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Research Article
Digital Fomites: Bacteria on College Lab Mice

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Abstract

Background and Objective: Shared computer equipment in academic settings can serve as fomites for microbial transmission, yet contamination of computer mice remains understudied. This study aimed to characterize microbial contamination on computer mice in two computer laboratories at Queensborough Community College (QCC), New York. **Materials and Methods:** Thirteen computer mice from each laboratory (12 student and 1 instructor computer per lab; total n = 26) were sampled using sterile swabs and Tryptic Soy Agar plates. Microbial growth was assessed using a 0-4 rating scale, followed by isolation and molecular identification of pure cultures. Statistical comparisons of mean colony counts and microbial diversity were performed at $p<0.05$. **Results:** Laboratory A exhibited higher mean colony counts (1.2 vs. 0.8) and greater microbial diversity than Laboratory B. Five species were isolated from Laboratory A-*Peribacillus simplex*, *Priestia megaterium*, *Bacillus amyloliquefaciens*, *Metabacillus halosaccharovorans* and *Micrococcus luteus*-while Laboratory B yielded four species-*Staphylococcus capitis*, *S. epidermidis*, *S. hominis* and *M. luteus*. Cocci predominated in Laboratory B (8 isolates vs. 5 in A), whereas *Bacillus* species were exclusive to Laboratory A (6 isolates). **Conclusion:** Computer mice harbor diverse microorganisms of human and environmental origin. Although only non-pathogenic organisms were detected, their presence highlights the need for routine surface disinfection and improved hygiene practices in shared academic computing environments. Future studies could explore temporal dynamics and potential pathogenic strains to further assess public health risks.

Key words: Microbial contamination, computer surfaces, environmental hygiene, public health

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Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

The use of shared computers in college laboratories is standard practice in multi-section courses. However, frequent use of these devices without routine disinfection can facilitate microbial accumulation, potentially transforming them into reservoirs for infectious agents[1]. Computer keyboards and other high-touch surfaces in institutional settings have been documented to harbor diverse microorganisms, including potential pathogens that may contribute to disease transmission[2,3]. Studies have specifically demonstrated microbial transfer from contaminated computer surfaces in academic environments[4-6].

Microorganisms such as *Staphylococcus aureus*, *Bacillus* spp. and various Gram-negative bacteria have been frequently recovered from computer hardware in hospitals, offices and educational institutions[7,8]. Neely and Maley[9] found that computer keyboards in educational laboratories were contaminated with *Staphylococcus* species, while another study by Bures *et al.*[10]. identified *Bacillus cereus* and *Micrococcus luteus* from student laboratory computers. Despite this body of research, computer mice, which experience equally frequent hand contact, remain relatively understudied compared to keyboards.

Computer mice function as high-touch fomites capable of harboring and transmitting potentially pathogenic microorganisms in shared environments, particularly in academic institutions, libraries, offices and healthcare settings, resulting in the accumulation of human and environmental microbes on their surfaces[7,11]. Studies have shown that computer mice can harbor bacteria such as *Staphylococcus aureus*, *Escherichia coli*, *Enterococcus* spp. and other environmental or opportunistic pathogens, sometimes including antibiotic-resistant strains[7,12]. Because these devices are not frequently disinfected and are often shared among multiple users, they may contribute to cross-contamination and the spread of infectious agents, particularly in settings with high user turnover[13]. Understanding contamination patterns is therefore essential for developing evidence-based hygiene practices, reducing microbial transmission risks and improving environmental health protocols in shared digital workspaces.

Given the regular use and shared nature of computer laboratories at Queensborough Community College (QCC), assessing microbial contamination of computer mice provides valuable insights into potential hygiene risks in academic settings. The objectives of this study were to: (1) Quantify microbial contamination levels on computer mice in two college computer laboratories, (2) Identify bacterial species present on these surfaces and (3) Characterize differences in contamination patterns between laboratories with different usage histories.

MATERIALS AND METHODS

Study site and sample collection: This study was conducted during the summer of 2023 at Queensborough Community College (QCC) in New York. Two computer laboratories, designated S-205 (Laboratory A) and S-208 (Laboratory B), were selected for sampling. Each laboratory contained 12 desktop computers used by students and one instructor computer (n = 13 computers per laboratory, 26 total). Samples were collected two weeks after the start of the semester, when student computers had been newly installed and in active use in Laboratory A. Computers in Laboratory B had been in use for more than 2 years. Instructor computers had been in continuous use for over five years and were not regularly cleaned between uses. Room temperature was about 25°C with RH 40-60%.

