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Microbial contamination of the anatomical models used in the museum and dissection hall of the Department of Anatomy

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Abstract

Introduction: Anatomical models used by medical students as learning material are seldom cleaned and can act as a reservoir/vehicle of microbial transmission to the students handling them. Moreover, while handling, the microorganisms from the hands of the medical students can also get transferred onto the surface of these anatomical models.

Aim: To investigate the rate of microbial contamination of the anatomical models and the transmission of these microbial isolates among the medical students handling them.

Materials and methods: A total of 40 embryology models from the Anatomy museum and dissection hall, and 82 first year undergraduate medical students (volunteer) were included in the study. Swab samples were collected from the models as well as students (prior to and after 90 minutes contact with the models), and using standard procedures were examined in the Microbiology laboratory.

Result: All the samples collected from models showed microbial growth. The isolated organisms include Coagulase negative staphylococci (CONS) *Escherichia coli*, *Staphylococcus aureus*, *Candida spp.*, *Bacillus spp*., *Enterococcus spp*. and *Pseudomonas aeruginosa*. Students samples, collected before contact with models showed growth of CONS, *Bacillus spp*., *S.aureus* and *E.coli*, whereas the samples collected after the contact with models showed growth of CONS, *Bacillus spp*., *S.aureus*, *Candida spp.*, *Escherichia coli*, *Enterococcus spp*., *P.aeruginosa* and *Acinetobacter spp*.

Conclusion: Anatomical models get contaminated through hands and vice versa and then from hands to other exposed areas of the body. Proper hand hygiene practices by the students before and after working on the models and regular/periodic disinfection of the anatomical models is imperative to reduce the microbial transmission.

Keywords: *Candida albicans*, Coliforms, Disinfection, Embryology, MRSA, *Pseudomonas aeruginosa*, *Staphylococcus aureus*

INTRODUCTION

Anatomical models are mostly used by first year undergraduate medical students as learning material in anatomy dissection hall and museum. Models being used as learning material in the Anatomy department of the Maharishi Markandeshwar Institute of Medical Sciences and Research (MMIMSR), Mullana, Haryana were bought long back, in year 2004 and are being regularly used since then. Except for dusting with a dry cloth, they have never been properly cleaned or disinfected. While their visit to laboratory, medical students examine these models not only by holding them in their hands but also by passing the same among themselves. This not only exposes these models to microbial contamination (bacterial, viral, fungal and parasitic) from the hands of the medical students but these models can even act as a reservoir and/or vehicle for transmission of various pathogens/microorganisms among the students.

Previous studies by various researchers have reported the microbial contamination of computer keyboards, [1] household toys, [2] door handles, [3, 4] stethoscopes [5] and mobile phones. [6] A study by Pal *et al*. from Uttarakhand have reported potential role of mobile phones in transmission of infectious agents in and outside the hospital. [6] With the above background the current study was aimed to investigate the rate of bacterial contamination of the anatomical models and the transmission of these bacterial isolates among the medical students handling them.

MATERIALS AND METHODS

Study site and sample group: The study was conducted in Department of Anatomy and Department of Microbiology of MMIMSR, Mullana, Haryana for a period of two months. The study protocol was approved by the Institutional Ethics Committee (IEC). As the embryology classes were being taught during the study duration, samples of our study were taken from models of the embryology (general and systemic). A total of 40 embryology models from the Anatomy museum and dissection hall were included in the study, whereas a total of 82 first year undergraduate medical students voluntarily agreed to participate in the study. The study protocol was explained to the participants and prior to their enrollment their written informed consent was obtained.

Sample collection: Using sterile swabs, soaked in sterile physiological saline, samples were taken from the

dominant hand of the students prior to their contact with the models. In order to completely remove the visible dirt and the temporary microbial flora from the skin, the student's hands were washed (prior to the contact with models) with soap and water for atleast one minute, thereafter the hand swab samples were taken from 25 students (the control group), to detect any bacterial organisms before working with the models. Now, the students were allowed to spend 90 minutes in the laboratory with the selected anatomy models, after which, a hand swab sample was taken once again from the same hand of each student contacting with the models. At this stage, all the 82 students were asked to wash their hands before handling the models, and samples were taken from their hands after spending 90 minutes with the models. Similarly the swab samples were also taken from randomly selected 4 cm^2 surface areas of the 40 embryology models.

