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Bacterial contamination of clinical coats of medical doctors: a cross-sectional study in Mulago National Referral Hospital in Uganda

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ABSTRACT:

— ***Objective:*** Contamination of medical doctors' clinical coats with potentially pathogenic organisms is one of the major vehicles for nosocomial infections. We determined the prevalence of bacterial contamination of clinical coats of medical doctors in a National Referral Hospital in Uganda.

— ***Subjects and Methods:*** We carried out a cross-sectional study of a convenience sample of medical doctors working in selected wards at Mulago National Referral Hospital. Sterile cotton swabs were used to take samples from 3 sites of each doctor's clinical coat (right and left cuffs, and edges of most used lower front pocket) at the end of their work shift. Samples were transported to the laboratory within 30 minutes from collection. Organisms were identified using conventional culture methods and standard biochemical tests. Antimicrobial susceptibility tests were done using the Kirby-Bauer disc diffusion method. Each participant completed a self-administered questionnaire which collected data on their handling habits of the clinical coats. Analysis was performed using STATA software.

— ***Results:*** A total of 294 swabs were collected from 98 clinical coats of 98 medical doctors, from which 332 bacteria were isolated. Out of the 98 clinical coats, 90 (91.8%) were found to be contaminated with at least one bacterial species. Gram-positive bacteria (n=293, 88.3%) were the most isolated, with Coagulase Negative Staphylococcus as the predominant bacteria (n=214, 64.5%). Among the gram-negative, Acinetobacter spp. was the most isolated (n=29, 8.7%). Thirteen (2.8%) isolates were multidrug-resistant (MDR). More than half of the isolates (n=223, 67.2%) were found in samples obtained from the cuffs.

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— ***Conclusions:*** This study revealed a high prevalence of bacterial contamination in clinical coats of medical doctors. Cuffs had the highest bacterial contamination among the clinical coat sites, thus posing a significant risk of transmitting such pathogens to patients.

— ***Keywords:*** *Medical doctors' clinical coats, Pathogenic bacteria contamination, Multi-drug resistant bacteria.*

INTRODUCTION

Nosocomial infections are those obtained by patients during their stay in hospital[1]. High incidence of nosocomial infections contributes to significant morbidity and mortality of patients especially in vulnerable populations like surgical patients, pediatrics, and those with chronic illnesses that frequently visit health facilities[2]. In developed countries, seven out of one hundred hospitalized patients at any given time get nosocomial infections, and in developing countries, ten out of a hundred hospitalized patients[3]. A systematic review and meta-analysis[4] by the World Health Organization showed nosocomial infection density in developing countries was 47.9 per 1,000 patient days (95% CI: 36.7-59.1), three times more than the density reported from the United States of America (USA). Some studies[5,6] conducted in Sub-Saharan Africa report prevalence rates ranging from 7-28% among admitted patients. A study done in Mulago National Referral Hospital by Seni et al[7] found that 10% of patients developed sepsis following surgery.

Health workers wear hospital attire to protect their clothes from contamination and as a way of indicating their role/profession to patients and other staff[8]. Despite their protective role, they are an important source of infection in and out of the hospital[9,10], including nosocomial infection[11,12]. Studies[9,13] carried out in USA and UK reveal that clinical coats can become contaminated with pathogenic and resistant bacteria, and contribute to the spread of nosocomial infections. This includes pathogenic bacteria like *Staphylococcus aureus,* some of which are methicillin-resistant (MRSA)[11,13]. A study conducted by Wiener-Well et al[14] in Israel, showed that 85 of 135 uniforms, and 50% of all samples were positive for pathogenic organisms, 11% of which were multidrug-resistant.

Contamination occurs when healthcare workers access their pockets to pick or drop items in their coats after checking patients[8,15,16]. Maximal contamination occurs in areas of greatest hand contact, such as pockets and cuffs[8,15]. With the increasing prevalence of nosocomial infections and multidrug-resistant bacteria in hospital settings, exploring the role of environmental factors, including clinical coats, in infection spread is crucial[16].

