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Short Communication

Contamination of Clinical White Coats with Potential Pathogens and their Antibiotic Resistant Phenotypes Among a Group of Sri Lankan Medical Students

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Abstract

Background: Clinical white coats worn by medical students can be contaminated at hospitals and act as a potential reservoir for pathogens, including antibiotic-resistant bacteria. This study aimed to identify the contamination rates of clinical white coats worn by medical students with selected potential pathogens and their antibiotic resistant phenotypes. **Methods:** A cross-sectional study was conducted among 151 fourth-year medical students of the Faculty of Medicine of University of Peradeniya, Sri Lanka in September 2020. The participants belonged to two batches undergoing clinical training at two settings. Swabs from pockets and sleeves of the clinical white coats were taken. Potential pathogens and their resistant phenotypes were identified with routine tests. **Results:** Fifty-three participants (35.1%) had coats contaminated with *Staphylococcus aureus* (*S. aureus*) and 15 (9.9%) had coats contaminated with Methicillin-Resistant *Staphylococcus aureus* (MRSA). One enterobacterales (0.7%) was an AmpC producer. Enterococcus species were isolated from 19 (12.6%) coats and 2 participants (1.3%) had coats contaminated with Vancomycin Resistant Enterococci (VRE). Molecular testing on the MRSA isolates identified that 5 (20%) of the MRSA isolates were *PVL* positive, while all were *mecA* positive. Sex, type of clinical appointment, and frequency of washing white coats were not associated with contamination. The "batch" was significantly associated with contamination with *S. aureus* and Enterococcus species. **Conclusions:** We found that clinical white coats worn by medical students recruited for the study were contaminated with *S. aureus*, MRSA, and Enterococcus species. There was a notably high rate of contamination with *S. aureus*. All MRSA isolates were *mecA* positive, while the rate of *PVL* positivity was low.

Key Words: Drug Resistance; Microbial; Infection Control; Microbiology; Students; Medical (Source: MeSH-NLM).

Introduction

Clinical white coats are worn by healthcare workers, including clinicians and medical students in many countries. While most developed countries have moved away from clinical white coats to scrubs, white coats remain a part of the hospital attire in many developing countries, such as Sri Lanka.

Clinical white coats, however, are considered to be possible vehicles for transmission of pathogens.[1] Microorganisms may live on the fabric of clinical coats for several days, even up to three months.[2] Therefore, these can act as potential reservoirs for the transmission of antibiotic resistant bacteria. Medical students spend long hours in different clinical settings as per their training requirements, such as wards, clinics, and in-hospital teaching areas, in the same attire. Therefore, the contamination of their white coats can contribute to horizontal transmission of potential pathogens from patient to patient as well as between different locations within a single healthcare institute. This could also lead to an increase in the rates of healthcare-associated infections, including those caused by antibiotic resistant bacteria. Furthermore, this may contribute to the spread of antibiotic resistant bacteria to the community. Therefore, identifying if clinical white coats worn by medical students are contaminated with potential pathogens and their antibiotic resistant phenotypes would provide evidence to convince university and hospital policy makers to implement preventive measures, such as implementing standard operating procedures to clean hospital-wear, and establishing a mechanism to provide hospital laundered outerwear to be worn during clinical training.

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This study aimed to describe the patterns of contamination of clinical white coats among medical students in a Sri Lankan medical school, with selected potential pathogens and their antibiotic resistant phenotypes. This included *Staphylococcus aureus,* Methicillin-resistant *Staphylococcus aureus* (MRSA), *Enterobacterales* species, Extended-spectrum Beta lactamase (ESBL)-producing *Enterobacterales,* AmpC producing *Enterobacterales*, *Enterococcus* species, and Vancomycin-resistant *Enterococcus* (VRE) species.

Methods

This cross-sectional study was conducted among fourth-year medical students of the Faculty of Medicine of University of Peradeniya, Sri Lanka in September 2020. The study site had two fourth-year batches (Batch A and B). Clinical training for the two batches were conducted predominantly in two separate institutes at the time of the study: the Teaching Hospital in Peradeniya, Sri Lanka and the National Hospital in Kandy, Sri Lanka. All except those who were wearing short or three-quarter-sleeved white coats were eligible to participate in the study. A self-administered data collection sheet was used to gather demographic data, current clinical appointment, predominant method of wearing the sleeve of the coat (rolled up or not), frequency of washing the coat, the date of when the coat was last washed, and the wearer's perception of the cleanliness of the white-coat. A pilot-test was done on ten medical students of the third-year batch. Ethics approval was obtained from the Ethics Review Committee of the Faculty of Medicine, University of Peradeniya, Sri Lanka (2020/EC/SP/01). Informed, written consent was obtained from all participants.

