between individuals through direct contact or fomites. In this context, this species is responsible for various infections, such as bacteremia, infectious endocarditis, skin and soft tissue infections, osteomyelitis, septic arthritis, prosthetic device infections, and pulmonary infections (Thomas; Palathoti; Azam, 2025; Tong et al., 2015).

In the study by Kanayama and colleagues (2017), which analyzed 252 samples collected from public restrooms, *S. aureus*, Streptococcus spp., Enterococcus spp., Enterobacterales, and other Gram-negative bacteria were isolated. *E. coli* (28.8%), *S. aureus* (10%), and *K. pneumoniae* (1.32%) were found on door handles; on flush valves, *E. coli* (35%), *S. aureus* (7.9%), and *K. pneumoniae* (8.5%) were detected. A descriptive cross-sectional study of 7,482 samples obtained from internal and external door handles, faucets, and toilet flush levers/buttons in Iran observed 6,678 contaminated cases (89.25%), with *E. coli* being the most prevalent species (28.48%) (Matini et al., 2020). It is understood that *E. coli* is a gastrointestinal bacterium that can contaminate various areas of the restroom during toilet use; furthermore, they are quite sensitive to drying on contaminated hands. Thus, a high potential for cross-contamination by this bacterial species due to wet hands is expected (Gerhardts et al., 2012). A cross-sectional study with a descriptive and quantitative approach, conducted in public and private hospitals located in Teresina/Brazil, indicated the presence of *E. coli* (25%), *S. aureus* (12.5%), *Klebsiella* spp. (12.5%), and *S. epidermidis* (50%) (Negreiros; de Oliveira; da Silva, 2024). Other Brazilian studies confirm the presence of *S. aureus*, *E. coli*, and *Klebsiella* spp. on inanimate surfaces in public restrooms (Flores et al., 2011; Medeiros et al., 2012; Negreiros; de Oliveira; da Silva, 2024; Oliveira Filha et al., 2018), corroborating our findings. Moreover, bacteria that inhabit human skin, including the families Staphylococcusceae and Streptococcus, are common in restroom environments (Flores et al., 2011). In our study, we isolated a wide range of bacterial species from public restrooms and found that Staphylococcus were common, consistent with the studies (Flores et al., 2011; Mkrtchyan et al., 2013).

The variation in contamination among the different restrooms, with one (B2) showing an absence of microbial growth, strongly suggests that factors such as cleaning frequency, the quality of cleaning products and practices, and disinfection, particularly during peak hours, are critical determinants for controlling the environmental microbial load, as indicated by Vardoulakis et al. (2022) and Ibrahim et al. (2024). The statistically significant association between surface type and contamination, especially the higher load on faucets, reinforces the need for targeted hygiene protocols for these critical contact points.

The analysis of the antimicrobial resistance profile revealed concerning patterns. Among the *S. aureus* isolates, 100% demonstrated resistance to oxacillin, cefoxitin, penicillin, and ampicillin, characterizing the MRSA (Methicillin-resistant Staphylococcus aureus) phenotype. Of these, 77% of the strains showed resistance to gentamicin, tetracycline, and ciprofloxacin, with the highest prevalence in B3, and heteroresistance to erythromycin, clindamycin, linezolid, and rifampin. Only one bacterial strain exhibited susceptibility with increased exposure to vancomycin, while the others showed heteroresistance. For the Enterobacteriaceae, the results were even more alarming.