In 2007, the UK Department of Health[17] implemented 'bare below the elbows' policy, a dress code requiring healthcare workers to wear attire with short sleeves, and no white coats, jewelry, ties, watches, or rings when seeing patients at the bedside, to decrease nosocomial infections. This policy was associated with a decrease in nosocomial infections over a 5-year period[17,18]. This prohibition is not applied in most African countries including Uganda.

Multiple studies[19,20] from African countries have been published on the health workers' clothing and potential for contamination. However, most of the studies have limitations such as one sample per coat and a small sample size[19], therefore making it difficult to ascertain the problem with any confidence. Therefore, this study, sought to assess bacterial contamination and the frequently contaminated sites of the clinical coats of medical doctors in a Ugandan hospital setting.

SUBJECTS AND METHODS

Study Design

There were two aspects: (1) a cross-sectional study based on samples from clinical coats and (2) a questionnaire survey of doctors. This study was conducted from 19th April, 2022, to 10th June, 2022.

Study Site

The study was carried out from Mulago National Referral Hospital (MNRH), which is the largest hospital in Uganda and doubles as the teaching hospital for Makerere University. The hospital is located on Mulago Hill, 5 kilometers North of Kampala city. MNRH has both outpatient and inpatient departments offering services in most surgical and medical subspecialties. The hospital has over 1,880 staff with an established bed capacity of 1,790[21]. The study was carried out in surgical, medical, and pediatric wards due to the high patient load in these wards, hence greatest risk of clinical coats contamination.

Study Population

Medical doctors at MNRH (interns, medical officers, senior house officers, and specialists) were included in the study. To be eligible, doctors had to have been wearing a standard white long-sleeved clinical coat. Written informed consent had to be given by the medical doctors before inclusion into the study.

Sample Size

The required sample size was estimated using Kish Leslie's formula[22]:

$$N = \frac{Z^2 \alpha/2\, p(1-p)}{d^2}$$

N – number of participants required, Z – the level of confidence at 95% - 1.96, d – tolerable sampling error (precision) – 5%, p – the estimated proportion of the clinicians' coats with microbial contamination = 45.1% obtained from a study in India among dental surgeons[23]. Estimated sample size = 381 medical doctors.

Scaling down of sample size[24]

This was done because the total number of medical doctors in the selected wards was 132, lower than the estimated sample size.

$$S = \frac{N}{1 + \frac{N}{populationsize}}$$

S – the adjusted sample size, N – the estimated sample size, and population size is the expected number of subjects within the time frame. Population size is the total number of medical doctors on selected wards on duty during the study period = 132. S = 98 Participants.

Sampling Technique

We aimed to enroll every medical doctor who had just finished working duty in the selected wards till the required number was reached.

Data Collection

A self-administered questionnaire was used to collect data on socio-demographics, and habits regarding the use of clinical coats. Questions on habits regarding the use of clinical coats were adopted from previous studies[19,25,26]. The questionnaire was thereafter pretested among 10 medical doctors at Mulago Women's and Neonatal Specialized Hospital (MWNSH). Irregularities were reviewed by a microbiologist from the Department of Microbiology, Makerere University, and corrected till a final version of the questionnaire was produced. Data from pre-testing were not included in the final data set.

Sample Collection and Transportation

The standardized time for sample collection was after a doctor had finished his/her working shift. Upon completing the questionnaire, a trained laboratory member collected three samples from each participant's clinical coat (right and left cuffs and the edges of most used lower front pocket) using commercial sterile cotton swabs (Fisherbrand™, Thermo Fisher Scientific Inc., Waltham, Massachusetts, USA) soaked with sterile normal saline. Briefly, a sterile swab was rubbed up and down or transverse at the left/right edge of pockets, and cuffs of the clinical coat. Sample collection was performed similarly for all the 98 clinical coats. The collected sample from each clinical coat was placed in a labeled test tube containing a 5 ml solution of nutrient broth. The test tubes with samples were then transported in a cooler box at room temperature to the Microbiology laboratory at Makerere University, College of Health Sciences, within 30 minutes after sample collection, as described by Shooriabi et al[27].