Two sterile swabs moistened with sterile 0.9% saline were used to obtain samples from both the pockets and the cuffs of the sleeves of each clinical white coat, as these are the sites that, respectively, are frequently handled by the wearers and come into contact with patients. Swabs were collected by the investigators according to a fixed protocol, with measures to prevent cross-contamination. The protocol called for the swab to be, inserted into individual plastic sheaths, transported to the lab immediately, and inoculated in 10 ml of Brain Hearn Infusion (BHI) broth (Oxoid, UK). BHI broth was incubated overnight at 37°C. The next day, 10 µl of each broth was plated on three different agars, a Mannitol Salt agar (MSA) (Oxoid, UK) plate, a MacConkey agar (Oxoid, UK) plate supplemented with Cefotaxime at 1 µg/ml (HiMedia, India) concentration to screen for potential *Enterobacterales,* and a Chromogenic agar plate (BioMaxima, Poland) to identify potential *Enterobacterales* and *Enterococcus* species. All plates were prepared according to manufacturer's instructions. Potential isolates were selected and identified using routine biochemical testing.[3]

S. aureus isolates were tested for sensitivity to cefoxitin in order to identify MRSA and Methicillin sensitive *Staphylococcus aureus* (MSSA) isolates. Sensitivity to cefotaxime and ceftazidime were tested in the *Enterobacterales* species to screen for possible ESBL producers. The *Enterobacterales* species that fulfilled the criteria for potential ESBL producers were subjected to combined disc testing and were additionally tested for AmpC production using the disc diffusion method (Mast, UK). Sensitivity to other relevant antibiotics were tested according to the CLSI guidelines.[4-6] Enterococci was tested for sensitivity to ampicillin using the disc diffusion method, and minimum inhibitory concentration (MIC) for vancomycin (Sigma-Aldrich, Singapore) was tested using macro-broth dilution method.[7]

DNA was extracted from the 20 MRSA isolates by boil lysis and presence of PVL and mecA genes were assessed by previously established conventional PCR.[8,9]

Student placements were categorized into two groups for the analysis. Medicine, pediatrics, and psychiatry appointments were grouped together as medical placements, while surgery, gynecology, obstetrics, and other surgical sub-specialties were grouped together as surgical placements. Wearers' perception of the cleanliness of the coat was thematically analyzed. The two themes that emerged were clean and contaminated, which were then used as a binary variable in further analysis.

In data analysis, percentages were calculated for contamination of white coats in each site with the selected potential pathogens and their antibiotic resistant phenotypes. A Chi-square test or Fisher's exact test were used to test for associations, while the Mann-Whitney U test was used to compare the differences in continuous variable. A p-value of less than 0.05 was considered as statistically significant. All analysis was done on SPSS (IBM) version 21.

Results

A total of 151 participants were recruited. Of these, 72 (47.7%) were from fourth-year batch A and 79 (53.3%) were from fourth-year batch B.

The numbers of female and male students were 78 (51.7%) and 73 (48.3%), respectively. The mean and median number of days from the last wash to sample collection was 6.2 (SD 5.8) and 4.0 (IQR 3 – 7) days, respectively. Other parameters of the two batches are provided in *Table 1*.

Among the 151 participants, *S. aureus* was isolated from one or both swabs in 53 (35.1%) participants. The coats of 15 of the 151 (9.9 %) participants were contaminated with Methicillin-resistant *Staphylococcus aureus* (MRSA) isolates. Twelve (7.9%) of the coats were contaminated with bacteria of the order *Enterobacterales*. None of the isolates were found to be ESBL producers; however, one (0.7%) coat was contaminated with an AmpC producing *Enterobacterales* species. Nineteen (12.6%) participants had coats that were contaminated with the Enterococcus species and two (1.3%) participants had coats contaminated with VRE (*Table 2*). The differences in contamination rates between pockets and sleeves were not statistically significant.

At least one potential pathogen of interest was found to contaminate 74 (49.0%) of the coats, while 18 coats (11.9%) were contaminated with at least one of the resistant phenotypes of interest (MRSA, VRE, or AmpC producers). Ten (6.6%) coats were contaminated with two types of potential pathogens, whereas 64 (42.4%) were contaminated with only one type.

