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Contamination of Automated Teller Machines Surfaces with Multi-drug Resistance Gram-negative Bacteria in Dar es Salaam, Tanzania

Regan Zenas Shayo[a,b] Nsiande Lema[e], Mecky I. N. Matee[c, d]

[a]Central Tuberculosis Reference Laboratory, Dar es Salaam, Tanzania, [b]National Tuberculosis and Leprosy Program, Dodoma, Tanzania, [c]Department of Microbiology and Immunology, Muhimbili University of Health and Allied Science, Dar es Salaam, Tanzania, [d]SACIDS Africa Centre of Excellence for Infectious Diseases, Sokoine University of Agriculture, Morogoro, Tanzania, [e]Tanzania Field Epidemiology and Laboratory Training Programme, Dodoma Tanzania

Correspondence to Regan Shayo (shayoregan@gmail.com)

ABSTRACT

Background: In Tanzania, little is known about the proportion of Multi-drug resistance (MDR) Gram-negative bacteria contamination on Automated Teller Machine (ATMs) surfaces. The study aimed to determine the proportion of MDR Gram-negative bacteria contamination on ATMs surfaces, antimicrobial resistance patterns as well as associated factors.

Methodology: A cross-sectional study was conducted between January and March -2021 in Dar es Salaam, involving 298 ATMs. Cultures were performed on Mac-Conkey agar while antimicrobial susceptibility was done using the Kirby Bauer disc diffusion method with *Klebsiella pneumoniae* ATCC 700603 and *Escherichia coli* ATCC 25922 used as controls. Data analysis was done using STATA version 15.1. Chi-square and Modified Poisson regression was used to assess factors associated with MDR contamination. Data was presented as prevalence ratio (PR) and 95% Confidence Interval. A *p-value* of <.05 was considered statistically significant.

Results: More than half (55.4%) of ATMs in Dar es Salaam are contaminated with Gram negative bacteria, mostly by *Klebsiella pneumoniae* 18.5% (31/168). The highest level of resistance was observed against ampicillin (68.9%). About one-third (34.5%) of the isolates were MDR. About 35.7% were Extended-Spectrum Beta-Lactamases (ESBL) producers while 19.6% were quinolone/ fluoroquinolones-resistance. Risk factors for contamination of ATMs included highly populated location such as; Ubungo (PR adjusted = 3.62, 95%CI = 1.58-8.30, *P=.002*), Kigamboni (PR adjusted = 2.78, 95%CI = 1.20-6.42, *P=.017*), and Temeke (PR adjusted = 2.75, 95%CI = 1.04-3.72, *P=.023*), and less frequent cleaned ATMs (PR adjusted = 1.98, 95%CI = 1.04-3.73, *P=.04*)

Conclusions: More than half of ATMs in Dar es Salaam are contaminated with Gram-negative and one-third of them with MDR bacteria, especially those located in highly populated areas and those that are less frequently cleaned. This calls for interventional measures regarding public awareness of ATMs as potential vehicles for the transmission of infectious agents.

BACKGROUND

Automated Teller Machines (ATMs), regarded as mini-banks are important devices in the banking sector. ATMs make banking convinient and serve thousands of customers daily.[1] As helpful as ATM machines are, a number of studies across the world have identified them as a source of infections to the users.[2] Bacteriological examinations carried out on ATMs have reported that they are contaminated with various microorganisms,[3–6] associated with both community-acquired and hospital acquired infections.[7] Microbes bear the potentials for survival on dry fomites like ATM machine key pads. They have different physiological resting stages and thus are capable of surviving or hibernating due to low water activity. Some Gram-negative bacteria can remain active up to month on their resting surfaces.[8] *Klebsiella pneumoniae, Escherichia coli, Enterobacter species* as well as non-lactose fermenting bacteria such as *Pseudomonas aeruginosa* and *Acinetobacter species* have been identified as major cause of multi-drug resistant bacterial infections.[9,10] This group of bacteria developed resistance to a wide range of antibiotics, including third generation cephalosporins, carbapenems, and fluoroquinolones, which are the best antibiotics currently available for treating multi-drug resistant bacteria.[11]