Laboratory Procedures

Primary inoculation of each swab was done onto freshly prepared Blood and MacConkey agar (Biolab, Budapest, Hungary) and incubated aerobically overnight at 37°C for probable bacterial growth. The morphology of the bacterial colonies from the plates was studied, and a representative of each morphologically distinct colony was picked and sub-cultured on a new agar plate for further bacterial species identification. The isolates were subjected to gram-staining to differentiate the gram-positive from the gram-negative bacteria. Distinct colony characteristics, including hemolytic zones and additional tests such as catalase, coagulase, DNase, and bile esculin tests, were performed to identify the different gram-positive bacterial species. The gram-negative isolates underwent different biochemical tests for identification. The different biochemical tests include oxidase, indole, urease, citrate, and triple sugar iron, and were performed according to the standardized guidelines of Bergey's manual[28] for determinative bacteriology.

Antimicrobial Susceptibility Testing

The standard disc diffusion method was used to determine the antibiotic-resistant pattern of the isolated bacteria against commonly used antimicrobial agents. The antibiotic selection for the sensitivity tests was based on the 2017 Performance Standards from Clinical Laboratory Standards Institute (CLSI)[29]. A turbid suspension of each isolate equivalent to 0.5 Mc Farland standards was spread on the surface of freshly prepared Mueller-Hinton plates using sterile cotton swabs (Indoplas inc, Quezon city, Philippines) and the commercial antibiotic discs (Oxoid™, Fisher Scientific, Leicestershire, UK) were then placed on the surface of the seeded plates at appropriate spatial arrangement using sterile forceps. The inoculated plates were incubated at 37°C for 24 hours and observed for the clear zone of inhibition. After incubation, the zones of complete inhibition were measured. Isolated gram-negative bacteria were tested for Extended-Spectrum beta-lactamases (ESBL) by using ceftazidime and ceftazidime + Clavulanic acid discs (Thermo scientific™ Oxoid™, Fisher Scientific, Leicestershire, UK). Identification and minimum inhibitory concentration of gram-negative bacteria were confirmed using the automated BD Phoenix instrument (Beckton-Dickinson, USA). The sensitivity patterns were determined by a calibrated ruler and interpreted according to standard guidelines for CLSI criteria[30]. Those that were intermediate were classified as resistant to that particular bacterium. Multidrug-resistant (MDR) bacteria were those that were resistant to at least one agent in three or more antibiotic classes[29].

Quality Control

Samples were collected by highly trained Laboratory technicians while following standard aseptic techniques. Culture media sterility was tested by incubating overnight at 37°C and for performance by inoculating known standard strains (*Escherichia coli* ATCC 25922, *Pseudomonas aeruginosa* ATCC 27853, *Klebsiella pneumoniae* ATCC 700603 and *Staphylococcus aureus* ATCC 25923)[31]. The principal investigator and a highly trained research assistant administered questionnaires. Data was checked for completeness and accuracy at the end of every day of data collection.

Statistical Analysis

Fully completed questionnaires were entered into an electronic data collection tool, Kobotool box (Kobo, Cambridge, Massachusetts, USA)[32], for coding and cleaning. Cleaned data was thereafter analyzed using STATA software version 16 (STATA Corp, College Station, TX, USA). Descriptive data were reported as frequencies and percentages. Continuous variables were described as mean ± standard deviations (SD) and median (interquartile range). Fisher's Exact test was applied to assess associations. A *p*-value lower than 0.05 was considered statistically significant.

Ethical Considerations

The study was approved by the Makerere School of Biomedical Sciences Research and Ethics Committee (SBS-2021-107) and the Uganda National Council of Science and Technology (HS2177ES). Additional permissions were sought from Mulago National Specialized Hospital administration and the ward in-charges. The study was conducted according to the Declaration of Helsinki. All participants provided written informed consent prior to participating in the study

RESULTS

Social Demographic Characteristics

Samples were taken from 98 clinical coats of 98 unique participants were swabbed. Half of the participants (n=49, 50%) were males. Intern doctors were the majority (n=83, 84.69%) of the participants. Participants were recruited from 3 wards, half of them (n=49, 50%) being from the surgery ward, 21.4% (n=21) from medical wards, and 28.6% (n=28) from the Pediatric ward. Average daily working shift for the participants was 11 (1.71) hours with 32 (31.4%) of the participants visiting a cafeteria during their shift. The average age was 28 (3.97) years (Table 1).