Contamination rates with *S. aureus* and *Enterococcus* species was significantly different between the two fourth-year batches. Other parameters analyzed in relation to contamination with the selected bacteria did not differ significantly and are provided in *Table 3*.

Table 1. Description of the Study Population.

Variables	All participants n (%)	Batch A	Batch B	Difference
Sex				
Male	73 (48.3 %)	40 (55.6%)	33 (41.8%)	0.10
Female	78 (51.7 %)	32 (44.4%)	46 (58.2%)	
Appointment[1]				
Medical	86 (57 %)	47 (65.3%)	39 (49.4%)	0.07
Surgical	65 (43 %)	25 (34.7%)	40 (50.6%)	
Frequency of washing[2]				
< 1 once a week	118 (78.1 %)	62 (86.1%)	56 (70.9%)	0.03*
> Once a week	33 (21.8 %)	10 (13.9%)	23 (29.1%)	
Perception[2]				
Clean	30 (24 %)	12 (18.5%)	18 (30.0%)	0.147
Contaminated	95 (76 %)	53 (81.5%)	42 (70.0%)	
Time since washing				
Median (IQR)	4.0 (3 – 7)	3 (3 – 5)	4 (3- 10)	0.003^

Legend: 1: Medical includes medicine, pediatrics and psychiatry appointments. Surgery includes surgery, gynecology, obstetrics, and other surgical sub-specialty appointments. 2: Only 125 (83.8%) participants presented their perception on cleanliness of the coats. * Chi-square test, ^ Mann-Whitney U test.

Association between the pattern of wearing the sleeve (rolled up vs left long) and contamination with resistant bacteria was assessed. There was no significant association between rolling up the sleeves and colonization with *S. aureus* (18.8% vs 34.8%), MRSA (7.0% vs 8.7%), or *Enterococcus* species (6.3% vs 8.7%) ($p>0.05$, Fisher's Exact test).

Among the 53 white coats contaminated with *S. aureus*, 19 were contaminated only on the sleeves of the coats, 21 only on the pockets, and 13 were contaminated on both sites; leading to a total of 66 *Staphylococcus aureus* isolates. Among the *S. aureus* isolates, 20 (30.30%) were MRSA, while 46 (69.67%) were Methicillin-sensitive *S. aureus* (MSSA). The susceptibility rates for different antibiotics were higher among the MSSA isolates than the MRSA isolates, except for ciprofloxacin. The susceptibility rates for the different antibiotics among MSSA and MRSA isolates were; gentamycin (95.7% vs 85%), ciprofloxacin (50% vs 70%), clindamycin (91.3% vs 70.0%), erythromycin (58.7% vs 45%), and tetracycline (95.7% vs 90%) respectively.

Molecular testing on the MRSA isolates identified that five of the 20 MRSA isolates were PVL positive, while all were *mecA* positive. Of the 20 *Enterococcus* isolates, four were ampicillin resistant and two isolates were identified as VRE.

Table 2. Summary of Colonization Rates.

Organism	Sleeves only n (%)	Pockets only n (%)	Both n (%)	Either or both n(%)
S. aureus	19 (12.6%)	21 (13.9%)	13 (8.6%)	53 (35.1%)
MRSA	6 (4.0%)	4 (2.6%)	5 (3.3%)	15 (9.9%)
Enterobacterales species	5 (3.3%)	5 (3.3%)	2 (1.3%)	12 (7.9%)
ESBL producers	0	0	0	0
AmpC producers	0	1 (0.7%)	0	1 (0.7%)
Enterococcus species	9 (6.0%)	9 (6.0%)	1 (0.7%)	19 (12.6%)
VRE	0	2 (1.3%)	0	2 (1.3%)

Discussion

This study aimed to describe the pattern of contamination of clinical white coats with selected antibiotic-resistant bacteria. *S. aureus* was isolated from swabs of 53 participants (35.1%). Out of these, 15 were contaminated with MRSA (9.9%). All of the MRSA isolates were positive for *mecA* gene while only 5 were positive for *PVL* gene.

A number of studies has previously assessed the rates of *S. aureus* contamination of clinical white coats. Despite varying in frequency of contamination, *S. aureus* has been identified as the commonest isolate in many studies.[1,10,11,12] Similarly, MRSA isolation rates from white coats has ranged from 3.5%[13] to up to 79% (during outbreaks of infections in units).[14] These differences in contamination rates could be due to the differences in institutional environments, infection prevention, and control measures, as well as wearer habits such as hand hygiene.