Most of these bacteria are on the World Health Organization (WHO) priority list of pathogens that poses substantial threat to morbidity and mortality worldwide.[11] These bacteria are resistant to extended-spectrum beta-lactamase (ESBL)- producing bacteria and quinolone/ fluoroquinolone-resistant bacteria and have been linked to a number of environments,[12,13]

including ATMs,[14–16] and thus posing a serious public health threat.[17-19] ATMs, despite being used by people of various backgrounds, lack constant and frequent monitoring of hygienic measures. Some are not provided with disinfectants and have no instructions for clients. This raises their potential to be vehicles for the transmission of micro-organisms, which cause infections that are difficult to treat as substantiated in numerous studies conducted in Europe, Asia and Africa.[3,20–24]

In Tanzania, little is known about the presence of pathogenic bacteria on ATMs surfaces, however, there is literature indicating the existence of pathogenic bacteria including ESBLs and quinolone resistance bacteria in the community.[25–29] This study aimed to determine the proportion of MDR Gram-negative bacteria contamination on ATMs surfaces and antimicrobial resistance patterns as well as associated factors in Dar es Salaam, Tanzania. Surveillance of AMR and MDR pathogens is one of the strategic objectives in the Tanzania National action plan on antimicrobial resistance.[30] In its part, this study provide data on the burden of MDR Gram-negative bacteria contamination on ATMs in Dar es Salaam.

Data emanating from this study will sensitise both owners and users of these machines, of their potential to transmit pathogens. The study will provide evidence for better management of ATMs to curb transmission of pathogens. Our hypothesis is that ATMs are essential to our social life, localised in city centres, trade areas, and around hospitals and are used by hundreds of people of varying socio-economic levels and hygienic status are potential vehicles of microbial pathogens, including MDR bacteria.

MATERIAL AND METHODS

Study Area

This was a cross-sectional study, carried out in Dar es Salaam Tanzania from January to March 2021. Dar es Salaam is the most populated city in Tanzania, with approximately more than 7 million people.[31] The use of ATMs is significantly high since Dar es Salaam is a commercial city. In 2019, Dar es Salaam had 290 bank branches, which constituted 30.3% of all bank branches in the country and the use of ATMs was reported to be 6.4 ATMs per 100,000 adults.[32,33] (Figure 1).

Sample Size Estimation

The sampling frame included ATMs of the 3 largest banks in Dar es Salaam. A list of the ATMs was obtained from respective banks, which totalled to 432. The sample size was calculated using Kish Leslie formula (1965),[34] a prevalence of 21.4% (*E. coli* bacteria isolated on ATMs surfaces)[35] and margin error of 5% was used. The minimum required sample size was 258 ATMs which was raised to 298 ATMs so as to increase the power of the study. The proportion of ATMs of a specific bank included in the sample size (298) depended on the proportion of the given bank's number of ATMs that contributed to the sample frame. Thus, banks with high number of ATMs in the sample frame contributed higher number of ATMs in the sample size. Simple random technique was used to select the ATMs that were included in the sample size (298). Samples were distributed as follows: First bank (I) 121 out of 176 ATMs, second bank (II) 119 out of 173 ATMs, and third Bank (III) 58 out of 83 ATMs.

Information regarding frequency of ATM cleaning and disinfection, availability of hand-washing and cleaning facilities, and location of the ATM (Remote ATMs versus Branch ATMs) was collected using a structured observation checklist.

Sample Collection and Transportation

A Sterile swab[36] was moistened in sterile saline and moved several times over the surfaces of the most-used keys on the ATM keypad/screen in an aseptic procedure and placed into a nutrient broth media.[37] The collected samples were transported to the National Public Health Laboratory (NPHL) in cooler boxes packed with ice packs at temperatures ranging between 2 to 8^{0}C degrees for processing within 4 hours of collection.

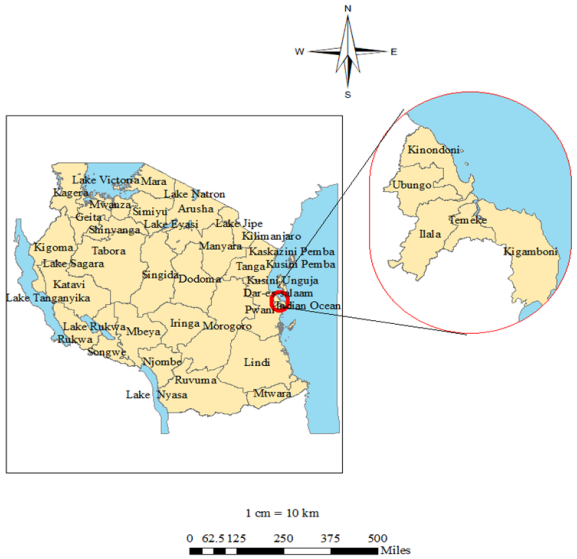
Sample Processing and Bacteria Isolation

Samples in nutrients broth were incubated at 37°C for 18 to 24 hours before culture. The culture was performed on Mac-Conkey (MCA) agar[37] with crystal violet and bile salt. Cultured plates were incubated aerobically at 37°C. Plate growths were noticed after 18 to 24 hours incubation, the isolates were then sub-cultured on fresh media plates until pure isolates were observed.

