

Isolation and Antibiotic Susceptibility Patterns of Airborne Bacteria from the In-Patient and Out-Patient Sections of Selected Primary Health Care Centers

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ABSTRACT

Airborne bacteria constitute an important source of environmental contamination in healthcare facilities and may contribute to healthcare-associated infections. This study assessed the load, diversity and antibiotic susceptibility of settled airborne bacteria in the in-patient (IP) and out-patient (OP) sections of six primary health care centres (three government-owned and three private-owned) in Obafemi-Owode LGA, Ogun State, Nigeria. Settle plates (Nutrient and MacConkey agar) were exposed in triplicate at 150 cm for 10-, 20- and 30-min during morning clinics across four wet-season visits (June 2025). OP loads were significantly higher than IP loads (one-way ANOVA, $P < 0.05$), with overall means of 21.1 ± 4.58 and 65.2 ± 7.06 CFU/plate, respectively (grand mean 43.1 ± 7.77). After 48 h, IP counts ranged from $8 \pm 0.63 - 22 \pm 2.71$ (10 min), $11 \pm 0.91 - 52 \pm 4.16$ (20 min) and $16 \pm 1.31 - 57 \pm 2.36$ CFU/plate (30 min); OP counts were $22 \pm 0.71 - 54 \pm 2.76$, $36 \pm 2.46 - 104 \pm 3.89$ and $82 \pm 2.23 - 144 \pm 5.16$. The highest OP means were at IHC (86.7 ± 17.28) and OHC (82.7 ± 17.92); the lowest was at MHC (39.3 ± 10.39). Several government-owned centres showed higher contamination than the private-owned. Gram-positive bacteria predominated, including *Staphylococcus* spp., *Streptococcus* spp. and *Bacillus* spp., alongside Gram-negative genera including *Escherichia coli*, *Klebsiella* spp., *Pseudomonas* spp. and *Serratia* spp. Mean panel resistance was about 52% (Gram-positive) and 48% (Gram-negative), especially to ampicillin, amoxicillin-clavulanate and erythromycin; while ciprofloxacin and gentamicin showed the best activity. The data indicate substantial settled airborne contamination that may increase healthcare-associated infection risk and underscore the need for routine microbiological surveillance, improved ventilation, and stringent infection-prevention protocols.

Received: 21 Jul. 2026

Accepted: 12 Oct. 2026

Published: 13 Oct. 2026

Keywords:

Airborne bacteria, Healthcare-associated infection, Primary health care, In-patient, Out-patient, Antibiotic resistance

INTRODUCTION

A substantial proportion of human time is spent in enclosed indoor environments, making indoor air quality (IAQ) a critical determinant of health and well-being (Mannan & Al-Ghamdi, 2021). Bioaerosols are particles suspended in the air that contain microorganisms and their products, and can spread respiratory and systemic disease and allergies among humans, a major public health risk (Othman et al., 2024). The most common microorganisms in healthcare settings are bacteria and fungi, with nosocomial infections (HCAs) being spread by airborne transmission (Chen et al., 2023; Al-Shaarani and Pecoraro, 2024).

Hospital environments act as important reservoirs for diverse airborne pathogens. Hospital-acquired infections (HAIs), also known as nosocomial infections, affect approximately 5–10% of hospitalized patients globally, with higher rates (up to 15–20%) reported in low- and middle-income countries (LMICs) such as Nigeria (WHO, 2022; Odoom & Donkor, 2025). In resource-limited primary health care settings, the burden is particularly heavy due to overcrowding, inadequate ventilation, and limited infection prevention infrastructure. Vulnerable populations, including children, the elderly, and immunocompromised individuals, are at greatest risk. Pathogens such as *Corynebacterium diphtheriae*, *Mycobacterium tuberculosis*, *Neisseria meningitidis*, and *Streptococcus pyogenes* are well-documented as being

transmitted via airborne droplets (Herfst et al., 2016; Ather et al., 2023).

Bioaerosols vary in size, shape, and composition depending on sources, aerosolization processes, and environmental conditions (Sajjad et al., 2023). Contamination in hospitals arises from multiple factors, including air currents, dust, visitors, patients, and outdoor influx (Nie et al., 2024). Poor IAQ exacerbates respiratory and systemic health issues among both patients and healthcare workers (Chamseddine et al., 2025). Human activities, high occupancy density, and clothing contribute significantly to elevated microbial loads. Bioaerosol exposure can lead to infections, hypersensitivity pneumonitis, and toxic reactions (Kim et al., 2017; Xhetani et al., 2026). Commonly implicated bacterial pathogens in nosocomial settings include *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, and *Escherichia coli*, while opportunistic fungi such as *Aspergillus* spp. and *Candida albicans* pose additional threats, particularly to immunocompromised patients (Kuznetsova et al., 2025).

Although there is increasing awareness, there is still less data available on the presence of airborne microbial contamination in Primary Health Care centres where most of the patients in LMICs will first encounter health services than in tertiary hospitals. This study therefore investigated the diversity, load, and antibiotic susceptibility profiles of airborne bacteria

in the IP and OP sections of selected primary health care centres in Obafemi-Owode LGA, Ogun State, Nigeria, with the aim of providing evidence-based recommendations for infection prevention and control strategies.

MATERIALS AND METHODS

Study Area and Duration

The study was carried out in six selected Primary Health Centres (PHCs) located within Obafemi-Owode Local Government Area (LGA) of Ogun State, Nigeria. These comprised three government-owned facilities (coded IHC, OHC and WHC) and three privately owned facilities (coded MHC, PHC and RHC). These codes are anonymised identifiers assigned for confidentiality and do not represent the official names of the centres.

Obafemi-Owode LGA contains a large network of primary-level facilities. Six operational centres were purposively selected to capture contrast in ownership (public versus private), typical patient throughput (low- versus high-attendance outpatient clinics, as judged from facility records and on-site occupancy during reconnaissance visits) and ward infrastructure (room size, number of beds and presence or absence of a dedicated in-patient/children's area). Centres that were closed, non-functional or declined permission were excluded.

Sampling was conducted in the in-patient (IP) sections (preferably children's wards where available) and out-patient (OP) sections of each centre. Settled airborne bacteria were collected weekly during the wet season (June 2025), yielding a total of four sampling days. Three replicate plates were collected from randomly selected positions in each section per sampling event to account for spatial variability within wards.

