IPS Interdisciplinary Journal of Biological Sciences
IPS Interdiscip J Bio Sci, 4(4): 144-149 (2025)
DOI: https://doi.org/10.54117/iijbs.v4i4.78

The Burden of Antibiotic Resistance: Evaluating the Impact of Multiple Antibiotic-Resistant Enteric Bacteria in Academic Environments

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Abstract

The increasing prevalence of multiple antibiotic-resistant enteric bacteria in academic environments poses a significant health risk to students and staff, potentially leading to outbreaks of difficult-to-treat infections. This study aims to evaluate the burden of antibiotic resistance and its impact on the academic community's health and well-being. A total of 45 swab samples from board dusters were screened for enteric bacterial isolates using standard microbiological techniques. The results revealed four bacterial species: *Escherichia coli* O157:H7, *Escherichia coli* JKHS016, *Klebsiella pneumoniae* 2014C06-125, and *Klebsiella pneumoniae* Kp2092. Antibiotic susceptibility testing showed 54.72% of isolates were resistant, while 45.28% were susceptible. Notably, 34.48% exhibited single antibiotic resistance, and 65.52% displayed multiple antibiotic resistance (MAR). Statistical analysis confirmed the significance ($p \leq 0.05$) of these findings. This study highlights the significant burden of antibiotic resistance in academic environments, particularly on board dusters. The prevalence of multiple antibiotic-resistant enteric bacteria, including *Escherichia coli* and *Klebsiella pneumoniae*, poses a considerable health risk to students and staff. The high rate of multiple antibiotic resistance (65.52%) underscores the need for improved hygiene practices, regular disinfection, and antimicrobial stewardship in academic settings to mitigate the spread of antibiotic-resistant bacteria and protect the health and well-being of the academic community.

Keywords: *Dusters, Microbiological, Strains, Enteric*

Article History
Received: 15 Jun 2025
Accepted: 12 Jul 2025
Published: 15 Aug 2025

Scan QR code to view•

How to cite this paper: Dim, C. N., Iheukwumere, I. H., Iheukwumere, C. M., Ugwu, C. H., Ike, V. E., Ezendianefo, J. N., Egbe, P. A., Oragwu, I. P., Orji, C. C., Ogbonnaya, O. C., Onwuasoanya, U. F., Okereke, F. O., Oduenyi, P. M., & Ochibulu, S. C. (2025). The Burden of Antibiotic Resistance: Evaluating the Impact of Multiple Antibiotic-Resistant Enteric Bacteria in Academic Environments. *IPS Interdisciplinary Journal of Biological Sciences*, *4*(4), 144–149. https://doi.org/10.54117/iijbs.v4i4.78

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Introduction

The presence of microorganisms on surfaces has contributed immensely to microbial distribution in the air (Flores *et al*., 2011). Microorganisms are encountered on virtually every surface, and this frequent exposure predisposes humans to disease by pathogenic strains, which could be antibiotic resistant or multiple antibiotics resistant strains such as enteric bacteria (*Escherichia coli*, *Klebsiella* species *Salmonella* species, *Shigella* species, *Proteus*, *Enterobacter* species etc.) (Flores *et al*., 2011).

These multiple antibiotic resistant strains have been incriminated in resisting the activity of antibiotics such as penicillin, amoxicillin, clindamycin, tetracycline, and erythromycin (Tacconelli *et al*., 2018). For any given indoor surface, microbial community composition is likely shaped by habitat-specific environmental constraints such as the type of surface material and dispersal sources, which include humans, bioaerosols, and other surfaces within the space (Flores *et al*., 2013). If dispersal among surfaces is a primary determinant of community structure, then adjacent surfaces should be more similar in community composition than surfaces further apart. If dispersal from humans is a major determinant, then community structure should vary with frequency and nature of human contact (Meadow *et al*., 2014).

It is worthy to note that different indoor surfaces could harbor different microbial communities, due to frequent contact with specific body parts (Meadow *et al*., 2014). Flores *et al*. (2013) observed that bacteria on restroom surfaces were similar to those isolated from specific human body parts, with the strongest association observed between toilet surfaces, gut, and vaginal communities.