Bacteria Identification

Isolated bacteria were identified by performing gram stain and standard biochemical tests, which included; oxidase, urease, Indole, Citrate test, and Triple Sugar Iron (TSI).[38] The TSI test is designed to differentiate among the different groups or genera of the Enterobacteriales, which are all Gram-negative bacilli, based on fermentation of glucose and lactose or sucrose and hydrogen sulphide production. For identification of Gram-negative bacteria with ambiguity, API 20 E systemm was used as per manufacture instructions.[38]

FIGURE 1: Map Showing Districts in Dar es Salaam City, Tanzania



Antibiotic Susceptibility Testing

Identified gram-negative bacteria were subjected to antibiotic sensitivity test using the Kirby Bauer diffusion disk method on Muller Hinton agar[37] to determine their susceptibility patterns against selected antimicrobial agents, as described by Clinical Laboratory Standards Institute (CLSI), 2020.[39] Antimicrobial classes used were; Aminoglycoside, Fluoroquinolone, Quinolones, Tetracycline, third generation cephalosporin, carbapenem, penicillins, chloramphenicol, cotrimoxazole and cephalosporin (cefotaxime/clavulanic acid-30/10µg). Bacteria that showed resistance or decreased susceptibility (intermediate) to any of the third generation cephalosporins were selected for phenotypic ESBL confirmation. The potential ESBL-producing gram-negative bacteria were screened by cefotaxime (30 µg) and were confirmed by the combination disk method. Cefotaxime (30 µg) and the combination disc cefotaxime plus clavulanic acid (30 µg+ 10 µg) were placed 25 mm apart. An increase of ≥ 5 mm in the zone of inhibition for cefotaxime plus clavulanic acid compared to cefotaxime alone was confirmed as an ESBL producer.[40] Bacteria showing resistance against ciprofloxacin and nalidixic acid were regarded as quinolones/fluoroquinolones-resistant.[41] Bacteria that showed resistance to at least one antimicrobial in 3 or more antibiotic classes was regarded as MDR.[42]

Quality Assurance

Culture media used for isolation and identification of organisms were controlled using standard organisms *E. coli* ATCC 25922 strains. For ESBL producing gram-negative bacteria, ESBL producing *K. pneumonia* ATCC 700603 and non-ESBL producing *E. coli* ATCC 25922 were used as positive and negative controls.

Data Analysis

Data management and analysis was done by using STATA version 15.1. Frequencies and proportions of bacteria isolated and their antibiograms were determined. A Chi-square test was used to determine the univariate association of factors that are associated with MDR contamination on ATM surfaces. Variables with $P<.25$ were subjected to multivariate analysis. Since the proportion of MDR was greater than 15%, Modified Poisson regression was used to determine independent predictors of ATM surface contamination. Results from modified Poisson regression analysis were presented as Prevalence Ratio (PR) and 95% Confidence Interval. A *p-value* of <.05 was considered statistically significant.

Ethical considerations

Ethical approval for this study was obtained from Muhimbili University of Allied Sciences (MUHAS) Senate Research and Publications Committee (Ref. No. DA.282/298/01.C/).

RESULTS

The Proportion of Gram-Negative Bacteria Recovered from ATM Surfaces

A total of 298 ATMs from 3 largest banks in 5 districts of Dar es salaam city namely; Kinondoni, Ubungo, Ilala, Temeke and Kigamboni were screened. The proportion of contaminated ATMs across the districts ranged from 35.7 % to 75% (Figure 2).

Of the 298 swabs collected from ATM surfaces (screen/key-pads), 55.5% (n=165/298) showed microbial growth, and 168 bacteria were isolated. The distribution of bacteria recovered from ATM surfaces is shown in Table 1. *Klebsiella pneumoniae* 18.5% (n=31/168) was the predominant isolate followed by *Acinetobacter* spp 12.5% (n=21/168) and *E. coli* 10.1% (n=17/168), while *Proteus* and *Providencia species* were the least recovered, each accounting for 0.6% (n=1/168) of the isolates.