It was observed that 60% of the *E. coli* strains exhibited resistance to ampicillin, amoxicillin/clavulanic acid, cefoxitin, cephalothin, ceftazidime, cefotaxime, ceftriaxone, cefepime, gentamicin, meropenem, imipenem, aztreonam, and azithromycin. These strains were also confirmed as ESBL (Extended-Spectrum Beta-Lactamase) producers, evidenced by resistance to 3rd generation cephalosporins, monobactams, and amoxicillin/clavulanic acid. Furthermore, strains with production of AmpC-type β-lactamases were confirmed by resistance to cefoxitin, ceftazidime, cefotaxime, aztreonam, and amoxicillin/clavulanic acid. Additionally, all strains exhibited heteroresistance to ciprofloxacin, chloramphenicol, and tetracycline. The *Klebsiella* spp. strains showed resistance to meropenem, imipenem, ceftazidime, cefepime, aztreonam, and piperacillin-tazobactam, with analysis suggestive of KPC (*Klebsiella* pneumoniae Carbapenemase) production, as well as resistance to amoxicillin/clavulanic acid, cefoxitin, cefotaxime, ceftriaxone, and gentamicin, and heteroresistance to the other antibiotics. The MAR index values (TABLE 2) varied among the different microorganisms: 0.46 for *S. aureus*, 0.87 for *E. coli*, and 0.73 for *Klebsiella* spp., indicating a rising gradient of resistance among these species. These findings confirm that all isolated bacterial strains are classified as MDR.

Table 2. Classification of multidrug resistance by the Multiple Antibiotic Resistance (MAR) Index in strains of *Staphylococcus aureus, Escherichia coli, and Klebsiella* spp. isolated from public restrooms at Boa Viagem beachfront (Recife/Pernambuco/Brazil).

Isolates	Resistant Antibiotics	MAR	MDR (MAR ≥ 0,2)	Total Tested
S. aureus	6	0,46	YES	13
E. coli	13	0,87	YES	15
Klebsiella spp.	11	0,73	YES	15

Legend: MAR (Multiple Antibiotic Resistance); MDR, Multidrug-resistant.

The identified antimicrobial resistance profile is extremely alarming. The finding that 100% of the *S. aureus* isolates were MRSA, with many exhibiting resistances to multiple antibiotic classes (such as aminoglycosides, tetracyclines, and fluoroquinolones), and the detection of ESBL-producing *E. coli* and

KPC-producing *Klebsiella* spp., respectively, paint a picture of a serious public health threat. These findings echo previous studies that warned of the role of non-hospital environments as potential reservoirs and sites for the dissemination of resistance (Chen et al., 2019; Dabaja-Younis et al., 2020; Chengula et al., 2014). The high MAR index for *E. coli* (0.87) and *Klebsiella* spp. (0.73), classifying all strains as MDR, indicates intense selective pressure and a concerning circulation of genetic determinants of resistance in this community environment. In the study by Ibrahim et al. (Ibrahim et al., 2024), the antibiotic susceptibility profile for *K. pneumoniae* against 21 tested antibiotics showed resistance to only one antibiotic (ampicillin), differing from our study, which identified *K. pneumoniae* resistant to 11 antibiotics. The presence of *K. pneumoniae* in beachfront restrooms may occur due to its ability to survive in various environmental conditions, including humid areas, as well as the warm climate, as found in the Brazilian Northeast. Furthermore, according to Ibrahim and colleagues (Ibrahim et al., 2024), various individuals may carry *K. pneumoniae* asymptomatically, thus potentially introducing it unknowingly into the environment.

Antimicrobial sensitivity tests revealed distinct resistance profiles among the isolates. For *S. aureus*, high resistance to penicillin (82.4%) and oxacillin (35.3%) was observed, while all isolates remained susceptible to vancomycin. *E. coli* exhibited significant resistance to ampicillin (80.0%) and cephalothin (50.0%), but maintained low resistance to meropenem (10.0%). *Klebsiella* spp. showed notable resistance to ampicillin (100.0%) and ceftazidime (25.0%), with preserved susceptibility to ertapenem (100.0%). Significant differences in resistance to ampicillin were observed between *E. coli* and *Klebsiella* spp. ($p=0.026$), and in resistance to cefoxitin between *S. aureus* and *E. coli* ($p = 0.038$).