The majority of the participants (n=80, 81.63%) had clinical coats made of cotton only. Thirty-nine (39.8%) participants left their clinical coats in the hospital after work. Almost all of them (n=96, 98%) carried out laundry from their homes. The mean number of days of the white coat before it was cleaned were 2.5 (1.32) days. Seventy-one participants (72.5%) perceived their clinical attire to be moderately clean (Table 2).

Prevalence of Bacterial Contamination

Of the 98 participants whose clinical coats were swabbed, 90 (91.8%, 95% CI: 86.4-97.2%) were found to be contaminated with at least one bacteria. Of the 98 unique clinical coats that were sampled, a total of 294 swabs were collected. Out of the 294 swabs, 332 bacteria were isolated. Of the 332 isolated bacteria, 120 (36%) were from the right cuff, 103 (31%) were from the left cuff, and 109 (33%) were from the lower front pocket. Gram-positive bacteria were the most commonly isolated (n=293, 88.3%). Coagulase Negative *Staphylococcus* (CoNS) were the most isolated bacteria (n=214, 64.5%), followed by *Bacillus spp.*, (n=41, 12.4%), *Acinetobacter ssp.*, (n=30, 8.9%), *Micrococcus spp.*, (n=22, 6.6%) and *S. aureus* (n=11, 3.3%). Other bacteria isolated in the study are in Table 3. Nearly half of the isolates (n=160, 48%) were obtained from samples of participants in the surgery ward (Table 3).

Antibiotic Resistance Profile

Gram-positive bacteria

Antimicrobial susceptibility testing was carried out for 14 Gram-positive bacteria. Eleven *S. aureus* were isolated, of which none were methicillin-resistant. All *S. aureus* isolated were sensitive to vancomycin. Two (18.2%) of the *S. aureus* were multidrug resistant. Two multidrug-resistant *Viridans streptococci* were isolated, and both of them were resistant to vancomycin and ceftriaxone. The only isolated *Enterococcus faecium* was multidrug-resistant, being resistant to ampicillin, ciprofloxacin, and erythromycin. It was sensitive to vancomycin. Table 4 shows the resistance profile of selected gram-positive bacteria to selected antibiotics.

Gram-negative bacteria

All the isolated gram-negative bacteria were resistant to at least one selected antibiotic. *Acinetobacter spp.* was the most isolated gram-negative bacteria (n=29, 8.7%). Among the isolated *Acinetobacter* spp., 17 (60%) were resistant to trimethoprim-sulfamethoxazole, and they were least resistant to aminoglycosides

Table 1. Socio-demographic characteristics of study participants.

Demographics	Frequency (n=98)	%
Sex		
Female	49	50.0
Male	49	50.0
Profession cadre		
Intern doctor	83	84.69
Medical officer	03	3.06
Senior house officer (resident doctor)	12	12.24
Current ward		
Surgical wards	49	50
Medical wards	21	21.43
Pediatrics	28	28.57
Movements during shift		
Visits other wards	13	40.2
Cafeteria	32	31.4
Office	7	6.9
**Other	10	9.8

**Others include blood bank, place of residence, Laboratory, Theatre.

Table 2. Handling of the clinical coats and perception on the level of clinical coat's cleanliness.