While contamination rates of clinical white coats are not available for Sri Lanka, Munasinghe et al. has reported a colonization rate of 22.0% and 4.3% for *S. aureus* and MRSA respectively, from nasal swabs obtained from a group of university students of the same study site.[9] In the same study, 21.4% of the identified MRSA isolated were found to be PVL positive. We did not assess to see if the wearers of the coats were colonized with any of the pathogens tested for. However, using the *PVL* positivity rates we can hypothesize that most of the isolates obtained from the white coats are of hospital origin, as the *PVL* positivity rates were lower in the current study when compared to the colonization study. This is because *PVL*, a virulence factor in MRSA, is more commonly found in isolates of community origin. All isolates were found to contain *mecA*. *MecA* gene codes for an alteration in the penicillin binding protein, leading to resistance in beta-lactam drugs.[15,16] These findings indicate that the white coats are likely to have got contaminated in the health-care setting, rather than from the community.

Nineteen (12.6%) participants of the present study had coats that were contaminated with *Enterococcus* species and two of them (1.3%) were vancomycin-resistant. A study by C. Kannangara et al. has shown that Vancomycin-resistant Enterococci (VRE) had a rectal colonization rate of 5% among 218 patients in an intensive care unit of the National Hospital of Colombo, Sri Lanka.[17] It is undeniable that VRE isolates are circulating in healthcare settings in Sri Lanka and that contaminated cloths may act as a vehicle of transmission. Given the possibility of horizontal gene transfer for vancomycin resistance, this is a concerning situation.

Twelve (7.9%) of the participants' coats were contaminated with Enterobacterales and none of the isolates were found to be ESBL producers. However, one (0.7%) coat was contaminated with an AmpC-producing Enterobacterales species. A study done at Kilimanjaro Christian Medical Center in Tanzania found that 3 out of 180 coats were contaminated with *E. coli*.[12] This, and other studies indicate that the contamination of clinical white coats with Gram negative isolates is relatively less common than contamination with Gram positive isolates. While our study did not identify any contamination by ESBL producers, they are common in Sri Lankan hospitals and the community, both as causative agents for infections and as colonizers.[9,18] However, clinical white coats are often kept dry and Gram negatives do not usually thrive in such conditions, unlike *S. aureus* or *Enterococcus* species.

In this study, the rate of contamination of clinical white coats with *S. aureus*, MRSA, *Enterobacterales*, and *Enterococcus* was assessed in relation to several variables such as sex, batch, current clinical placement, frequency of washing the coat, and one's perception of cleanliness of his/her clinical white coats. Out of these variables, only the batch was found to have a statistically significant association with the rate of contamination. Batch A had a significantly higher contamination rate with *Enterococcus* species, while batch B had a higher rate of contamination with *S. aureus*. At the time of the study, the two batches had their clinical training at two hospitals, where the predominant environmental contaminants could have been different, which may explain the difference in the contamination rates. Furthermore, the frequency of washing coats significantly differed between the two batches; however, the impact of this on the association with different potential pathogens remains to be further explored. It is of interest to note that the frequency of washing and the duration since the last wash was not significantly associated with contamination rates.

Table 3. Association of Variables Studied with Contamination of Coats.

Variable	Contamination with *Staphylococcus aureus*			Contamination with MRSA			Contamination with *Enterococcus* spp		
	Contamination absent	Contamination present	p-value	Contamination absent	Contamination present	p-value	Contamination absent	Contamination present	p-value
Sex									
Male (n=73)	52 (71.2 %)	21 (28.8 %)	0.11	64 (87.7 %)	9 (12.3 %)	0.34	62 (84.9%)	11 (15.1%)	0.37
Female (n=78)	46 (59.0 %)	32 (41.0 %)		72 (92.3 %)	6 (7.7%)		70 (89.7%)	8 (10.3%)	
Batch									
4th year batch A (n=72)	53 (73.6 %)	19 (26.4 %)	**0.03***	66 (91.7 %)	6 (8.3%)	0.53	56 (77.8%)	16 (22.2%)	**0.001***
4th year batch B (n=79)	45 (57.0 %)	34 (43.0 %)		70 (88.6 %)	9 (11.4%)		76 (96.2%)	3 (3.8%)	
Appointment									
Medical (n=86)	58 (67.4%)	28 (32.6%)	0.45	78 (90.7%)	8 (9.3%)	0.77	76 (88.4%)	10 (11.6%)	0.68
Surgical (n=65)	40 (61.5 %)	25 (38.5 %)		58 (89.2 %)	7 (10.8 %)		56 (86.2%)	9 (13.8%)	
Frequency of washing									
<=1 once a week (n=118)	78 (66.1 %)	40 (33.9 %)	0.56	107 (90.7 %)	11 (9.3 %)	0.74	102 (86.4%)	16 (13.6%)	0.77
> Once a week (n=33)	20 (60.6 %)	13 (39.4 %)		29 (87.9 %)	4 (12.1 %)		30 (90.9%)	3 (9.1%)	
Perception									
Clean (n=30)	20 (66.7 %)	10 (33.3%)	0.86	26 (86.7 %)	4 (13.3%)	0.29	29 (96.7%)	1 (3.3%)	0.07
Contaminated (n=95)	65 (68.4 %)	30 (31.6%)		88 (92.6 %)	7 (7.4%)		78 (82.1%)	17 (17.9%)	
Time since coats were cleaned						0.07			
Mean (SD)	6.5 (6.6)	5.6 (3.9)	0.62	6.1 (5.9)	7.4 (4.5)		6.2 (6.0)	6.1 (4.4)	0.94
Median (IQR)	3.5 (3 - 8)	4.0 (3 - 7)		4.0 (3 - 6)	5.0 (3 - 11)		4.0 (3 - 7)	3.0 (3 - 8.5)	