Antimicrobial Resistance Pattern of Isolates Recovered from ATM Surfaces

Bacteria were particularly resistant against ampicillin (68.9%), followed by cefotaxime (26.8%), and least resistant against gentamicin (1.3%). *K. pneumoniae*, *Acinetobacter species*, *E. coli* and *P. aeruginosa*, showed high, moderate and low levels of resistance ranging from 3.2% to 87.1%. (Table 2).

TABLE 1: The Pattern of Gram-Negative Bacteria Recovered from ATM Surfaces in Dar es Salaam, Tanzania

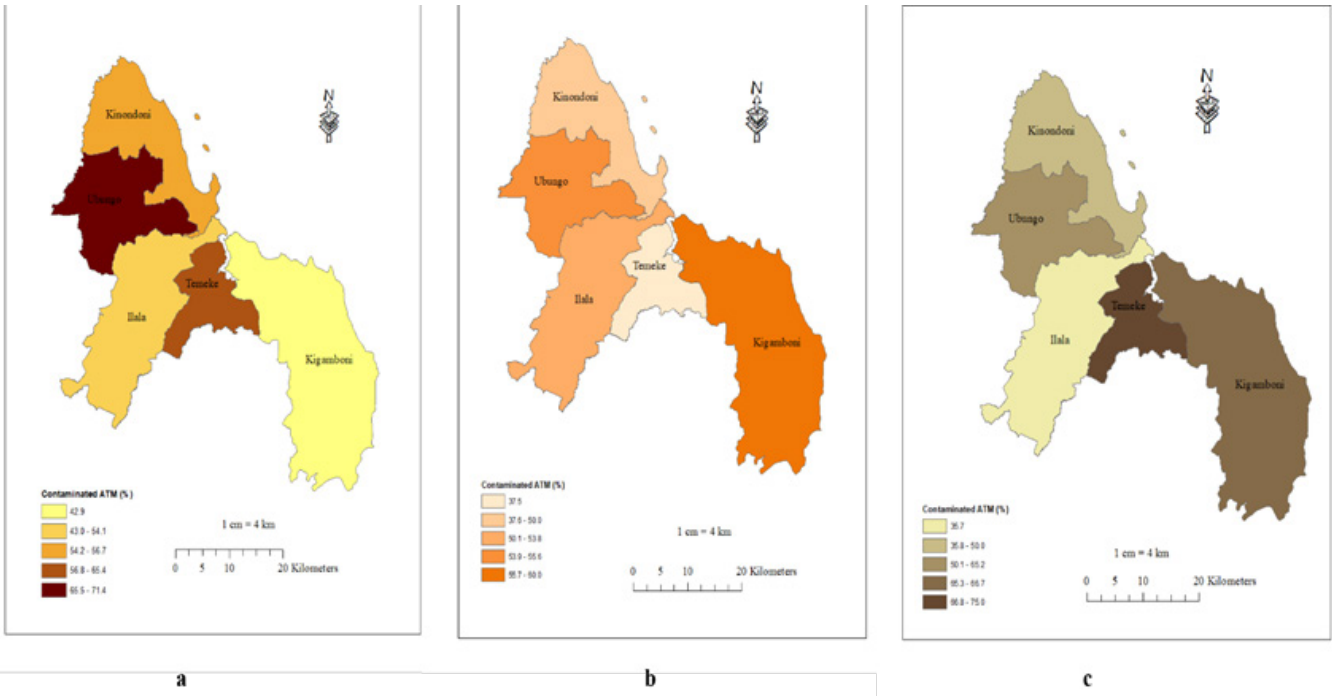
Organism	# isolates	Percent
Klebsiella pneumoniae	31	18.5
Acinetobacter spp	21	12.5
Escherichia coli	17	10.1
Pseudomonas aeruginosa	14	8.3
Enterobacter aerogenes	13	7.7
Shigella spp	13	7.7
Enterobacter spp	12	7.1
Serratia spp	11	6.6
Klebsiella oxytoca	9	5.4
Salmonella spp	8	4.8
Citrobacter spp	7	4.2
Pseudomonas spp	4	2.4
Yersinia spp	4	2.4
Morganella spp	2	1.2
Proteus spp	1	0.6
Providencia spp	1	0.6
Total	**168**	**100**

The Proportion of Multi-Drug Resistance Gram-Negative Bacteria from ATM Surfaces

Out of 168 isolates, 35.1% (n=59/168) were MDR against 3 to 7 classes of tested drugs. *Salmonella spp* had the highest proportion of MDR isolates 62.5% (n=5/8) compare to other Gram-negative bacteria, which ranged between 9.1% and 50% (Table 3).