Characteristics	Frequency N (%)	Surgical wards N (%)	Medical wards N (%)	Pediatrics N (%)	*p*-value (Fishers' Exact)
Fabric material for the clinical coat					
Cotton	80 (81.6)	38 (47.5)	18 (22.5)	24	0.655
Mixture of cotton and polyester	18 (18.4)	11 (61.1)	3 (16.7)	4 (22.2)	
Where do you keep your clinical coat after hospital work?					
Leave it in the hospital	28 (28.6)	12 (42.9)	4 (14.29)	12 (42.9)	0.380
Store in Locker	2 (2)	2 (100)	0	0	
Store in bag	29 (29.6)	16 (55.2)	8 (27.6)	5 (17.2)	
Carry it with hands up to place of residence	39 (39.8)	19 (48.7)	9 (23.1)	11 (28.2)	
Where do you carry out laundry for your clinical coat from?					
Home	96 (98)	49 (51.0)	21 (21.9)	26 (27.1)	0.124
Laundry services at hospital	2 (100)	0	0	2 (100)	
Professional laundry services	0	0	0	0	
Do you exchange clinical attire with colleagues?					
Yes	5 (5.1)	2 (40)	2 (40)	1 (20)	0.600
No	93 (94.9)	47 (50.5)	19 (20.4)	27 (29)	
From your perception, grade the current level of cleanliness of your clinical coat					
Very clean	15 (15.3)	5 (33.3)	4 (26.7)	6 (40)	0.024
Moderately clean	71 (72.5)	33 (46.5)	16 (22.5)	22 (31)	
Dirty	12 (12.2)	11 (91.7)	1 (8.3)	0	

(gentamicin and amikicin). Two *Acinetobacter spp.,* both isolated from samples obtained from clinical coats of participants in the surgery ward, were found to be multidrug resistant.

Four *E. coli* were isolated, of which three (75%) of them were resistant to piperacin. Half of them (n=2, 50%) were resistant to ampicillin, cefoxitin, and ceftazidime. One *E. coli* isolate was found to be an ESBL producer. The three isolated *Klebsiella pneumoniae* were resistant to ampicillin, while one of the three isolates was an ESBL producer. Table 5 shows the resistance profile of gram-negative bacteria to selected antibiotics.

Table 3. Type of Isolated bacteria from clinical coats.

Organisms	Total N=332 (%)	Wards			Site of clinical coat			
		Medical ward N (%)	Pediatric ward N (%)	Surgical ward N (%)	Left Cuff N (%)	Left Pocket N (%)	Right Cuff N (%)	Right Pocket N (%)
Gram-positive bacteria								
Coagulase Negative Staphylococcus	214 (64.5)	27 (12.6)	90 (42.1)	97 (45.3)	71 (33.2)	19 (8.9)	76 (35.5)	48 (22.4)
Bacillus spp.	41 (12.4)	8 (19.5)	14 (34.2)	19 (46.3)	9 (22.0)	4 (9.6)	14 (34.2)	14 (34.2)
Micrococcus spp.	22 (6.6)	15 (68.2)	3 (13.6)	4 (18.2)	7 (31.8)	1 (4.6)	9 (40.9)	5 (22.7)
Staphylococcus aureus	11 (3.3)	0	3 (27.3)	8 (72.7)	3 (27.3)	0	2 (18.2)	6 (54.6)
Viridans streptococcus	2 (0.6)	0	1 (50.0)	1 (50.0)	1 (50.0)	0	0	1 (50.0)
Enterococcus faecium.	1 (0.3)	0	0	1 (100)	0	0	1 (100)	0
Corynebacterium spp.	2 (0.6)							
Gram-negative bacteria								
Acinetobacter spp.	29 (8.7)	4 (13.8)	7 (24.1)	18 (62.1)	7 (24.1)	5 (17.2)	15 (51.7)	2 (7.0)
Pseudomonas spp.	1 (0.3)	0	0	1 (100)	1 (100)	0	0	0
Escherichia coli	4 (1.2)	0	1 (25.0)	3 (75.0)	1 (25.0)	0	2 (50.0)	1 (25.0)
Klebsiella Pneumoniae	3 (0.9)	0	1 (33.3)	2 (66.7)	1 (33.3)	0	1 (33.3)	1 (33.3)
Citrobacter spp.	1 (0.3)	0	0	1 (100)	0	1 (100)	0	0
Enterobacter spp.	1 (0.3)	0	0	1 (100)	1 (100)	0	0	0

Table 4. Antibiotic resistance profile for gram positive bacteria to selected bacteria.