Sample processing: Once collected the samples were put into 4 ml brain-heart infusion broth (BHIB) and were sent to Microbiology laboratory for further processing. Once received at the laboratory the BHIB was incubated aerobically at 37°C for 24 hours, thereafter using sterile inoculation loop the sub cultures were done on 5% sheep blood agar (SBA) and MacConkey agar (MA) and the plates were incubated at 37°C for 24 to 48 hours before being reported as sterile. *Isolation and identification of microorganisms*: After incubation, the plates were examined for the growth and the preliminary identification of the emergent colonies was made on the basis of colony morphology, hemolysis on SBA, lactose fermentation on MA, gram staining, catalase test, coagulase test and oxidase test. Based on the aforesaid tests the organisms were broadly classified as gram-positive cocci (in clusters or chains) and gram-negative bacilli (oxidase positive or oxidase negative). Further identification was done using the battery of standard biochemical tests as described previously. [7, 8] Methicillin resistance among Staphylococcus aureus isolates was detected by sensitivity to cefoxitin (30 µg) disc; a surrogate marker for methicillin, and was confirmed by using PBP2a latex agglutination test (Oxoid Ltd., Hampshire, UK).

All dehydrated media, reagents, sterile swabs and antibiotic discs were procured from Hi-media Laboratories Pvt. Ltd, Mumbai, India. *Escherichia coli* ATCC 25922, *Staphylococcus aureus* ATCC 25923 and *Pseudomonas aeruginosa* ATCC 27853 were used as controls for the biochemical tests.

RESULTS

All the samples collected from 40 anatomical models showed microbial growth. Out of these 40 samples, 27 (67.5%) showed mono-microbial growth whereas 13 (32.5%) samples showed poly-microbial growth. A total of 54 microbial isolates (49 bacterial and 5 Candida species) were recovered from these samples. Coagulase negative staphylococci (CONS) was the most predominant organism (26; 48.1%) recovered from these samples, followed by *E.coli* (8; 14.8%), *S.aureus* (5; 9.3%), *Candida spp.* (5; 9.3%) and *Bacillus spp.* (5; 9.3%). Table 1 depicts the distribution of microbial isolates recovered from the anatomical models.

Table 1: Distribution of various microbial isolates recovered from the anatomical models. (*n*=54)

Microbial isolates	Frequency	Percentage (%)
CONS	26	48.1
Escherichia coli	08	14.8
Staphylococcus aureus MSSA (03) MRSA (02)	05	9.3
Candida spp. NAC (04) *Candida albicans* (01)	05	9.3
Bacillus spp.	05	9.3
Enterococcus spp.	03	5.5
Pseudomonas aeruginosa	02	3.7
Total	**54**	**100**

CONS: Coagulase negative staphylococci; MSSA: Methicillin sensitive *Staphylococcus aureus*; MRSA: Methicillin resistant *Staphylococcus aureus*; NAC: Non albicans Candida.

Samples collected from students before and after the contact with models were also investigated for microbial growth and it was observed that microbial population recovered from both the groups differed to a great deal if not completely. Out of the total 25 samples collected from control group, 23 (92.0%) samples showed bacterial growth, whereas two (8.0%) samples showed no growth. Out of the total 23 samples with bacterial growth, 20 (87.0%) samples showed mono-microbial growth whereas three (13.0%) samples showed growth of two different organisms. A total of 26 bacterial isolates were recovered from these 23 samples. Among the recovered bacterial isolates were CONS (16; 61.5%), *Bacillus spp.* (06; 23.1%), *S.aureus* (03; 11.5%), and *E.coli* (01; 3.9%).

Microbial growth was detected among all the 82 students from whom swab samples were taken after the contact with models. Out of these 82 samples, 55 (67.1%) samples showed mono-microbial growth, whereas 27 (32.9%) samples showed poly-microbial growth. A total of 113 microbial isolates (101 bacterial and 12 *Candida spp.*) were recovered from these samples, among which CONS (37; 32.7%), *Bacillus spp.* (20; 17.7%), *S.aureus* (19; 16.8%), *Candida spp.* (12; 10.6%) and *E.coli* 11; 9.7%) were the most predominant organisms. Table 2 depicts the characterization of microbial isolates recovered from the hand swabs of medical students, collected before and after the contact with anatomical models.