Research has shown that surfaces in the classroom such as walls, desks, chairs, and floors harbor different bacterial species (Meadow *et al.*, 2014). According to their observation, some of the bacterial isolates in the study are similar to human pathogens such as *Salmonella* species, *Staphylococcus aureus*, *Streptococcus* species, and *Corynebacterium* species. This clearly indicates that these bacteria in the surfaces are not far from human sources, especially the body surfaces (Meadow *et al*., 2014).

Several researchers have worked on the bacteria found on the surfaces of inanimate objects in the classroom (papers, chairs, desks, walls, and floors) such as Hubner *et al*. (2011) and Meadow *et al*. (2014) but no study is available on assessing the burden of multiple antibiotic resistant enteric bacteria on board dusters used at Chukwuemeka Odumegwu Ojukwu University, Uli Campus. Hence, the aim of this study is to assess the burden of multiple antibiotic resistant enteric bacteria on board dusters used at Chukwuemeka Odumegwu Ojukwu University, Uli Campus.

Materials and Methods

Study Area

Uli is a town located at the end southeast angle of Ihiala local government area of Anambra state in Nigeria. Its closest neighboring towns are Ohakpu, Ihiala, Amorka, Ubulu, Ozara, and Egbuoma.Uli communities stretch westward over Usham Lake to the lower Niger region and to the confluence of the Atamiri and Enyinja rivers. Its coordinates are 5.783°N 6.687°E and 5°47'N 6°52'E. It occupies a landmass of 99square miles (256-kilometer square). The people of Uli are basically traders and farmers. The climate of the town is typically and equatorial rainforest type characterized by two main seasons; the rainy, which lasts between April and October and the dry season which lasts between November and march, with temperature which is usually high throughout the year and average minimum temperature at about 32℃ and 25℃ respectively.

Sample Collection, Handling and Transportation

The samples (40) used for this study were collected from different board dusters used at different lecture halls at Chukwuemeka Odumegwu Ojukwu University, Uli Campus. The samples were collected using sterile swab sticks. All the samples were put in a sterile polythene bag and were transported to the laboratory for immediate analysis.

Culture and Isolation of Enteric Bacteria

This was carried out using the modified method of Cheesbrough. The swab sticks were stricked on Petri dishes (60 mm OD × 55 mm ID × 13mm high) containing MacConkey agar medium (MA/Biotech). All the plates in triplicates were incubated in inverted at 37±2˚C for 24-48 h. (Cheesbrough, 2010; Ekesiobi *et al*., 2025a; Ekesiobi *et al*., 2025b; and Ekesiobi *et al*., 2025c)

Characterization and Identification of the Isolates

The isolates were sub-cultured on nutrient agar (Biotech), incubated in an inverted position at 37±2˚C for 24 h. The isolates were characterized and identified using their colonial and morphological descriptions (Cheesbrough, 2010), biochemical reactions (Cheesbrough, 2010) and molecular characterization (Iheukwumere *et al*., 2018; and Ekesiobi *et al*., 2025d). The colonial description was carried out to determine the colours of the isolates on agar media plates, their sizes, edges, consistencies and optical properties of the isolates.

Susceptibility Patterns of the Pathogenic Bacterial Isolates against Conventional Antibiotics

Preparation of test isolate: The test isolates were prepared using the method described by Cheesbrough (2010), Ekesiobi *et al*. (2025e) and Ekesiobi *et al*. (2025f). The isolates were aseptically subcultured into a broth culture and incubated at 35 + 2^0C for 24 h. The broth culture of each isolate was centrifuged using an electric centrifuge. The sediment from each culture was diluted to a turbidity that matched 0.5 MacFarland standard that was prepared by mixing 0.5 mL of 1.175% $BaCl_2$ $2H_2O$ and 99.5 mL of 1% Conc. H_2SO_4. The prepared isolates were standardized by comparing the absorbance with that of 0.5 McFarland standards at 640 nm using UV/visible spectrophotometer.

***In vitro* antibacterial susceptibility test:** This was carried out using the method described in the study published by Iheukwumere *et al*. (2018). Each labeled plate was uniformly inoculated with the test organism using pour plate method. An antibiotic sensitive disk (MAXI Disk) was aseptically placed

https://doi.org/10.54117/iijbs.v4i4.78

on the surface of the seeded plate, labeled and then incubated at 37±2ºC for 24 h. Antibacterial activity was determined by measuring the diameter of the zones of inhibition (mm) produced after incubation.