Study Approval and Ethical Considerations

This study involved passive sampling of indoor air only; no human clinical specimens, blood, swabs, or other patient-derived materials were collected. Consequently, formal institutional ethical approval and an ethics approval number were not required under the institutional guidelines of Mountain Top University for purely environmental microbiological surveys. Administrative permission and written informed consent for facility access were obtained from the management of each participating primary health care centre prior to sampling. The purpose of the study was explained to the heads of the respective wards. Facility identifiers were anonymised (coded as MHC, PHC, RHC, IHC, OHC and WHC); no personal identifiers of patients or staff were recorded at any stage. All data were used solely for research purposes.

Air Sampling Procedure

Settled airborne bacteria were isolated using the passive settle-plate (sedimentation) method (Jalili *et al.*, 2021; Aleruchi *et al.*, 2024). Sterile Petri dishes (90 mm diameter) containing sterile Nutrient Agar (for total aerobic bacteria) and sterile MacConkey Agar (for Gram-negative enteric bacteria) were used. Media were prepared according to the manufacturer's instructions, autoclaved at 121 °C for 15 minutes, and poured aseptically into plates (approximately 20–25 mL per plate). Plates were allowed to solidify and dried briefly in a laminar-flow hood before use.

During sampling, plates were exposed to indoor air at a height of 150 cm above floor level (breathing-zone height) and at least 1 m away from walls, windows, doors and high-traffic

areas to minimise direct disturbance. Exposure durations were 10, 20 and 30 minutes per set of plates. Sampling was performed during peak morning clinic hours under normal operational conditions, with minimal interference from researchers (sterile gloves, laboratory coats and masks). Environmental parameters including ward dimensions (length × breadth in metres), IP and OP occupancy during sampling, number of beds, ward temperature (°C) and ambient outdoor temperature were recorded simultaneously. After exposure, plates were immediately covered, sealed with parafilm, placed in sterile transport containers and transported to the laboratory within 2 hours. Plates were incubated aerobically at 37 ± 1 °C for 24–48 hours. Colonies were counted after 24 h and 48 h using a digital colony counter (LALCO, 537 Micro), and results were expressed as colony-forming units per plate (CFU/plate). Plates with no visible colonies were recorded as 0 CFU/plate. Plates with more than 300 colonies were recorded as too numerous to count (TNTC) and were excluded from mean calculations; TNTC observations are noted in the Results where they occurred.

Morphological and Biochemical Characterization of Isolates

Representative colonies were subcultured onto fresh Nutrient Agar plates for purity. Morphological characterisation was based on colony appearance (size, shape, colour, margin, elevation), cellular morphology (Gram staining) and pigmentation (Olutiola *et al.*, 2000). Biochemical identification included Gram staining, catalase, oxidase, methyl red/Voges-Proskauer (MR-VP), coagulase, starch hydrolysis, sugar fermentation (glucose, lactose, sucrose, mannitol), Simmons citrate utilisation and indole tests. Standard reference strains were used as controls. Isolates were identified to genus level using standard microbiological identification keys and Bergey's Manual (Olutiola *et al.*, 2000).

Antibiotic Susceptibility Testing

One representative isolate from each identified genus was selected for susceptibility testing. The disc-diffusion method (Kirby-Bauer) was performed on Mueller-Hinton agar according to Clinical and Laboratory Standards Institute (CLSI) standard M02 (CLSI, 2024) description. Standardised bacterial suspensions equivalent to 0.5 McFarland standard ($\approx 1.5 \times 10^8$ CFU/mL) were prepared and swabbed evenly onto the agar surface. Commercially prepared antibiotic discs containing ampicillin 30 µg, amoxicillin-clavulanate (augmentin) 30 µg, chloramphenicol 30 µg, ciprofloxacin 15 µg, cotrimoxazole 25 µg, erythromycin 15 µg, gentamicin 10 µg, pefloxacin 5 µg, rifampin 5 µg, streptomycin 10 µg and vancomycin 30 µg were placed on the inoculated plates. Plates were incubated at 37 °C for 24 hours. Zones of inhibition were measured in millimetres (mm) using a calibrated ruler and interpreted as Sensitive (S), Intermediate (I) or Resistant (R) according to CLSI guidelines (CLSI, 2025) (Table 1). *Escherichia coli* ATCC 25922 and *Staphylococcus aureus* ATCC 25923 were used as quality-control strains. Vancomycin disc-diffusion zones are reported as observed phenotypes only. Because both CLSI and European Committee on Antimicrobial Susceptibility Testing (EUCAST) do not recommend disc diffusion for determining vancomycin susceptibility in staphylococci as the drug diffuses poorly in agar; these results were therefore interpreted with caution and were not used as standalone clinical breakpoints.

Table 1: Zone-diameter interpretative standard chart for the selected antibiotics

Antibiotics	Code	Potency (µg/disk)	Sensitive (mm)	Intermediate (mm)	Resistant (mm)
Ampicillin	AMP	30	≥18	14–17	≤13
Amoxicillin–Clavulanate	AUG	30	≥18	13–17	≤12
Chloramphenicol	CHL	30	≥18	13–17	≤12
Ciprofloxacin	CPX	15	≥21	16–20	≤15
Cotrimoxazole	CXT	25	≥16	11–15	≤10
Erythromycin	ERY	15	≥23	14–22	≤13
Gentamicin	GEN	10	≥15	13–14	≤12
Pefloxacin	PFX	5	≥18	15–17	≤14
Rifampin	RFP	5	≥20	17–19	≤16
Streptomycin	STR	10	≥15	12–14	≤11
Vancomycin	VAN	30	≥15	12–14	≤11

Code: AMP = ampicillin; AUG = Augmentin (amoxicillin–clavulanate); CHL = chloramphenicol; CPX = ciprofloxacin; CXT = cotrimoxazole; ERY = erythromycin; GEN = gentamicin; PFX = pefloxacin; RFP = rifampin; STR = streptomycin; VAN = vancomycin. S = susceptible; I = intermediate; R = resistant. Interpretative ranges follow CLSI M100 as applied in this study.

Data Analysis

All countable plates were processed from triplicate exposures. Data were analysed using descriptive statistics (means ± standard error of the mean, calculated from the actual replicate counts). One-way ANOVA was used to test differences ($P \leq 0.05$) among IP and OP sections, private and government-owned facilities, and exposure times. Means were separated using Duncan's Multiple Range Test where applicable. TNTC plates were excluded from parametric means.