From the most frequently isolated bacteria, the common resistant pattern observed were Cephalosporin's/Penicillin's/Phenicals, Cephalosporin's/Sulphonamides/Fluoroquinolone/ Penicillin's/ Quinolones and Sulphonamides/ Penicillin's/ Quinolones. One isolate each from *E. coli*, *P. aeruginosa*, *and Acinetobacter species*, were resistant to 6 and up to 7 classes of antibiotics (Table 4).

FIGURE 2: Proportion of contaminated ATM among three banks in each Districts of Dar es Salaam city, Tanzania



Key: a- bank (I), b-bank (II), c-bank (III)

TABLE 3: Proportion of MDR Isolates Recovered from ATM Surfaces in Dar es Salaam, Tanzania

Bacteria name	#Isolates	#MDR Isolates	%MDR Isolates
Klebsiella pneumoniae	31	7	22.58
Acinetobacter spp	21	10	47.62
Escherichia coli	17	8	47.06
Pseudomonas aeruginosa	14	7	50.00
Enterobacter aerogenes	13	6	46.15
Shigella spp	13	5	38.46
Enterobacter spp	12	4	33.33
Serratia spp	11	1	9.09
Klebsiella oxytoca	9	3	33.33
Salmonella spp	8	5	62.50
Citrobacter spp	7	1	14.29
Pseudomonas spp	4	2	50.00
Yersinia spp	4	0	-
Morganella spp	2	0	-
Proteus spp	1	0	-
Providencia spp	1	0	-
Total	168	59	35.12

TABLE 4: Multi-Drug Resistance Pattern among most Frequently Isolated Gram-Negative Bacteria Recovered from ATM Surfaces in Dar es Salaam, Tanzania

Organism	Resistant Profile	# Resistant classes	# Isolates
Acinetobacter spp	CEPH3, FQ, QUIN	3	2
	FOLATE, PEN, QUIN	3	3
	CEPH3, PEN, PHEN	3	1
	CEPH3, PEN, PHEN, QUIN	4	1
	CEPH3, FOLATE, FQ, PHEN, QUIN	5	1
	AG, CEPH3, FOLATE, PEN, PHEN	5	1
	CARB, CEPH3, FOLATE, FQ, PEN, QUIN	6	1
E coli	FOLATE, PEN, QUIN	3	1
	FOLATE, PEN, PHEN	3	2
	CEPH3, PEN, PHEN	3	1
	FOLATE, FQ, PEN, QUIN	4	1
	CEPH3, FOLATE, FQ, PEN, QUIN	5	2
	CARB, CEPH3, FOLATE, FQ, PEN, QUIN	6	1
Klebsiella oxytoca	FOLATE, FQ, PEN, QUIN	4	2
	CARB, CEPH3, FOLATE, PEN, PHEN, QUIN	6	1
Klebsiella pneumoniae	CEPH3, FOLATE, PEN	3	2
	FOLATE, FQ, PEN	3	1
	CEPH3, PEN, PHEN, QUIN	4	1
	CARB, CEPH3, PEN, QUIN	4	1
	CEPH3, FOLATE, FQ, PEN, QUIN	5	2
Pseudomonas aeruginosa	CEPH3, FQ, QUIN	3	1
	FOLATE, PEN, PHEN	3	1
	CEPH3, PEN, PHEN	3	2
	CEPH3, FQ, PEN	3	1
	CEPH3, FOLATE, PEN, PHEN	4	1
	CARB, CEPH3, FOLATE, FQ, PEN, PHEN, QUIN	7	1

Key: QUIN, quinolones; PHEN, phenicol's; AG, aminoglycosides; PEN, penicillin's; FQ, Fluoroquinolone; FOLATE, sulphonamides; CEPH3, cephalosporin's; CARB, carbapenems

TABLE 5: Proportion of ESBL Producers Isolated from ATM Surface in Dar es Salaam, Tanzania

Organism	#Isolates	# ESBLs producers	% ESBLs
E.coli	7	4	57.14
P. aeruginosa	8	0	-
K. Oxytoca	2	1	50.00
K. pneumoniae	11	5	45.45
Total	**28**	**10**	**35.71**