Bacterial isolates	Antibiotics (% resistant)										
	ERY	TET	CLI	LZD	VAN	CHL	GEN	AMK	CIP	G PEN	CRO
Staphylococcus aureus (n=11)	63.6	18.2	27.3	0	0	0	0	9.1	18.2	45.5	-
Viridans streptococci (n=2)	50	0	50	0	100	50	0	0	0	-	100
Enterococcus Spp. (n=1)	100	0	-	100	0	0	0	-	100	0	

ERY- Erythromycin, TET – Tetracycline, CLI – Clindamycin, LZD – Linezolid, VAN – Vancomycin, CHL – Chlorampenicol, GEN – Gentamycin, AMK – Amikacin, CIP – Ciprofloxacin, G PEN – Penicillin G, CRO – Ceftriaxone.

Table 5. Antibiotic resistance profile for gram negative bacteria to selected antibiotics.

Bacterial isolates	Antibiotics (% Resistant)														
	AMP	PIP	TZP	AMC	CAZ	FEP	IPM	ATM	CRO	FOX	CXM	CHL	GEN	AMK	CIP	SXT
Acinetobacter spp. (n=29)	-	60	6.7	-	46.7	13.3	10	-	60	16.7	-	3.3	10	10	20	36.7
Enterobacter spp (n=1)	100	100	0	100	100	-	0	100	100	100	100	100	100	0	100	100
Escherichia coli (n=4)	50	50	0	0	50	25	0	0	25	50	25	0	75	0	0	25
Citrobacter spp. (n=1)	1	100	0	100	0	0	100	-	0	-	100	0	100	-	0	0
Klebsiella Pneumoniae (n=3)	100	33	0	33.3	66.7	0	0	33.3	33.3	0	33.3	0	0	-	33.3	33.3
Pseudomonas spp. (n=1)	-	100	0	100	100	0	0	0	-	-	-	-	0	0	100	100

AMP – Ampicillin, PIP – Piperacillin, TZP – Piperacillin + Tazobactam, AMC – Amoxicillin Clavulanic acid, CAZ – Ceftazidime, FEP – Cefepime, IPM – Imipenem, ATM – Aztreonem, CRO – Ceftriaxone, FOX – Cefoxitin, CXM – Cefuroxime, CHL – Chloramphenicol, GEN – Gentamycin, AMK – Amikacin, CIP – Ciprofloxacin, SXT – Trimethoprim sulfamethoxazole.

MDR

The overall prevalence of the MDR bacteria was 13 (2.8%) (95% CI: 2.22-2.62%). The MDR bacteria included *Viridans streptococci* (n=2), *S. aureus* (n=2), K. *pneumonae* (n=1), *Enterobacter faecium* (n=1), *E. coli* (n=1), and *Acinetobacter spp.* (n=6). Of the ESBL-producing bacteria, 2 (1 *E. coli* and 1 *k. pneumonia*) were MDR.

DISCUSSION

This current study was carried out to determine the prevalence of bacterial contamination of clinical coats of medical doctors. We found the prevalence of bacterial contamination of clinical coats of medical doctors was 91.8%, similar to another study[33] carried out in Nigeria where contamination was at 91.3%. Our prevalence of bacterial contamination of clinical coats was higher compared to provenances reported in Tanzania (73.3%)[20] and in Columbia (75%)[20,34]. The differences in adherence to Infection Prevention and Control (IPC) measures in the different hospital settings could explain the discrepancy in the report prevalence. This finding could as well be attributed to the fact that most of the participants in our study were intern doctors with minimal experience in IPC measures.