RESULTS AND DISCUSSION

Physical Conditions of the Sampling Locations

Table 2 summarises occupancy and physical conditions at the time of sampling. Ward dimensions ranged from 4.25×2.5

m (PHC) to 6.25×5.5 m (RHC). Mean in-patient (IP) occupancy across the six centres was 4.0 ± 0.58 persons and differed significantly among locations ($P \leq 0.05$), being highest at IHC (6 ± 0.87^a) and lowest at MHC (2 ± 0.50^e). Mean out-patient (OP) occupancy was substantially higher (13.2 ± 4.28 persons) and more variable, ranging from 4 ± 0.71^e at WHC to 32 ± 2.00^a at OHC. The number of beds averaged 5.7 ± 0.76 (range 3 ± 0.00^e at MHC to 8 ± 0.00^a at WHC). The overall SE for beds describes differences among centres; bed number within each centre was fixed. Ward temperatures were narrow (23.6 ± 0.20 °C; range 23.0 – 24.0 °C) and did not differ significantly among locations ($P > 0.05$). Outdoor temperature averaged 23.8 ± 0.40 °C. These records show that OP sections were more densely occupied than IP sections during sampling.

Table 2: Occupancy and Physical Conditions of the Sampling Locations during the Study

Sampling category	Sampling location	Dimension (m)	IP pop.	OP pop.	Beds	Ward Temp. (°C)	Outdoor Temp. (°C)
Private-owned	MHC	5.13×3.25	2 ± 0.50^e	5 ± 0.79^d	3 ± 0.00^e	24.0 ± 0.20^a	23.0 ± 0.25^e
	PHC	4.25×2.5	4 ± 0.71^c	10 ± 1.12^c	6 ± 0.00^c	23.0 ± 0.25^c	25.0 ± 0.30^a
	RHC	6.25×5.5	4 ± 0.71^c	10 ± 1.12^c	6 ± 0.00^c	24.0 ± 0.20^c	25.0 ± 0.30^a
Government-owned	IHC	5.75×4.0	6 ± 0.87^a	18 ± 1.50^b	7 ± 0.00^b	24.0 ± 0.20^a	23.0 ± 0.25^c
	OHC	5.25×3.5	3 ± 0.61^d	32 ± 2.00^a	4 ± 0.00^d	23.5 ± 0.22^b	24.0 ± 0.28^b
	WHC	4.75×3.0	5 ± 0.79^b	4 ± 0.71^e	8 ± 0.00^a	23.0 ± 0.25^c	23.0 ± 0.25^c
Overall mean ± SE	—	—	4.0 ± 0.58	13.2 ± 4.28	5.7 ± 0.76	23.6 ± 0.20	23.8 ± 0.40

Code: MHC, PHC, RHC = anonymised private-owned centres; IHC, OHC, WHC = anonymised government-owned centres; IP = in-patient section; OP = out-patient section. Means followed by different superscript letters within a column are significantly different ($P \leq 0.05$, Duncan's Multiple Range Test). Overall mean ± SE is the mean of the six facilities ± ($s/\sqrt{6}$).

Settled Airborne Bacterial Loads

Table 3 presents settled bacterial counts (CFU/plate) on Nutrient Agar after 10, 20 and 30 min exposure and 24 h or 48 h incubation. One-way ANOVA showed a significant difference between sections ($P \leq 0.05$). OP areas consistently carried higher loads than IP areas: the overall OP mean was 65.2 ± 7.06 CFU/plate compared with 21.1 ± 4.58 CFU/plate in IP sections (grand mean 43.1 ± 7.77 CFU/plate).

Counts increased with both exposure time and incubation period. Grand means rose from 13.58 ± 3.37 CFU/plate at 10 min/24 h to 26.25 ± 4.33 at 10 min/48 h, 38.25 ± 8.20 at 20 min/24 h, 49.92 ± 8.01 at 20 min/48 h, 57.92 ± 12.61 at 30 min/24 h and 72.83 ± 12.27 CFU/plate at 30 min/48 h. The same gradient was clearer in OP sections, where the column

mean increased from 22.17 ± 4.20 (10 min/24 h) to 107.83 ± 10.27 CFU/plate (30 min/48 h). IP column means increased more modestly, from 5.00 ± 1.69 to 37.83 ± 8.17 CFU/plate. Among individual centres, the highest overall OP load was at IHC (86.7 ± 17.28 CFU/plate), followed by OHC (82.7 ± 17.92). The highest single cell count was IHC OP after 30 min and 48 h (144 ± 5.16^a CFU/plate). The lowest overall OP load was at MHC (39.3 ± 10.39 CFU/plate), not at WHC. IP loads were highest at IHC (37.7 ± 7.16 CFU/plate) and lowest at MHC (7.5 ± 2.20 CFU/plate). Private-owned centres did not uniformly have lower contamination than government-owned centres when compared site by site (Table 3). Longer plate exposure was associated with higher deposited counts in most OP locations.

Table 3: Colony Counts (CFU/Plate) on Nutrient Agar by Exposure Time and Incubation Period