Sample collection and processing: Samples were collected on the same day between 6:00 and 8:00 PM when the laboratories were not in use. The entire surface and sides of each computer mouse were swabbed using sterile cotton swabs pre-moistened with sterile distilled water. Each swab was immediately placed into a sterile transport tube and transported to the microbiology laboratory for analysis within 2 hrs of collection. Samples were aseptically streaked onto Tryptic Soy Agar (TSA) plates using the T-streak method to facilitate isolation of individual colonies. Plates were incubated aerobically at 37°C for 48 hrs.

Table 1: Growth score of bacteria grown on tryptic soy agar in the laboratory

Growth description	Score	Growth coverage on plate
No growth	0	No growth on petri dish
Scant	1	Growth on the 1st quadrant
Light	2	Growth on the 1st and 2nd quadrants
Moderate	3	Growth on the 1st, 2nd and 3rd quadrants
Heavy	4	Growth on all four quadrants

Microbial enumeration and isolation: Following incubation, microbial growth on each plate was scored using a 0-4 scale based on the extent of colony coverage (Table 1): 0 = no growth; 1 = growth in first quadrant only (scant); 2 = growth in first and second quadrants (light); 3 = growth in first, second and third quadrants (moderate); 4 = growth in all four quadrants (heavy). Colony counts and Gram reaction characteristics were recorded for each sample.

Growth scores represent the extent of bacterial colony coverage on Tryptic Soy Agar plates, assessed using a four-quadrant streaking method to estimate relative abundance.

Well-isolated colonies representing distinct morphologies were subcultured to obtain pure cultures. Pure cultures were maintained in Nutrient Broth and subsequently transferred to Eppendorf tubes for transport to Quantus, Inc. (Blue Bell, PA, USA) for molecular identification via matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) on a Bruker MALDI Biotyper® system following the manufacturer's standard analytical procedures.

Data analysis: Descriptive statistics, including mean colony counts and standard deviations, were calculated for each laboratory. Comparisons between Laboratory A and Laboratory B were performed using GraphPad Prism version 11.0 (GraphPad Software, San Diego, CA, USA) using the Mann-Whitney test, with statistical significance set at $p<0.05$.

RESULTS

Microbial load and growth assessment: Bacterial colony counts were recorded in Laboratory A and Laboratory B (n = 13 each). In Laboratory A, counts ranged from 0 to 4 colonies (mean $\pm$ SD = 1.231 $\pm$ 1.301 colonies), while Laboratory B ranged from 0 to 2 colonies (mean $\pm$ SD = 0.769 $\pm$ 0.725 colonies). A Mann-Whitney test showed no significant difference between laboratories ($U = 70.5$, exact two-tailed $p = 0.4497$) (Fig. 1a).

A total of 14 microbial isolates were recorded in Laboratory A and 9 isolates in Laboratory B. In Laboratory A, isolates comprised cocci (n = 5), rods (n = 6) and fungi (n = 3). In Laboratory B, isolates comprised cocci (n = 8), rods (n = 0) and fungi (n = 1). Fisher's exact test indicated a significant association between laboratory location and microbial category ($p = 0.0370$), showing that microbial composition differed between the two laboratories (Fig. 1b).

Morphological distribution: Coccal bacteria were more abundant in Laboratory B (8 isolates, representing 89% of bacterial isolates) than in Laboratory A (5 isolates, 45% of bacterial isolates). *Bacillus* species dominated Laboratory A with 6 isolates (55% of bacterial isolates) but were completely absent from Laboratory B. Fungal growth was detected primarily in Laboratory A (3 isolates) with only one fungal isolate recovered from Laboratory B.

Species identification: Molecular identification revealed nine distinct bacterial species across both laboratories (Table 2). Laboratory A yielded five bacterial species: Four belonging to the *Bacillus* group (*Peribacillus simplex*, *Priestia megaterium*, *Bacillus amyloliquefaciens* and *Metabacillus halosaccharovorans*) and one coccal species (*Micrococcus luteus*).

Bacterial isolates were identified based on colony morphology, Gram staining and biochemical characteristics. Morphological classifications reflect the predominant cell shape observed under microscopy (coccus or bacillus). Laboratory A yielded mostly Bacillus-type organisms, whereas Laboratory B showed a higher prevalence of coagulase-negative Staphylococcus species.