Statistical Analysis

The results of the data generated were expressed as mean, percentage and Table, Data were analyzed by two-way Analysis of Variance (ANOVA) to determine the significance of the study at 95 % confidence level. Pair wise comparison of mean was done by Student "t" test sa described in the study published by Iheukwumere *et al* (2018), Ekesiobi *et al*. (2017), Abiodum *et al*. (2024a), Abiodum *et al*. (2024c), Ekesiobi *et al*. (2025g), Iheukwumere *et al*. (2025c), Iheukwumere *et al*. (2025d), Iheukwumere *et al*. (2025e), Iheukwumere *et al*. (2025f), Iheukwumere *et al*. (2025g), Iheukwumere *et al*. (2025h), Iheukwumere *et al*. (2025i), Iheukwumere *et al*. (2025j), Iheukwumere *et al*. (2025k), Egbe *et al*. (2025a) and Egbe *et al*. (2025b).

Results

The characteristics of the enteric bacterial isolates are shown in Table 1. The results revealed that the isolates varied in appearances on MacConkey agar. Isolate C1 appeared pink, isolate C2 appeared red and isolate D1 and D2 showed similar appearance whereby they appeared red and mucoid. Isolate C1 and C2 had convex elevation and isolates D1 and D2 were slightly raised. They were all Gram-negative rods. All the isolate were catalase positive. Isolate C1 and C2 were citrate negative whereas isolate D1 and D2 where citrate positive; isolate C1 and C2 were indole positive and only isolate D1 and D2 were methyl red negative. The isolates showed complete utilization to glucose and maltose but varied in the utilization to xylose, sorbitol, inositol and Dulcitol.

The molecular characteristics of the enteric bacterial isolates revealed the presence of *Escherichia coli* 0157:H7 strain NE1127 chromosome with complete genome (ECNE11), *Escherichia coli* strain JKHS016 (ECJ6), *Klebsiella pneumoniae* strain 2014C06-125 (KP2) and *Klebsiella pneumoniae* strain KP2092 (KPK2) as shown in Table 2.

The susceptibility of bacterial isolates to conventional antibiotics revealed that isolates D2 was the most susceptible strain with a percentage of 63.64% followed by isolate C1 (61.54%) isolate C2 (40.91%) and then isolate D1 (0.00%) as shown in Table 3.
The degree of resistance exhibited among the isolates revealed that isolate D1 showed the highest resistance with a percentage of 100.00% followed by isolate C1 (80.00%), Isolate D2 (75.00%) and then isolate C2 (38.46%) as shown in Table 4.

Table 1: Characteristics of the enteric bacterial isolates

Parameter	C1	C2	D1	D2
Appearance on MacConkey agar	Pink	Red	Red and Mucoid	Red and Mucoid
Elevation	Convex	Convex	Slightly raised	Slightly raised
Motility	+	+	-	-
Gram reaction	-	-	-	-
Cell morphology	Rods	Rods	Rods	Rods
Catalase	+	+	+	+
Citrate	-	-	+	+
Indole	+	+	-	-
MR	+	+	-	-
VP	-	-	+	+
Glucose	+	+	+	+
Maltose	+	+	+	+
Xylose	+	+	+/-	+/-
Sorbitol	-	+	+/-	-
Inositol	+/-	+/-	+	+/-
Dulcitol	+/-	+	+/-	+/-

Table 2: Molecular characteristics of the enteric bacterial isolates

Isolate code	Max score	Toal score	Query cover (%)	E-value	Percent identity (%)	Accession Number	Description
C1	1681	1681	100	0.0	100	CP038321.1	*Escherichia coli* 0157:H7 strain NE1127 chromosome complete genome (ECNE11)
C2	1936	1936	100	0.0	100	CP147059.1	*Escherichia coli* strain JKHS016 (ECJ6)
D1	1552	1552	100	0.0	100	CP170972.1	*Klebsiella pneumoniae* strain 2014C06-125 (KP2)
D2	1552	1552	100	0.0	100	CP141801.1	*Klebsiella pneumoniae* strain Kp2092 (KPK2)

https://doi.org/10.54117/iijbs.v4i4.78

Table 3: Susceptibility of the bacterial isolates to conventional antibiotics

Isolate	N	Susceptible Strain (%)	Resistance Strain (%)	Implicated antibiotics
C1	13	8 (61.54)	5 (38.46)	S, PN, CEP, SXT, AU, CN
C2	12	9 (40.91)	13 (59.09)	AMX, AU, CEP, S, PN, SXT, CN
D1	7	0 (0.00)	7 (100.00)	PN, S, CEP, SXT, AU
D2	11	7 (63.64)	4 (36.36)	AU, PN, S, CEP, SXT, CN
Total	53	24 (45.28)	29 (54.72)	