Sampling Category	Sampling Location	Sampling Section	Plate Exposure Time (Minutes)						Mean $\pm$ SE Overall
			10 min		20 min		30 min		
			24 h	48 h	24 h	48 h	24 h	48 h	
Private-owned	MHC	In	1 $\pm$ 0.58 ^c	8 $\pm$ 0.63 ^c	4 $\pm$ 0.15 ^g	11 $\pm$ 0.91 ^g	5 $\pm$ 0.29 ^h	16 $\pm$ 1.31 ^h	7.5 $\pm$ 2.20
		Out	8 $\pm$ 0.63 ^c	24 $\pm$ 0.83 ^d	34 $\pm$ 1.37 ^c	36 $\pm$ 2.46 ^c	52 $\pm$ 2.16 ^c	82 $\pm$ 2.23 ^{de}	39.3 $\pm$ 10.39
	PHC	In	2 $\pm$ 0.82 ^c	21 $\pm$ 2.65 ^d	3 $\pm$ 1.00 ^g	48 $\pm$ 4.00 ^d	7 $\pm$ 1.53 ^h	56 $\pm$ 2.32 ^f	22.8 $\pm$ 9.69
		Out	22 $\pm$ 0.71 ^b	47 $\pm$ 0.96 ^b	62 $\pm$ 1.55 ^b	66 $\pm$ 1.69 ^c	84 $\pm$ 2.29 ^d	89 $\pm$ 2.45 ^d	61.7 $\pm$ 10.09
	RHC	In	2 $\pm$ 0.82 ^c	10 $\pm$ 1.83 ^c	14 $\pm$ 1.15 ^f	16 $\pm$ 2.31 ^g	18 $\pm$ 1.73 ^g	21 $\pm$ 2.65 ^g	13.5 $\pm$ 2.75
		Out	20 $\pm$ 0.58 ^b	42 $\pm$ 1.74 ^b	56 $\pm$ 3.32 ^c	64 $\pm$ 4.62 ^c	88 $\pm$ 4.02 ^d	92 $\pm$ 2.12 ^d	60.3 $\pm$ 11.20
Government-owned	IHC	In	11 $\pm$ 1.91 ^c	22 $\pm$ 2.71 ^d	46 $\pm$ 2.94 ^d	52 $\pm$ 4.16 ^d	40 $\pm$ 3.16 ^f	55 $\pm$ 4.28 ^f	37.7 $\pm$ 7.16
		Out	40 $\pm$ 1.65 ^a	54 $\pm$ 2.76 ^a	68 $\pm$ 2.58 ^b	82 $\pm$ 2.23 ^b	132 $\pm$ 2.88 ^a	144 $\pm$ 5.16 ^a	86.7 $\pm$ 17.28
	OHC	In	9 $\pm$ 1.73 ^c	19 $\pm$ 2.52 ^d	12 $\pm$ 2.00 ^f	32 $\pm$ 3.27 ^c	49 $\pm$ 2.52 ^e	57 $\pm$ 2.36 ^f	29.7 $\pm$ 8.12
		Out	23 $\pm$ 0.41 ^b	35 $\pm$ 2.16 ^c	90 $\pm$ 1.83 ^a	104 $\pm$ 3.89 ^a	112 $\pm$ 2.02 ^b	132 $\pm$ 3.63 ^b	82.7 $\pm$ 17.92
	WHC	In	5 $\pm$ 1.29 ^d	11 $\pm$ 1.91 ^c	17 $\pm$ 1.53 ^f	24 $\pm$ 2.45 ^f	12 $\pm$ 2.00 ^g	22 $\pm$ 2.71 ^g	15.2 $\pm$ 2.94
		Out	20 $\pm$ 0.58 ^b	22 $\pm$ 0.71 ^d	53 $\pm$ 1.20 ^c	64 $\pm$ 1.62 ^c	96 $\pm$ 2.66 ^c	108 $\pm$ 3.01 ^c	60.5 $\pm$ 14.95
Mean $\pm$ SE (IP)	-	-	5.00 $\pm$ 1.69	15.17 $\pm$ 2.52	16.00 $\pm$ 6.41	30.50 $\pm$ 6.84	21.83 $\pm$ 7.49	37.83 $\pm$ 8.17	21.1 $\pm$ 4.58
Mean $\pm$ SE (OP)	-	-	22.17 $\pm$ 4.20	37.33 $\pm$ 5.20	60.50 $\pm$ 7.54	69.33 $\pm$ 9.20	94.00 $\pm$ 11.06	107.83 $\pm$ 10.27	65.2 $\pm$ 7.06
Grand Mean $\pm$ SE	-	-	13.58 $\pm$ 3.37	26.25 $\pm$ 4.33	38.25 $\pm$ 8.20	49.92 $\pm$ 8.01	57.92 $\pm$ 12.61	72.83 $\pm$ 12.27	43.1 $\pm$ 7.77

Code: In = in-patient section; Out = out-patient section. Means followed by different superscript letters within a column are significantly different ($P \leq 0.05$, Duncan's Multiple Range Test).

Biochemical Profile of Morphologically different Bacterial Isolates

The biochemical reactions of the morphologically distinct isolates are presented in Table 4. On the basis of Gram reaction, cell shape and the biochemical panel described in Section 2.4, isolates were assigned to genus level. Gram-

positive isolates included *Staphylococcus* spp., *Micrococcus* spp., *Bacillus* spp., *Streptococcus* spp. and *Arthrobacter* spp. Gram-negative isolates included *Serratia* spp., *Aeromonas* spp., *Proteus* spp., *Pseudomonas* spp., *Citrobacter* spp., *Enterobacter* spp., *Providencia* spp., *Escherichia coli* and *Klebsiella* spp.

Table 4: Biochemical Profile of Morphologically Different Bacterial Isolates

Isolat e Code	G S	Shape s	C A	M R	V P	O X	I N	C O	S H	E D	Different Bacterial Isolates																		Probable Identity
											GLU		FRU		GAL		SUC		MAL		MAN								
											A	G	A	G	A	G	A	G	A	G	A	G							
IHC4	+	Cocci	+	-	-	-	-	-	-	-	+	-	+	-	+	-	+	-	+	-	+	-	<i>Micrococcus</i> <i>s sp.</i>						
IHC8	-	Rods	+	+	-	-	-	-	+	-	+	G	+	G	+	G	+	G	+	G	+	G	<i>Serratia sp.</i>						
MCH 2	+	Cocci	+	-	+	-	-	+	-	-	+	G	+	G	+	G	+	G	+	G	+	G	<i>Staphylococ</i> <i>us sp.</i>						
MCH 5	-	Rods	+	+	-	+	+	-	+	-	+	G	+	G	+	G	+	G	+	G	+	G	<i>Aeromonas</i> <i>sp.</i>						
OHC 10	-	Rods	+	+	-	-	+	-	-	-	+	G	+	G	+	G	+	G	+	G	+	G	<i>Proteus sp.</i>						
OHC 5	-	Rods	+	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<i>Pseudomon</i> <i>as sp.</i>						
OHC 7	+	Cocco id	+	-	-	-	-	-	+	-	+	-	+	-	+	-	+	-	+	-	+	-	<i>Arthrobacte</i> <i>r sp.</i>						
OHC 9	-	Rods	+	+	-	-	+	-	-	-	+	G	+	G	+	G	+	G	+	G	+	G	<i>Citrobacter</i> <i>sp.</i>						
PHC1	+	Cocci	-	-	-	-	-	-	-	-	+	G	+	-	+	-	+	-	+	-	+	-	<i>Streptococc</i> <i>us sp.</i>						
PHC4	-	Rods	+	-	+	-	-	-	-	-	+	G	+	G	+	G	+	G	+	G	+	G	<i>Enterobacte</i> <i>r sp.</i>						
RHC 12	+	Rods	+	+	-	-	-	-	+	+	+	G	+	G	+	G	+	G	+	G	+	G	<i>Bacillus sp.</i>						
WHC 2	-	Rods	+	+	-	-	+	-	-	-	+	G	+	G	+	G	+	G	+	G	-	-	<i>Providencia</i> <i>sp.</i>						
WHC 4	-	Rods	+	+	-	-	+	-	-	-	+	G	+	G	+	G	+	G	+	G	+	G	<i>E. coli</i>						
WHC 6	-	Rods	+	-	+	-	-	-	-	-	+	G	+	G	+	G	+	G	+	G	+	G	<i>Klebsiella</i> <i>sp.</i>						

Codes: GS – Gram staining; CA – catalase; MR – methyl red; VP – Voges-Proskauer; OX – oxidase; IN – indole; CO – coagulase; SH – starch hydrolysis; ED – endospore staining; GLU, FRU, GAL, SUC, MAL, MAN – fermentation of glucose, fructose, galactose, sucrose, maltose and mannitol; A – acid; G – gas.