Most of the isolated bacteria were gram-positive, the predominant being CoNS. This result is different from other studies, which reveal *S. aureus* as the most dominant pathogen isolated from clinical attire of health workers[12,18,35,36]. This difference can partly be explained by the different geographical locations and hospital settings in which our study was carried out. Gram-negative bacteria were isolated however, these were significantly lower in number as compared to the gram-positive bacteria. This is similar to findings from other studies in Malaysia, and Iran conducted by Muhadi et al[36] and Moravvej et al[37], respectively. Gram-positive bacteria predominantly CoNS have similarly been isolated from studies in India by Naik et al[15], and Kumar et al[38]. CoNS are normal flora on hands and human skin. Thus, it is not surprising that they are the most isolated bacteria. CoNS were previously considered harmless; however, due to advances in medical technology like the use of in-dwelling medical devices, CoNS have emerged as potential pathogens

in a hospital setting[37]. In our study, eleven *S. aureus* were isolated, of which none was *MRSA*. This finding is contrary to studies done by Kumar et al[38], in India, and Uneke et al[33] in Nigeria where they isolated ten MRSA. This could be due to the fact that our study was conducted in a tertiary care level which is aware of antibiotic resistance with antibiotic usage policies.

In our study, other potential pathogens isolated included commonly implicated agents in nosocomial infections, such as *E. coli, K. pneumonae, Pseudomonas spp.,* and *Enterobacter faecium*. This is comparable to other findings from previous studies[18,38,39]. All these isolated potential pathogens have been found in hospital environments and have been implicated as agents for nosocomial infections[39]. All the isolated gram-negative bacteria were resistant to at least one antibiotic, with nearly half of them being multidrug-resistant. Carbapenems are the antibiotics of choice for the treatment of infections caused by gram-negative bacteria[40]. In our current study, three *Acinetobacter spp.* (10%) were resistant to the carbapenems. From our study, the most resistant isolated bacterium was *Enterobacter faecium*. The high level of antibiotic resistance shown by the isolates is of significant public health importance because they are capable of causing severe nosocomiasis in a hospital environment[33].

We found that 2.1% of bacterial isolates were multidrug resistant. This finding is similar to that from a study conducted in a health facility in Tanzania by Qaday et al[20], who isolated four contaminants that were multidrug resistant. However, our finding was contrary to studies that were conducted in Germany and Austria by Lenski et al[43], and Berktold et al[44], respectively, which found no multidrug resistant bacteria in their contaminants. The most likely cause for this is the different hospital geographical environment in which our study was carried out. Furthermore, in the study carried out in Austria by Berktold et al[44], patients with multidrug-resistant infections were treated using isolation precautions like use of protective gowns. From their study, samples were obtained from clinical coats of doctors who had not come in contact with patients harboring multidrug-resistant pathogens, which was different from our study, where we sampled every doctor who had just finished their duty on the ward.

From our study, the cuffs of the clinical coats were the most contaminated sites. This finding is in accordance with that of a previous study[10], which found that bacteria are most likely to be isolated from cuffs of clinical coats since these are sites of frequent contact. As a result, there is a need to encourage scrupulous hand washing among medical doctors before and after attending to patients.

In our study, participants reported that they regularly moved out of their wards with clinical coats during their shifts, with the cafeteria and other wards as the most visited places. This finding is similar to results from multiple studies[20,25,41]. These movements could be a potential source of cross-contamination between the contaminated clinical coats and the external environment, such as the cafeteria.

Nearly all the clinical coats in this study were home-laundered. This is similar to a study conducted in the United Kingdom (UK) by Perry et al[35]. Numerous infection outbreaks have been reported[42,43] due to the laundering of hospital linen where guidelines have not been followed. The outbreaks led to the setting up of the guidelines entailing how hospital linen can be disinfected[44]. It is still unclear how these guidelines can be followed with home-laundering, given that recommendations like temperature of 65°C are hardly available in healthcare workers' homes. A study done by Nordstrom et al[42] in the USA, revealed a higher bacterial contamination on home-laundered scrubs as compared to hospital-laundered scrubs. Therefore, more guidance is needed so that home laundering can be performed safely.

All the participants had clinical coats made of cotton or a blend of both cotton and polyester. A study done by Chacko et al[43], found that bacteria can survive on clinical attire for 10-98 days, depending on the fabric. Polyester alone had the shortest survival time in comparison to cotton or a blend of both cotton and polyester. Therefore, the bacterial contamination found on the clinical coats of our participants might have been acquired prior to the day when a sample was taken off from them since their clinical coats were worn on average for 2.5 days without washing. This finding reveals the need for frequent laundering of clinical coats, and, if possible, wearing newly laundered clinical coats at the start of every working shift.