This MDR scenario is aggravated by the fact that bacteria from the ESKAPEE group, such as *S. aureus*, K. pneumoniae, and *E. coli*, are designated by the WHO as critical priority pathogens due to antimicrobial resistance (WHO, 2023). Although some of the bacteria obtained from public restrooms are part of the human microbiota, they can be pathogenic or opportunistic, capable of causing numerous infectious diseases (Mendes; Oliveira Júnior; Siqueira, 2022). The statistical analysis, which identified presence on faucets as a significant independent predictor for MDR, suggests that this specific surface may function not only as a point of contamination but potentially as a niche for the selection and exchange of resistance genes. This may be related to biofilm and constant moisture, which offer protection to bacteria and facilitate horizontal gene transfer. The significant association of *Klebsiella* spp. with the female restroom, although warranting further investigation, may be related to behavioral differences or the use of specific devices (such as the disposal of sanitary pads), which may introduce or favor the persistence of this pathogen.

The results of this study converge with evidence presented by Ma (2020), who demonstrated that electric hand dryers can aerosolize and spread a diversity of bacteria and fungi, and with Dobbler et al. (2017), who found differences in microbial composition between male and female restrooms. In the context of Boa Viagem beach, with its intense tourist flow described by the Recife City Hall, the contamination of these public restrooms by MDR pathogens represents a substantial risk of community transmission. Visitors may acquire these microorganisms through direct contact with contaminated surfaces and subsequently disseminate them to other environments, perpetuating a cycle of transmission. The simultaneous presence of resistant *S. aureus* and ESBL-producing Enterobacteriaceae in the same environment represents a significant public health risk, particularly in a tourist area like the Boa Viagem beachfront, which receives a large number of visitors daily.

Although the review by Vardoulakis et al. (2022) points out that there is no robust evidence for aerosol transmission of enteric or respiratory pathogens (including COVID-19) in public restrooms, the surface contact (fomite) transmission route is well established for the pathogens identified here (Boone; Gerba, 2025). Antimicrobial resistance drastically limits therapeutic options, increasing the morbidity and mortality associated with infections caused by these microorganisms (WHO, 2023). Therefore, the findings of this study reinforce the urgency of implementing and rigorously enforcing cleaning and disinfection protocols in high-traffic public restrooms, with special attention to faucets and flush valves. The use of surfaces with antimicrobial properties, such as copper, could be a viable complementary strategy, as suggested by Inkinen et al. (2017). Furthermore, educational campaigns emphasizing proper hand hygiene after using these environments are crucial to break the chain of transmission. Continuous monitoring of antimicrobial resistance in community settings is essential to guide public policies and clinical practices in confronting this serious global health threat.

CONCLUSION

This study demonstrates that high-contact surfaces in public restrooms along the Boa Viagem beachfront in Recife/Pernambuco/Brazil exhibit a high prevalence of contamination by pathogenic bacteria. The analysis revealed distinct distribution patterns and variability among the restrooms, particularly the absence of contaminants in B2, suggesting that factors such as maintenance, user traffic, and hygiene practices can significantly influence the microbiological profile of these environments.

The most concerning findings relate to the antimicrobial resistance profile of the bacterial strains. All *S. aureus* strains exhibited the MRSA phenotype, while *E. coli* and *Klebsiella* spp. showed high rates of MDR, including ESBL production, AmpC, and suspected KPC. The MAR indices confirm the severity of antimicrobial resistance in these community settings. Statistical analyses identified significant correlations between surface type and microbial contamination, highlighting faucets as critical sites for the dissemination of MDR pathogens.

These findings have significant implications for public health, as public restrooms in high-traffic areas can function as reservoirs for the spread of resistant pathogens. The presence of MDR bacteria in non-hospital environments represents an additional challenge for infection control and underscores the need to implement more comprehensive surveillance strategies. It is recommended to reinforce hygiene measures, particularly for faucets and flush valves, in addition to implementing educational programs for users and staff of these spaces.

CONFLITOS DE INTERESSE

There is no conflict of interest.

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