Occurrence and Distribution of Bacterial Genera

Figure 1 shows the percentage occurrence of bacterial genera isolated from IP and OP sections. Gram-positive genera dominated, with *Staphylococcus* spp. (29.5% IP, 24.4% OP) and *Bacillus* spp. (20.5% IP, 19.8% OP) the most prevalent.

Gram-negative bacteria were more diverse in OP sections and included low counts of *Citrobacter* spp. and *Escherichia* spp. (0.8% each). The distribution is consistent with higher occupancy in OP areas, although source attribution was not directly measured in this study.

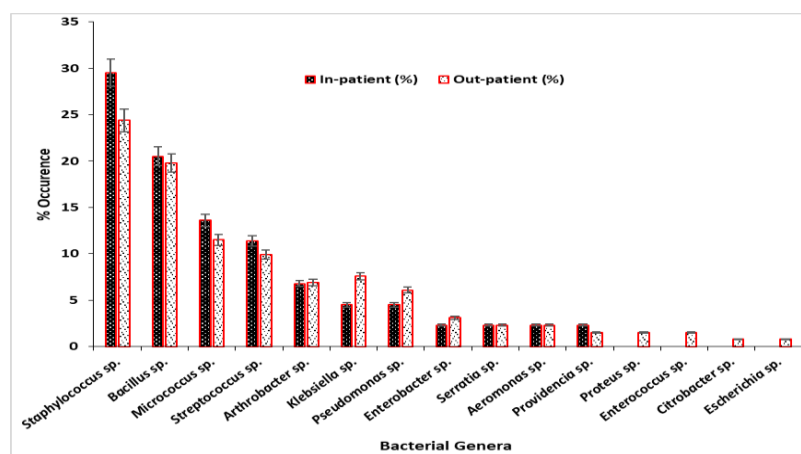


Figure 1: Percentage occurrence of bacterial genera isolated from in-patient (IP) and out-patient (OP) sections

Antibiotic Susceptibility Profiles of Selected Bacterial Isolates

The antibiotic susceptibility patterns of representative isolates from each bacterial genus are presented in Table 5 and summarised in Figure 2. Overall, the tested isolates showed high levels of resistance, with a mean proportion of resistant isolate–antibiotic reactions of approximately 52% among Gram-positive isolates and 48% among Gram-negative isolates across the 11 discs evaluated. These figures describe average resistance across the panel, not the proportion of isolates that were multidrug-resistant.

Ciprofloxacin (CPX) and gentamicin (GEN) exhibited the highest antimicrobial activity, with the greatest susceptibility rates among bacterial isolates across most genera. Gram-positive isolates exhibited very high resistance to ampicillin (AMP), amoxicillin–clavulanate (AUG) and erythromycin (ERY). Vancomycin (VAN) produced measurable inhibition zones against some Gram-positive isolates, but these zones

are reported only as observed phenotypes: disc diffusion is not recommended by CLSI for vancomycin susceptibility in staphylococci, and Gram-negative isolates are intrinsically resistant.

Gram-positive isolates generally displayed higher panel resistance. *Enterococcus* sp. (PHC8) recorded the highest resistance rate (86%), followed by *Staphylococcus* sp. (MCH2) at 77%. *Streptococcus* spp., *Bacillus* spp., *Micrococcus* spp. and *Arthrobacter* spp. showed moderate to high panel resistance (40–50%).

Gram-negative isolates exhibited slightly lower overall panel resistance. Notable patterns include high resistance in *Providencia* sp. (59%), *Enterobacter* sp. (50%), *Klebsiella* sp. (50%) and *Escherichia* sp. (50%). *Proteus* sp. (OHC10) was relatively more susceptible (27% panel resistance). *Pseudomonas* sp. and *Aeromonas* sp. showed better susceptibility to fluoroquinolones and aminoglycosides.

Table 5: Antibiotic Susceptibility Profile of Selected Bacterial Isolates

Isolate Codes	Bacterial Genera	Antibiotics										
		AUG	GEN	ERY	CPX	PEF	CXT	STR	RFP	CHL	AMP	VAN
MCH5	<i>Aeromonas</i> sp.	S	S	R	S	S	S	S	S	S	R	R
OHC7	<i>Arthrobacter</i> sp.	R	S	S	S	S	R	I	R	S	R	S
RHC12	<i>Bacillus</i> sp.	R	S	R	S	S	R	R	I	S	R	R
OHC9	<i>Citrobacter</i> sp.	R	S	I	S	S	S	S	R	I	R	R
PHC4	<i>Enterobacter</i> sp.	R	R	R	S	S	S	S	I	R	R	R
PHC8	<i>Enterococcus</i> sp.	R	R	R	S	R	R	R	R	R	R	R
WHC4	<i>Escherichia</i> sp.	R	S	R	S	S	S	R	R	I	R	R
WHC6	<i>Klebsiella</i> sp.	R	S	I	S	S	I	R	R	R	R	I
IHC4	<i>Micrococcus</i> sp.	R	S	S	S	S	R	R	R	S	R	S
OHC10	<i>Proteus</i> sp.	I	R	S	S	S	S	S	R	S	R	S
WHC2	<i>Providencia</i> sp.	R	R	S	R	R	S	S	R	R	R	R
OHC5	<i>Pseudomonas</i> sp.	I	S	S	S	S	I	R	R	R	R	S
IHC8	<i>Serratia</i> sp.	R	R	I	S	S	S	S	R	S	R	R
MCH2	<i>Staphylococcus</i> sp.	R	R	R	S	R	R	R	R	R	R	R
PHC1	<i>Streptococcus</i> sp.	R	S	R	R	R	S	S	I	I	R	R

Codes: S = susceptible; I = intermediate; R = resistant. % resistance = percentage of R reactions per genus across all antibiotics tested.