We found that clinical coats of medical doctors working in the surgical ward were the most contaminated, contrary to the study conducted in Nepal by Mishra et al[45], which revealed healthcare workers in the surgical ward as the least contaminated. This difference could be due to the high patient load in the surgery ward as compared to the other wards.

Medical doctors from our study had worn clinical coats for 2.5 days on average. A study conducted by Wong et al[12] revealed that the rate of bacterial contamination on white coats did not vary with time in use of the coat. Several studies reveal a 'plateau effect' where contamination does not change significantly regardless of the number of days the white coat has been worn[4,41]. For the study of Wong et al[12], the plateau effect was reached within one week of use of the clinical coats.

Limitations

We conveniently selected medical doctors who had finished their working duties in their respective wards, which could have created a selection bias. Therefore, findings may not be generalizable to all doctors across the hospital. Our study was carried out at a point in time; hence, these results may not represent the year-round pathogen contamination distribution. Self-reports on clinical coat-handling habits could have created an information bias due to the desire for social acceptability by medical doctors. Further research should be car-

ried out to know more about the clonal spread of the organisms within the hospital using Pulsed-Field gel electrophoresis (PFGE).

CONCLUSIONS

This study revealed a high degree of bacterial contamination of medical doctors' white coats. Pathogens on the WHO global priority list, in addition to multidrug-resistant pathogens, were isolated. There was high contamination of potential pathogens on the cuffs of the white coats. This may reflect a gap in carrying out adequate infection prevention and control measures, thus calling for regular hand washing by the medical doctors to minimize the degree of contamination and potential transmission of these organisms to patients.

Recommendations

Regular IPC training of medical doctors should be organized to ensure that all medical doctors are aware about hospital IPC guidelines such as hand washing.

Efforts to discourage medical doctors from moving with clinical coats in places outside the hospital environment, like cafeterias and homes of residence, should be stressed in order to avoid transmission of the in-hospital bacteria on clinical coats to the community.

Given that most medical doctors do home laundering, written guidelines on home laundry, including the minimum temperature to use while laundering, should be given to them.

Conflicts of Interest:
The authors declare no conflict of interest.

Data Availability:
All data generated and analyzed during this study are included in this article. De-identified data can be requested from the corresponding author.

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Informed Consent:
Written informed consent was given by the medical doctors before inclusion into the study.

Ethics Approval:
The study was approved by the Makerere School of Biomedical Sciences Research and Ethics Committee (SBS-2021-107) and the Uganda National Council of Science and Technology (HS2177ES). Additional permissions were sought from Mulago National Specialized Hospital administration and the ward in-charges. The study was conducted according to the Declaration of Helsinki.

Authors' Contributions:
Conceptualization, Nelson Twinamasiko and Joseph Byamugisha; Data curation, Nelson Twinamasiko and Joseph Byamugisha; Formal analysis, Nelson Twinamasiko, Andrew Semulimi, Ronald Kasoma, John Mukisa, Josephine Tumuhamye, Charles Batte, Margaret Lubwama and Cecily Banura; Funding acquisition, Nelson Twinamasiko, Joseph Byamugisha, Roger Harrison and Cecily Banura; Investigation, Andrew Semulimi; Methodology, Nelson Twinamasiko, Joseph Byamugisha, Ronald Kasoma, Charles Batte, Margaret Lubwama, Roger Harrison and Cecily Banura; Project administration, Nelson Twinamasiko; Resources, Ronald Kasoma; Supervision, John Mukisa, Charles Batte, Margaret Lubwama, Roger Harrison and Cecily Banura; Validation, Nelson Twinamasiko, Andrew Semulimi, Josephine Tumuhamye, Margaret Lubwama and Roger Harrison; Visualization, John Mukisa; Writing – original draft, Nelson Twinamasiko and Joseph Byamugisha; Writing – review & editing, Nelson Twinamasiko, Andrew Semulimi, Ronald Kasoma, John Mukisa, Josephine Tumuhamye, Charles Batte, Margaret Lubwama, Roger Harrison and Cecily Banura.

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