Key: ESBL- Extended spectrum beta-lactamase; #, number of; Spp- Species; % Percentage

Isolation Frequency of ESBL-Producing Gram-Negative from ATM Surfaces

A total of 28 Gram-negative bacteria isolates, (*K. pneumoniae, E. coli, K. oxytoca and P. aeruginosa*) that showed resistance or decreased susceptibility (intermediate) to any one of the third generation cephalosporin's were screened for ESBL production, and 35.7% (n=10/28) were positive for the test. Among screened isolates, the proportion of ESBL producers was highest among *E. coli* isolates 57.1 % (n=4/7) (Table 5).

Quinolone-Resistant Gram-Negative Bacteria Recovered from ATM Surfaces

Out of 168 isolates tested, 19.6% (n=33/168) were found

TABLE 2: Antibiotic resistance pattern among the 168 isolates recovered from ATM surfaces in Dar es Salaam, Tanzania

Organism	#Isolates	AMP	CIP	MEM	CTX	SXT	GEN	CHL	NAL	DOX
K. pneumoniae	31	87.1	3.2	0	32.3	16.1	0	3.2	0	6.5
Acinetobacter spp.	21	28.6	4.8	4.8	14.3	38.1	4.8	9.5	47.6	0
Escherichia coli	17	70.6	5.9	0	23.5	41.2	0	11.8	17.6	11.8
P. aeruginosa	14	78.6	0	0	42.9	21.4	0	28.6	7.1	14.3
Enterobacter spp.	13	61.5	15.4	7.7	15.4	30.8	7.7	7.7	30.8	7.7
Shigella spp.	13	38.5	15.4	7.7	38.5	15.4	0	7.7	38.5	0
E. aerogenes	12	83.3	8.3	8.3	58.3	16.7	8.3	8.3	16.7	8.3
Serratia spp.	11	81.8	0	0	36.4	0	0	0	0	0
Klebsiella oxytoca	9	88.9	0	0	11.1	44.4	0	11.1	22.2	0
Salmonella spp.	8	62.5	12.5	12.5	62.5	12.5	0	0	37.5	25
Citrobacter spp.	7	71.4	14.3	0	42.9	0	0	14.3	14.3	28.6
Pseudomonas spp.	4	100	0	0	25	25	0	0	0	25
Yersinia spp.	4	50	0	0	25	0	0	0	0	0
Morganella spp.	2	0	0	0	0	0	0	0	0	0
Proteus spp.	1	100	0	0	0	0	0	0	0	0
Providencia spp.	1	100	0	0	0	0	0	0	0	0
Total	**168**	**68.9**	**4.9**	**2.6**	**26.8**	**16.4**	**1.3**	**6.4**	**14.7**	**7.9**

Key: CIP, ciprofloxacin; CHL, chloramphenicol; NAL, nalidixic acid; GEN, gentamycin; AMP, ampicillin; DOX, doxycycline; SXT, trimethoprim/sulfamethoxazole; CTX, cefotaxime; MEM, meropenem; ESBL, Extended spectrum beta-lactamase;#,number of; Spp, Species; %R, Percentage resistance

TABLE 7: Comparison of resistance levels between ESBL vs non-ESBL producers, and Quinolone's resistance versus non-Quinolone's resistance among gram-negative bacteria recovered from ATMs surfaces in Dar es Salaam, Tanzania

Drug	ESBL producers (n=10) %R (n)	Non-ESBL producers (n=18) %R(n)	P-Value	Quinolone's resistance (n=33) %R(n)	Non-quinolone resistant (135) %R(n)	P-Value
STX	50(5)	22.2(4)	0.23	51.5(17)	14.8(20)	<.001
MEM	30(3)	0(0)	0.04	27.3(9)	3.7(5)	<.001
DOX	20(2)	5.6(1)	0.24	5.4(4)	4.4(6)	.38
GEN	0(0)	0(0)	1.00	0.0(0)	2.2(3)	1.00
CHL	10(1)	11.1(2)	1.00	9.1(3)	8.15(11)	1.00

Key: CHL, chloramphenicol; GEN, gentamycin; AMP, ampicillin; DOX, doxycycline; SXT, trimethoprim/sulfamethoxazole; MEM, Meropenem; ESBL, Extended spectrum beta-lactamase, %R, percentage resistance; (n), number of isolates