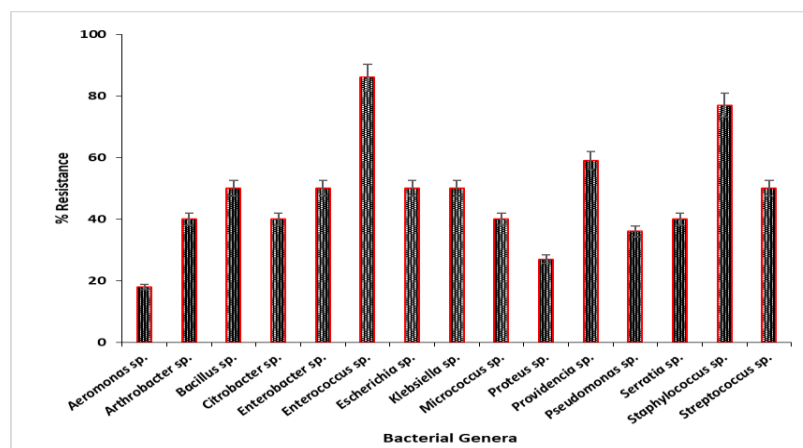


Figure 2: Percentage resistance of the isolated bacterial genera against the selected antibiotic discs

Discussion

Settled Airborne Bacterial Loads and Physical Factors

The significantly higher settled airborne bacterial loads in out-patient (OP) sections compared with in-patient (IP) sections (overall means of 65.2 ± 7.06 versus 21.1 ± 4.58 CFU/plate) are likely attributable to increased human occupancy and activity, as reported elsewhere (Tselebonis *et al.*, 2020; AlRayess *et al.*, 2022). Foot traffic, coughing frequency and visitor movement were not measured directly in this study and are therefore proposed as plausible contributing factors rather than demonstrated causes. This pattern agrees with previous work in Nigerian and other African hospitals, where high-occupancy areas such as OP departments harbour elevated microbial burdens (AlRayess *et al.*, 2022; Odoyo *et al.*, 2023).

Colony counts increased with plate-exposure time (10 to 30 min) and with incubation (24 h to 48 h). This pattern is expected for the settle-plate method, which recovers particles large enough to sediment onto agar; longer exposure increases the opportunity for deposition, while extended incubation allows slower-growing colonies to become visible (Fernandez *et al.*, 2019). Counts exceeding 200 CFU/plate in some OP locations after 30 min exceed values often cited as acceptable for general healthcare environments and indicate a substantial burden of sedimented bacteria (Monteiro *et al.*, 2021). This does not, by itself, prove airborne transmission of infection.

Government-owned facilities tended to show higher contamination than private-owned centres in several pairwise comparisons, which may reflect differences in patient volume, building fabric and routine cleaning, although these operational variables were not quantified beyond occupancy and ward dimensions recorded at the time of sampling. Ward temperatures occupied a narrow range (23–24 °C). Temperature was not formally tested against bacterial load (no correlation or regression analysis was performed); accordingly, no inference is made about a temperature effect within this range. Human occupancy remains the more plausible driver of the differences observed (Al-Shaarani & Pecoraro, 2026).

Distribution of Bacterial Genera

The predominance of Gram-positive bacteria is consistent with their thick peptidoglycan cell walls, which enhance resistance to desiccation and environmental stress. In addition, *Staphylococcus* and *Micrococcus* are common skin commensals readily dispersed by human activity, while *Bacillus* spp. persist through endospore formation.

Gram-negative organisms such as *E. coli*, *Klebsiella* spp., *Pseudomonas* spp. and *Enterobacter* spp. were more prominent in OP sections. Hand hygiene, sanitation and faecal contamination were not assessed in this study; the recovery of these genera may therefore reflect contamination from human activities, environmental reservoirs or inadequate infection-prevention practices rather than a documented faecal source (Singh *et al.*, 2025). These genera include opportunistic pathogens capable of causing respiratory, wound and other healthcare-associated infections, particularly among children and the elderly (Szabó *et al.*, 2022). The observed distribution aligns with previous reports of airborne microflora in Nigerian healthcare settings. Although not isolated in the present study, previous investigations have frequently reported *Corynebacterium* spp., *Acinetobacter* spp. and fungal genera such as *Aspergillus*, *Penicillium* and *Cladosporium* in similar indoor environments, where they pose additional risks to immunocompromised patients (Al-Shaarani & Pecoraro, 2026; Haddad & Hallak, 2026).

Antibiotic Resistance Patterns

The recovery of resistant bacteria from indoor air suggests that hospital air may function as an environmental reservoir of antimicrobial resistance. Airborne dissemination increases opportunities for resistant organisms to contaminate surfaces, equipment and susceptible patients, thereby contributing to healthcare-associated infections and facilitating transmission within healthcare environments. Horizontal gene transfer on shared fomites and selection pressure from empirical antibiotic use in primary care are additional mechanisms that may maintain this reservoir, although neither gene transfer nor prescribing intensity was measured here.

The high panel resistance observed, especially among *Enterococcus* sp. (86%) and *Staphylococcus* sp. (77%), mirrors global and local trends (Ahmed *et al.*, 2024; Roy *et al.*, 2025). *Staphylococcus* species readily acquire resistance genes and *mecA* is often associated with, and encodes, methicillin resistance; PCR for *mecA* was not performed in this study, so methicillin-resistant *S. aureus* cannot be confirmed from the present data (Li *et al.*, 2025). *Enterococcus* possesses intrinsic resistance mechanisms and efficiently acquires mobile genetic elements (Lu *et al.*, 2025). Ciprofloxacin and gentamicin exhibited the highest activity against the isolates tested. Possible explanations include less frequent outpatient misuse of these agents in the study setting relative to inexpensive oral beta-lactams and macrolides, concentration-dependent killing (aminoglycosides and

fluoroquinolones), and a broader spectrum against the genera recovered. These explanations are interpretive; local consumption data were not collected. High resistance of isolates to ampicillin, amoxicillin-clavulanate and erythromycin is comparable to findings from Ogun State and southwestern Nigeria, where ESBL-producing Gram-negative bacteria and macrolide-resistant Gram-positive organisms are increasingly reported (Adekanmbi *et al.*, 2026; Mohamed *et al.*, 2026). Together, these patterns support the view that settled airborne bacteria can contribute to the environmental dissemination of antimicrobial resistance in resource-limited primary-care settings.

Limitations and Implications

Limitations include reliance on the passive settle-plate method, which recovers sedimented particles and under-samples smaller, longer-suspended aerosols, and restriction of fieldwork to the wet season. Identification was to genus level only; molecular methods would have provided species-level resolution and would have been required to confirm genes such as *mecA*. Vancomycin disc-diffusion results for Gram-positive isolates should be interpreted with caution because CLSI does not recommend this method for staphylococci. The uniform ± 0.02 error terms originally attached to individual colony counts have been withdrawn; remaining overall SEs will be recomputed from raw triplicate counts.