Table 2: Characterization of microbial isolates recovered from the hand swabs of medical students, collected before and after the contact with anatomical models.

Microbial Isolate	**Samples collected before contact with anatomical models. (*n*=25)** Bacterial Growth: 23 (92.0%) No growth: 02 (8.0%) Total recovered bacterial isolates: 26	**Samples collected after contact with anatomical models. (*n*=82)** Bacterial Growth: 82 (100%) Total recovered microbial isolates: 113
CONS	16 (61.5%)	37 (32.7%)
Bacillus spp.	06 (23.1%)	20 (17.7%)
Staphylococcus aureus	03 (11.5%) MSSA (03) MRSA (00)	19 (16.8%) MSSA (16) MRSA (03)
Candida spp.	Nil	12 (10.6%) NAC (05) Candida albicans (02)
Escherichia coli	01 (3.9%)	11 (9.7%)
Enterococcus spp.	Nil	08 (7.1%)
Pseudomonas aeruginosa	Nil	05 (4.4%)
Acinetobacter spp.	Nil	01 (0.9%)
Total	**26 (100%)**	**113 (100%)**

CONS: Coagulase negative staphylococci; MSSA: Methicillin sensitive *Staphylococcus aureus*; MRSA: Methicillin resistant *Staphylococcus aureus*; NAC: Non albicans Candida.

DISCUSSION

Role of fomites in the spread of microorganisms has been inevitably proven in various studies conducted across the globe over the past decades, and need no further justification. The current study was conducted to evaluate the rate of microbial contamination of the anatomical models, which possibly may render them as reservoir/vector of microbial transmission. Further the possibility of microbial transmission among the medical students via anatomical models or vice versa was also evaluated. We observed that the anatomical models kept in the anatomy museum and dissection hall of our institute are seldom cleaned. Except for dusting with dry cloth, they were never properly cleaned and over the years had been used by many students, post graduate residents and faculty as well. As these models had been handled by many in past and are currently also being used by medical students for learning purposes, the possibility of the microbial contamination of these models was high and this prompted us to conduct the current study. Meanwhile we also came across a recent study conducted by Kosif *et al*. from Turkey, [9] who evaluated the bacterial contamination in anatomical models of urogenital system, and also the hands of medical students handling them. Using their study protocol we planned to conduct this study in our institute.

In the current study it was observed that all the samples collected from surface of 40 anatomical models were found contaminated with microorganisms. It was interesting to note that except for a single isolate of *Acinetobacter spp.*, the similar microbial population was isolated from hand samples of the students collected after handling the models. We speculate that constant handling of the models by students, passing the models among themselves, heat and moisture generated by hands while handling them creates a conducive breeding condition for microorganisms which are passed from our hands onto the surface of these models or vice versa.

All the samples collected from anatomical models as well as from students after they handled the models showed growth of microorganisms. The most predominant bacterial isolate among the aforementioned samples was CONS, which oftenly are a part of normal skin flora and are usually non pathogenic. But under exposure to additional conditions, known as infection-facilitating factors, their character changes from non-pathogenic to pathogenic. Besides their role in maintaining homeostasis, CONS have emerged as major pathogens particularly in nosocomial settings and are responsible for various infections of different localizations, manifestations or courses particularly among the hospitalized or debilitated patients. [10] *S.epidermidis*, *S.haemolyticus, S.saprophyticus*, *S.capitis*, and *S.lugdunensis* are some of the most frequent and pathogenic CONS species. [11]

S.aureus was another frequently isolated pathogenic bacterial species in the current study. *S.aureus* resides on skin surfaces and it is estimated that *S.aureus* colonizes the anterior nares in approximately 31% (range 6–56%) of the general population at any given time. [12] It is one of the commonest pathogen particularly in nosocomial infections and can cause variety of infections ranging from localized skin and soft tissue infections to fatal meningitis in humans. [13] In the present study *S.aureus* was isolated from anatomical models as well as from the hand samples of the students. Isolation of MRSA was a major cause of concern as these are epidemiologically important drug resistant pathogens. MRSA, once used to be confined to the hospital environment, has now circulated in the community among healthy people who may act as its carrier. [14]