TABLE 6: Proportion of Quinolone/ Fluoroquinolone Resistant Bacteria Recovered from ATM Surfaces in Dar es Salaam, Tanzania

Organism	#Isolates	# FQ/QUIN resistant	%FQ/QUIN resistant
Klebsiella pneumoniae	31	8	25.81
Acinetobacter spp	21	0	-
Escherichia coli	17	5	29.41
Pseudomonas aeruginosa	14	3	21.43
Enterobacter aerogenes	13	1	7.69
Shigella spp	13	4	30.77
Enterobacter spp	12	5	41.67
Serratia spp	11	0	-
Klebsiella oxytoca	9	0	-
Salmonella spp	8	0	-
Citrobacter spp	7	2	28.57
Pseudomonas spp	4	0	-
Yersinia spp	4	4	100.00
Morganella spp	2	1	50.00
Proteus spp	1	0	-
Providencia spp	1	0	-
Total	168	33	19.64

Key: FQ- quinolone, QUIN-fluoroquinolone, #-number of, %-Percentage

to be quinolone/fluoroquinolones -resistant. *Yersinia species* were observed to be more resistant to quinolones 100% (4/4) than the other Isolated Gram-negative bacteria which ranged from 7.7% to 50 % (Table 6).

Antibiotic Resistance Levels among ESBL and Quinolone Resistance Isolates

ESBL producing bacteria were more significantly resistant to meropenem (*P=.04*), while quinolone/ fluoroquinolone resistant isolates were more significantly resistant to trimethoprim/sulfamethoxazole (*P <.001*), and meropenem (*P<.001*). (Table 7) Additionally, out of 10 isolates that were ESBLs producers, almost 50% (n=5/10) of those isolates were also resistant to quinolone/fluoroquinolone.

Factors Associated with MDR Bacteria Contamination on ATM Surfaces

Table 8 show independent predictors of ATM surface contamination. ATM surface contamination were more likely significantly associated with ATMs located in Ubungo ($PR_{adjusted}$ = 3.62, 95%CI = 1.58-8.30, *P=.002*), Kigamboni ($PR_{adjusted}$ = 2.78, 95%CI = 1.20-6.42, *P=.017*), and Temeke ($PR_{adjusted}$ = 2.75, 95%CI = 1.04-3.72, *P=.023*) compared to those located at Ilala municipal. On the other hand, ATMs with less frequency of cleaning were significantly associated with an increased likely hood of MDR bacteria contamination compared to those cleaned at least once a day ($PR_{adjusted}$ = 1.98, 95%CI = 1.04-3.73, *P=.04*). There was a decreased risk of MDR bacteria contamination on remote ATMs, though the decrease was not statistically significant ($PR_{adjusted}$ = 0.79, 95%CI = 0.43-1.46, *P=.46*).

DISCUSSION

This study revealed that more than half of ATMs in Dar es Salam were contaminated with gram-negative bacteria and one-third of these bacteria were MDR against 3 to 7 classes of common antibiotics used in hospital settings. ATMs located in Ubungo, Kigamboni and Temeke as well as less cleaned ATMs were observed as risk factors for MDR bacteria contamination.

The current study found 55.4% of ATMs contaminated with Gram-negative bacteria. This finding is lower than what was reported in a study conducted in India where 95.7% of ATMs were found to be contaminated with such bacteria.[43] This variation is probably contributed by the fact that the current study took place in the middle of the COVID-19 pandemic, where the use of hand sanitisers was high. Nonetheless, this poses a public health risk given the fact that half of the machines inspected were contaminated with pathogenic bacteria, including multi-drug resistant bacteria.

In this study, *K. pneumoniae* was the most frequent isolate, followed by *Acinetobacter* sp and *E. coli*. These results conform to observation reported in a study conducted in India where *K. pneumoniae* was the most isolated bacteria from ATM surfaces.[44] However, this finding is contrary to the findings of a study conducted in west Iran[45] where *E.coli* was the predominant isolate followed by *Klebsiella spp*. Collectively, numerous studies report the predominance of *K. pneumoniae* and *E. coli* as the most significant gram-negative bacteria in contamination of ATM surfaces.[44-46] These microbes are members of Enterobacteriaceae.