Nevertheless, this study provides baseline data for under-researched primary health care settings. The results show that primary health care centres can harbour substantial loads of settled airborne bacteria, including genera of clinical importance and isolates with high panel resistance. Strengthening infection prevention and control (IPC) improved ventilation, routine air and surface monitoring; hand-hygiene enforcement and staff training is warranted. Integration of these findings into local health policies could reduce the environmental contribution to healthcare-associated infection risk.

CONCLUSION

This study demonstrates substantial loads of settled airborne bacteria in the in-patient and out-patient sections of selected primary health care centres in Obafemi-Owode LGA, Ogun State, Nigeria. Significantly higher bacterial loads were recorded in out-patient areas, with several government-owned facilities also showing higher counts than private-owned centres. Gram-positive genera predominated, while clinically important Gram-negative pathogens and isolates with high panel resistance were also recovered. These findings indicate substantial airborne bacterial contamination that may increase the risk of healthcare-associated infections. They do not demonstrate that nosocomial infections occurred in the sampled centres. The recovery of resistant isolates from indoor air further suggests that primary-care air may act as an environmental reservoir of antimicrobial resistance.

Routine microbiological surveillance of hospital air, combined with enhanced IPC practices, improved ventilation and antimicrobial stewardship, is recommended to protect patients, staff and the community. Further longitudinal studies using complementary active sampling and molecular identification are warranted to monitor trends, resolve isolates to species level and assess intervention effectiveness. Addressing these environmental and resistance challenges is important for improving healthcare quality and patient safety across primary care facilities in Nigeria.

REFERENCES

- Adekanmbi, A. O., Ishola, L. T., Ogunsakin, E. B., Ajamu, T. A., & Lawal, F. T. (2026). Antibiotic resistance profiles and co-occurrence of ESBL and AmpC β -lactamase genes in ESBL-producing Gram-negative bacteria of clinical origin. *BMC Microbiology*. <https://doi.org/10.1186/s12866-026-05129-x>
- Ahmed, S. K., Hussein, S., Qurbani, K., Ibrahim, R. H., Fareeq, A., Mahmood, K. A., & Mohamed, M. G. (2024). Antimicrobial resistance: Impacts, challenges, and future prospects. *Journal of Medicine Surgery and Public Health*, 2, 100081. <https://doi.org/10.1016/j.gjmed.2024.100081>
- Aleruchi, O., Robinson, V. K., Okpokiri, M., & Egedeye-Fubara, I. V. (2024). Assessment of Airborne Microbial Composition and Antibiotic Susceptibility Profiles in Dumpsite Environments within Rivers State University. *Journal of Advances in Microbiology*, 24(1), 19–29. <https://doi.org/10.9734/jamb/2024/v24i1782>
- AlRayess, S., Sleiman, A., Alameddine, I., Fayad, A. A., Matar, G. M., & El-Fadel, M. (2022). Airborne bacterial and PM characterization in intensive care units: correlations with physical control parameters. *Air Quality Atmosphere & Health*, 15(10), 1869–1880. <https://doi.org/10.1007/s11869-022-01222-y>
- Al-Shaarani, A. A., & Pecoraro, L. (2026). The influence of environmental factors on the diversity and structure of airborne fungal and bacterial communities. *Mycology: an International Journal on Fungal Biology*. <https://doi.org/10.1080/21501203.2026.2627697>
- Al-Shaarani, A. Q. A., & Pecoraro, L. (2024). A review of pathogenic airborne fungi and bacteria: unveiling occurrence, sources, and profound human health implication. *Frontiers in Microbiology*, 15, 1428415. <https://doi.org/10.3389/fmicb.2024.1428415>
- Ather B, Mirza TM, Edemekong PF. Airborne Precautions. [Updated 2023 Mar 13]. In: StatPearls [Internet]. Treasure Island (FL): StatPearls Publishing; 2026 Jan-. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK531468/>
- Chamseddine, A., Elzein, I. M., & Hassan, N. (2025). Indoor Air Quality in Critical Indoor Environments: A review paper. *Water Air & Soil Pollution*, 236(13). <https://doi.org/10.1007/s11270-025-08512-y>
- Chen, L., Song, Z., Zhou, X., Yang, G., & Yu, G. (2023). Pathogenic bacteria and fungi in bioaerosols from specialized hospitals in Shandong province, East China. *Environmental Pollution*, 341, 122922. <https://doi.org/10.1016/j.envpol.2023.122922>
- Clinical and Laboratory Standards Institute (CLSI), (2024). *Performance standards for antimicrobial disk susceptibility tests* (14th ed., CLSI standard M02). Clinical and Laboratory Standards Institute.
- Clinical and Laboratory Standards Institute (CLSI), (2025). *Performance standards for antimicrobial susceptibility testing* (35th ed., CLSI supplement M100). Clinical and Laboratory Standards Institute.