Legend: * Chi-square test

One major disadvantage of this study is that we did not determine the contamination of *Clostridium difficile*. This was not possible, as the study site lacked anaerobic culture facilities. Also, the selection of the isolates depended on the available funding as it prevented us from focusing on all ESKAPE pathogens.

In conclusion, we identified a considerable high rate of contamination with potential pathogens, particularly Gram-positive isolates. This is a reason for concern. Furthermore, the association of *S. aureus* and *Enterococcus* species with the two batches, where the main difference was the hospital they were trained at, indicates that hospital environment may play a role in this.

The current study highlights the importance of establishing a protocol to ensure that the attire worn in healthcare settings are cleaned appropriately. While our study population is from a single university, in the current times of global travel, these findings are of global concern. With the escalation of the COVID-19 pandemic, Sri Lankan universities transitioned from white coats to scrubs as the attire for medical students. We hope that this will have had a positive impact on the possible contamination with potential pathogens, as scrubs directly contact the wearer's skin, and therefore, unlike white coats, are likely to be washed more frequently. Further, providing standard operating procedures for cleaning hospital wear and implementing mechanisms to provide faculty or hospital laundered cloths to be worn in the clinical setting along with adequate facilities for changing rooms could be considered.

Summary – Accelerating Translation

Contamination of white coats with germs

Clinical white coats had been switched for other alternatives in many countries, but in some countries like Sri Lanka it continued to be a part of the attire of medical students till the emergence of COVID-19 pandemic. In this study, we took samples from 151 white coats worn by medical students of the Faculty of Medicine, University of Peradeniya, Sri Lanka and tested to see if any germs causing infections are found. Regular laboratory methods were used for testing and samples were obtained from the cuffs and pockets of the white coats. We identified three types of infection-causing germs on the coats. We also found two types of germs that are resistant to antibiotics, namely Methicillin Resistant *Staphylococcus aureus* (MRSA) on 15 (9.9%) coats and Vancomycin Resistant Enterococci (VRE) on two (1.3%) coats. We emphasize the importance of having strict guidelines to ensure that those who wear white coats, including medical students, clean them more frequently so that their role as potential reservoirs of germs may be lessened.

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Author Contributions

Study conceptualization: HD, OD, AD, PD, SD, KD, DeDeS, SDS, NDeS, DiDeSi, DiDeZ, VL, Proposal writing and obtaining ethics: HD, OD, AD, PD, SD, KD, DeDeS, SDS, NDeS, DiDeSi, DiDeZ, VL, Sample collection: HD, OD, AD, PD, SD, KD, DeDeS, SDS, NDeS, DiDeSi, DiDeZ, Initial laboratory work: HD, OD, AD, PD, SD, KD, DeDeS, SDS, NDeS, DiDeSi, DiDeZ, RD, AE, GV, VL, Confirmatory laboratory work: RD, AE, GV, VL, Data-anaylsis, HD, OD, AD, PD, SD, KD, DeDeS, SDS, NDeS, DiDeSi, DiDeZ, VL, Drafting the paper: HD, GV, VL, Refining the paper: VL, Final approval of the paper: HD, OD, AD, PD, SD, KD, DeDeS, SDS, NDeS, DiDeSi, DiDeZ, RD, AE, GV, VL.

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