The current study revealed that the risk of contamination was higher in less cleaned ATMs. This observation conforms to a study that showed that cleaning and disinfection reduce microbial contamination by 94.1%.[47] The risk of contamination of ATMs with MDR bacteria was also significantly associated with the location of the ATM. The risk was high in densely populated areas namely; Ubungo, Kigamboni, and Temeke. This observation is in keeping with a study conducted in Nigeria where ATMs from the Abakaliki metropolis had higher isolation of bacteria compared to ATMs in low populated Afikpo town.[16] Collectively, these findings support the need for maintaining strict hygienic measures on frequently touched public surfaces especially in overcrowded areas. This is supported by multiple studies.[30,48,49]

Regarding AMR pattern, isolates recovered from this study showed high levels of resistance against ampicillin, moderate levels of resistance against, cefotaxime (CTX), trimethoprim/sulfamethoxazole (SXT) and nalidixic acid (NAL), and low level against meropenem (MEM) and gentamicin (GEN). An estimated one-third of all isolates were MDR, with some exhibiting resistance to more than 6 different classes of antibiotics and could be classified as pan-drug resistant (PDR).[50] Notably, most MDR combinations included penicillin, tetracycline, and ciprofloxacin, which is in keeping with several studies conducted in Dar es Salaam, showing high resistance to such antibiotics.[51,52] Resistance to these antibiotics can be explained by the fact that there is irrational use of antibiotics in the community, as most antibiotics are relatively cheap and can be obtained over the counter without a prescription,[53] which fuels the occurrence of the resistance.[54] Furthermore, this study showed that *Salmonella* species had high to moderate levels of resistance against CTX and MEM respectively. This observation supports other studies' findings, where the emergence of ESBL- producing *Salmonella spp* and carbapenem resistance have been reported in the community.[55,56] An increase in resistance to *Salmonella spp* especially to meropenem (MEM) is alarming, as there are few options available to treat extensive drug-resistance (XDR) Typhoid. This is high time to take an important step to study the resistance pattern of *salmonella spp* to detect new stains timely.

Our study showed that among isolates screened for ESBL, 35.7% were ESBL producers. Compared with non-ESBL producers, ESBL-producing bacteria had insignificant resistance to trimethoprim/sulfamethoxazole, chloramphenicol; gentamycin, and doxycycline except meropenem.

On the other hand, 19.6% of isolates were quinolone/fluoroquinolones-resistant whereby quinolone/fluoroquinolones resistance isolates were more significantly resistant to trimethoprim/sulfamethoxazole, and meropenem except for gentamicin, doxycycline, and chloramphenicol when compare to non-quinolone/fluoroquinolones resistance. These findings are in contrary to a study in Dar es Salaam[57] which shows that ESBL producers and quinolone resistant isolates were more significantly resistant to all other tested antibiotics including, gentamicin, meropenem, chloramphenicol, doxycycline, and trimethoprim/sulfamethoxazole. This variation is presumably because the current study used samples from inanimate surfaces while the other study used poultry and pig, whose farming has been associated with intense use of antibiotics.[58] *Yersinia spp* were more resistance to quinolones/flouriquinolones than other Gram-negative bacteria, this is similar to a study conducted in china which showed that *Yersinia spp* isolated from animal feaces, raw/cooked livestock, poultry meat, and frozen food had high resistance to quinolones.[59,60] Nonetheless, 50% of ESBL producers were also resistant to quinolones/ fluoroquinolones, indicating and supporting shared mechanisms of resistance.[61] These findings are important since beta-lactams and quinolones/fluoroquinolones are the cornerstones for treatment of majority of infections occurring in humans and animals[62,63] and resistance to them has severe consequences on public health and animal production.[64,65]

CONCLUSION

More than half of ATMs in Dar es Salaam are contaminated with Gram-negative bacteria, with one-third of these bacteria exhibiting multi-drug resistance against the tested antibiotics. Contamination occurred especially in ATMs that were not regularly cleaned and those located in densely populated areas, calling for interventional measures such as regular disinfection of the machines and clients' precautionary measures, such as hand sanitation. The owners of the ATMs need to ensure constant application of hygienic measures, including the provision of sanitisers, and constant monitoring of compliance.

Study Limitations

The current study provides important preliminary information about the proportion of Gram-negative MDR bacteria contamination on ATM surfaces, as well as associated factors. However, the study has several limitations. Users' hand hygiene practices were not observed, which could have provided evidence of the association of hand hygiene practices with contamination of ATMs with MDR bacteria. Secondly, the preparation of the sanitisers, their composition, and expiry dates could not be verified since such information was not available.

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