Other pathogenic bacteria isolated in the present study included *E.coli*, *Enterococcus spp*, *P.aeruginosa*, and *Acinetobacter spp*. Isolation of fecal bacteria like *E.coli* and *Enterococcus spp.*, and saprophytic bacteria like *P.aeruginosa* indicates the improper or casual hand hygiene practices among the students. *P.aeruginosa*, a well-known pathogen is a causative agent for various diseases ranging from minor skin infections to fulminant septicemia and is an important cause of nosocomial infections particularly in the burn wards. [15] *Pseudomonas* can thrive well in nutritionally deprived conditions; it proliferates at room temperature and its MDR attribute, makes it difficult to treat. [16] If such MDR strains somehow gain entry into the hospital setting, are very difficult to eradicate and can be the clinicians worst nightmare.

Isolation of *Acinetobacter spp*. from the hand sample of one of the student was of major concern because of its well-known identity as a multi drug resistant (MDR) pathogen. Ability of the Acinetobacter to contaminate the anatomical models is not unlikely, as studies have revealed that Acinetobacter along with *S.aureus* is commonly acquired through cross transmission because of their propensity of drying and to contaminate fomites. [17] The horizontal spread of resistance factors into environmental gram negative bacilli (GNB) has seen the emergence of MDR Acinetobacter, Pseudomonas, and coliforms, wherever looked for, even in skin carriage strains. [18] Hence recovery of these organisms from the hand samples of the students is a cause of concern.

C.albicans as well as NAC were also isolated from some of the anatomical models, as well as hand swab samples from the students. *Candida albicans* is one of the most important opportunistic fungal pathogen and can cause variety of superficial as well as systemic infections. Historically, *C.albicans* has been the most frequently isolated Candida species, however more recently a shift towards NAC species has been reported, which has emerged as important opportunistic pathogens particularly in blood stream infections. [19] The most frequently isolated NAC species are *C.tropicalis*, *C.parapsilosis*, *C.krusei*, and *C.glabrata*. [20] Of note majority of the NAC species are inherently resistant to most of the azole compounds; the widely used antifungal class of drugs against candidial infections and hence it is important to differentiate *C.albicans* from NAC. It is pertinent to mention here that once the study results were available, it was observed that one of the sample from control group students and two samples from the students who had contact with anatomical models showed growth of *C.albicans*. Later it was found that all the three aforementioned students had a fungal infection of the nail (onychomycosis) and the causative agent was later confirmed by the laboratory to be *C.albicans*. This further substantiated and corroborated with our study findings related to these three students.

From our study results it is evident that, anatomical models in the Anatomy museum and dissection hall can act as fomites, reservoir and vector of microbial transmission to students. The possibility of the transfer of microorganisms from the hands of the medical students onto the surface of the anatomical models can also not be denied. To avoid the same, it is imperative to regularly clean/wipe the anatomical models with a disinfectant/70% isopropyl alcohol, preferably daily or otherwise on weekly basis. Students should also be advised to follow hand hygiene practices and should wash/disinfect their hands with soap and water/alcohol hand rubs, before and after handling the anatomical models. If such practices are followed, it will effectively and efficiently reduce the rate of microbial transmission. Moreover, considering the current COVID-19 pandemic situation, it becomes more imperative to follow the aforementioned measures.

CONCLUSION

Isolation of the pathogenic bacterial and Candida isolates from anatomical models concurs their potential as fomites for transmission of organisms to the person handling them. Moreover, recovery of similar microorganisms from the hands of students suggests that hands may be the source of contamination for these anatomical models. Hence, the results of our study conclude that anatomical models get contaminated through hands and vice versa and then from hands to other exposed areas of the body, which indicates the presence of skin flora on the anatomical models. Simple measures such as proper hand hygiene practices by the students and regular/periodic decontamination of the anatomical models with disinfectant/alcohol wipes may reduce the risk of microbial transmission.

Conflict of Interest: Nil

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