- Fernandez, M. O., Thomas, R. J., Garton, N. J., Hudson, A., Haddrell, A., & Reid, J. P. (2019). Assessing the airborne survival of bacteria in populations of aerosol droplets with a novel technology. *Journal of the Royal Society Interface*, 16(150), 20180779. <https://doi.org/10.1098/rsif.2018.0779>
- Haddad, G., & Hallak, M. A. (2026). Microbial contamination in the indoor environment of Arabian Gulf: a review. *Frontiers in Microbiology*, 17, 1796861. <https://doi.org/10.3389/fmicb.2026.1796861>
- Herfst, S., Böhringer, M., Karo, B., Lawrence, P., Lewis, N. S., Mina, M. J., Russell, C. J., Steel, J., De Swart, R. L., & Menge, C. (2016). Drivers of airborne human-to-human pathogen transmission. *Current Opinion in Virology*, 22, 22–29. <https://doi.org/10.1016/j.coviro.2016.11.006>
- Jalili, D., Dehghani, M., Fadaei, A., & Alimohammadi, M. (2021). Assessment of airborne bacterial and fungal communities in Shahrekord Hospitals. *Journal of Environmental and Public Health*, 2021, 1–7. <https://doi.org/10.1155/2021/8864051>
- Kim, K., Kabir, E., & Jahan, S. A. (2017). Airborne bioaerosols and their impact on human health. *Journal of Environmental Sciences*, 67, 23–35. <https://doi.org/10.1016/j.jes.2017.08.027>
- Kuznetsova, M. V., Nesterova, L. Y., Mihailovskaya, V. S., Selivanova, P. A., Kochergina, D. A., Karipova, M. O., Valtsifer, I. V., Averkina, A. S., & Erjavec, M. S. (2025). Nosocomial *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Staphylococcus aureus*: Sensitivity to Chlorhexidine-Based Biocides and Prevalence of Efflux Pump Genes. *International Journal of Molecular Sciences*, 26(1), 355. <https://doi.org/10.3390/ijms26010355>
- Li, J., Cheng, F., Wei, X., Bai, Y., Wang, Q., Li, B., Zhou, Y., Zhai, B., Zhou, X., Wang, W., & Zhang, J. (2025). Methicillin-Resistant *Staphylococcus aureus* (MRSA): Resistance, Prevalence, and Coping Strategies. *Antibiotics*, 14(8), 771. <https://doi.org/10.3390/antibiotics14080771>
- Lu, Z., McInnes, R. S., Allen, F., Gadar, K., & Van Schaik, W. (2025). Resistance to last-resort antibiotics in enterococci. *FEMS Microbiology Reviews*, 49. <https://doi.org/10.1093/femsre/fuaf057>
- Mannan, M., & Al-Ghamdi, S. G. (2021). Indoor air quality in buildings: A comprehensive review on the factors influencing air pollution in residential and commercial structure. *International Journal of Environmental Research and Public Health*, 18(6), 3276. <https://doi.org/10.3390/ijerph18063276>
- Mohamed, F. I., Ibrahim, M. A., Abdel-Latef, G. K., Abdel-Rahim, M. M., Shany, S. a. S., Mahmoud, R., Mahgoub, S. M., Othman, S. I., & Aziz, S. a. a. A. (2026). Enhanced nanoencapsulation of gentamicin, ciprofloxacin, and lysozyme in chitosan-MIL-53 metal-organic frameworks for a synergistic activity against drug-resistant *Salmonella* from poultry and human origins. *RSC Advances*, 16(22), 19991–20014. <https://doi.org/10.1039/d5ra09975g>
- Monteiro, A., Almeida, B., Paciência, I., Rufo, J. C., Ribeiro, E., Carolino, E., Viegas, C., Uva, A. S., & Verde, S. C. (2021). Bacterial Contamination in Health Care Centers: Differences between Urban and Rural Settings. *Atmosphere*, 12(4), 450. <https://doi.org/10.3390/atmos12040450>
- Nie, C., Qiu, Y., Pei, T., & Qin, Y. (2024). Specific sources exert influence on the community structures of bioaerosols. *Aerobiology*, 2(4), 72–84. <https://doi.org/10.3390/aerobiology2040006>
- Odoom, A., & Donkor, E. S. (2025). Prevalence of Healthcare-Acquired Infections among Adults in Intensive Care Units: A Systematic Review and Meta-Analysis. *Health Science Reports*, 8(7), e70939. <https://doi.org/10.1002/hsr2.70939>
- Odoyo, E., Matano, D., Tiria, F., Georges, M., Kyanya, C., Wahome, S., Mutai, W., & Musila, L. (2023). Environmental contamination across multiple hospital departments with multidrug-resistant bacteria pose an elevated risk of healthcare-associated infections in Kenyan hospitals. *Antimicrobial Resistance and Infection Control*, 12(1), 22. <https://doi.org/10.1186/s13756-023-01227-x>
- Olutiola P. O., Famurewa, O., Sonntag, H. S. (2000). An Introduction to General Microbiology (A practical Approach). Measurement of Microbial Growth, pp. 101-111. <https://www.sciepub.com/reference/231610>
- Othman, M., Latif, M. T., Hamid, H. H. A., Bakar, N. H. A., Mohamad, N. H., Haron, N. F., & Noraini, N. M. R. (2024). Variability and health impact of air pollutants and bioaerosols in multi-functional indoor environments with mechanical ventilation system. *Journal of Building Engineering*, 90, 109436. <https://doi.org/10.1016/j.jobbe.2024.109436>
- Roy, S., Barua, H. T., Sujan, M. J., Hossain, A., Paul, S. K., Nasreen, S. A., Ahmed, S., Haque, N., Habib, Z. H., Rahman, A., Rizvi, S. M. S., Hasnat, M. A., Kwon, S. Y., Stelling, J., Gautam, S., Shaw, A., Marks, F., & Poudyal, N. (2025). Trends and patterns of antimicrobial resistance in a tertiary care hospital in Bangladesh. *Microbiology Research*, 16(2), 30. <https://doi.org/10.3390/microbiolres16020030>
- Sajjad, B., Hussain, S., Rasool, K., Hassan, M., & Almomani, F. (2023). Comprehensive insights into advances in ambient bioaerosols sampling, analysis and factors influencing bioaerosols composition. *Environmental Pollution*, 336, 122473. <https://doi.org/10.1016/j.envpol.2023.122473>
- Singh, K. V., Puraswani, M., Ningombam, A., Ashita, A., Thomas, J. M., Ambashta, N. K., Deuri, R. R., Sam, S., Ranic, D., Victor, D., Gunjiyal, J., Farooque, K., & Mathur, P. (2025). Environmental sampling reveals reservoirs of antimicrobial resistance in a tertiary care Indian hospital: an observational study to strengthen infection control practices. *IJID Regions*, 17, 100782. <https://doi.org/10.1016/j.ijregi.2025.100782>
- Szabó, S., Feier, B., Capatina, D., Tertis, M., Cristea, C., & Popa, A. (2022). An overview of healthcare associated infections and their detection methods caused by pathogen bacteria in Romania and Europe. *Journal of Clinical Medicine*, 11(11), 3204. <https://doi.org/10.3390/jcm11113204>
- Tselebonis, A., Nena, E., Panopoulou, M., Kontogiorgis, C., Bezirtzoglou, E., & Constantinidis, T. (2020). Air contamination in different departments of a tertiary hospital.

Assessment of microbial load and of antimicrobial susceptibility. *Biomedicines*, 8(6), 163. <https://doi.org/10.3390/biomedicines8060163>

World Health Organization: WHO. (2022, May 6). WHO launches first ever global report on infection prevention and control. *WHO*. <https://www.who.int/news/item/06-05-2022-who-launches-first-ever-global-report-on-infection-prevention-and-control>

Xhetani, M., Parllaku, B., Bakiri, F., Lugaj, A., Hamzaraj, E., Lika, M., Metaliaj, A., Beca, V., & Bennewitz, B. (2026). Optimizing Molecular Tools for Bioaerosol Monitoring: A Case Study of *Staphylococcus aureus* in a Crowded Workplace. *Aerobiology*, 4(1), 4. <https://doi.org/10.3390/aerobiology4010004>



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