Table 4: Degree of resistance among the isolates

Isolates	NR	Single resistant strain (%)	Multiple resistant strain (%)
C1	5	1 (20.00)	4 (80.00)
C2	13	8 (61.54)	5 (38.46)
D1	7	0 (0.00)	7 (100.00)
D2	4	1 (25.00)	3 (75.00)
Total	29	10 (34.48)	19 (65.52)

Discussion

Genetic mutation and other environment factors have been implicated as the chief contributors to multiple antibacterial resistant worldwide. The burden of multiple antibiotics resistant has been heavy on man as revealed in the alarming rate of disease occurrence and death. Understanding the pattern of antibiotic resistant is paramount in disease prevention and control globally. The bacterial species isolated in this study are similar to the bacteria isolated by several researchers (Hubner *et al.*, 2011; Meadow *et al.*, 2014) that evaluated the presence of bacteria in different surfaces in classrooms. The antibiotic resistant bacteria detected in this study corroborate to the resistant bacteria isolated by other researchers (Hubner *et al.*, 2011; Meadow *et al.*, 2014). The ability of the bacterial species to exhibit antibiotics resistance could be attributed to the presence of resistance gene in their plasmid and poor efficacy of the antibiotics. This corroborates to the findings of several researchers (Hubner *et al.*, 2011; Meadow *et al.*, 2014) who studied bacterial species found in the surfaces of inanimate objects in the classroom otherwise known as fomites. The ability of the bacterial species to exhibit antibiotics resistance could be attributed to the presence of resistance gene in their plasmid and poor efficacy of the antibiotics. Similar observation was made by several researchers (Hubner *et al.*, 2011; Meadow *et al.*, 2014). Molecular characterization of the bacterial isolates revealed certain bacterial strains such as *Escherichia coli* 0157:H7 strain NE1127, *Escherichia coli* strain JKHS016, *Klebsiella pneumoniae* strain 2014C06-125, and *Klebsiella pneumoniae* strain Kp2092. However, there was variation in the bacterial isolates reported by other researchers (Murad *et al.*, 2014; Adzitey *et al.*, 2015; Kunad, 2018), which could be attributed to the degree of contamination by the handlers and climatic condition of the area study area.

Furthermore, the antibiotics that were implicated in the resistant menace are Streptomycin, Amoxil, Ciprofloxacin, Augmentin, Ceporex, Penicillin, and Trimethoprim. Similar antibiotics were reported by other researchers (Elshebrawy *et al.*, 2022; Hossain *et al.*, 2022) but there was deviation in the antibiotics documented by Enayat *et al.* (2012), which could be attributed to efficacy of the active pharmaceutical ingredients.

Conclusion

This study highlights the significant burden of antibiotic resistance in academic environments, particularly on board dusters. The prevalence of multiple antibiotic-resistant enteric bacteria, including *Escherichia coli* and *Klebsiella pneumoniae*, poses a considerable health risk to students and staff. The high rate of multiple antibiotic resistance (65.52%) underscores the need for improved hygiene practices, regular disinfection, and antimicrobial stewardship in academic settings to mitigate the spread of antibiotic-resistant bacteria and protect the health and well-being of the academic community.

Acknowledgment

We are grateful to all our study participants who join the study voluntarily. We are grateful to ZAHARM Analytical and Research Laboratory, Amawbia, Awka Anambra State, Nigeria for providing enabling environment, resources and techniques for this study. We really salute their wonderful efforts.

Conflict of interests: The authors declare that they have no conflict of interests.

Funding: This research did not receive specific grant from any funding agencies.

Ethical approval: Not applicable

Authors Contributions: All contributed towards the study design, experiment execution, data analysis, and manuscript drafting.

Availability of Data and Materials: All datasets analyzed and described during the present study are available from the corresponding author upon reasonable request.

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