Laboratory B yielded four coccal species exclusively: Three *Staphylococcus* species (*S. capitis*, *S. epidermidis* and *S. hominis*) and *Micrococcus luteus*. Notably, *M. luteus* was the only species recovered from both laboratory groups.

DISCUSSION

This study recovered nine distinct bacterial species from computer mice in two college computer laboratories, demonstrating that these frequently touched surfaces harbor diverse microbial communities. Laboratory A yielded five species (four *Bacillus* and one coccus), while Laboratory B yielded four coccal species exclusively. The isolation of both *Bacillus* and coccal bacteria corroborates previous findings in similar environments[7,14,15].

The predominance of spore-forming *Bacillus* species in Laboratory A may reflect the absence of routine cleaning protocols in that laboratory. *Bacillus* species are ubiquitous environmental organisms capable of surviving on inert surfaces for extended periods through endospore formation[16]. While most *Bacillus* species are non-pathogenic, opportunistic infections have been documented in immunocompromised individuals[17,18]. The presence of four distinct *Bacillus* species suggests environmental inoculation from air, dust, or contact with contaminated surfaces rather than direct human transfer[19].

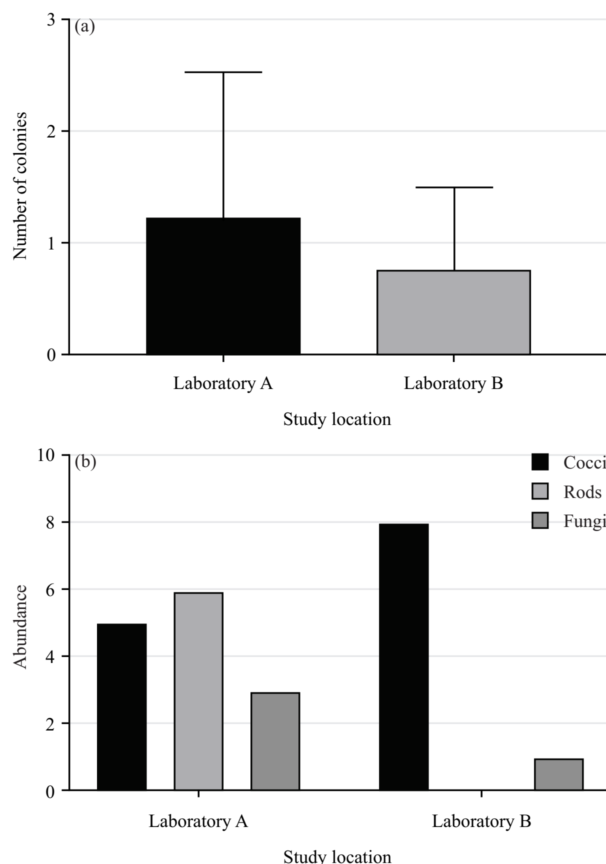

Fig. 1(a-b): (a) Colony counts in laboratory A (n = 13) and laboratory B (n = 13), (b) Microbial isolates by category (cocci, rods, fungi) in two computer laboratories

(a) Laboratory A: 1.231±1.301 (0-4), Laboratory B: 0.769±0.725 (0-2). Mann-Whitney test: U = 70.5, p = 0.4497 and (b) Laboratory A: 5, 6, 3, Laboratory B: 8, 0, 1. Fisher's exact test: p = 0.0370

Table 2: Bacterial isolates from two computer laboratories at Queensborough Community College

Laboratory A	Morphology	Laboratory B	Morphology
Peribacillus simplex	Bacillus	*Staphylococcus capitis*	Coccus
Priestia megaterium	Bacillus	*Staphylococcus epidermidis*	Coccus
Micrococcus luteus	Coccus	*Staphylococcus hominis*	Coccus
Bacillus amyloliquefaciens	Bacillus	*Micrococcus luteus*	Coccus
Metabacillus halosaccharovorans	Bacillus		

In contrast, the dominance of coccal bacteria in Laboratory B strongly suggests direct transfer from human skin flora. *Staphylococcus epidermidis* and *S. hominis* are common skin commensals but can act as opportunistic pathogens, particularly in nosocomial settings and in individuals with compromised immune systems[20,21]. *Staphylococcus capitis* has been specifically associated with neonatal sepsis and infections related to prosthetic devices[22]. The recovery of *Micrococcus luteus* from both laboratories further supports human skin as a contamination source, as this organism is a common component of the human skin microbiome[23].

The marked differences in microbial diversity and composition between the two laboratories warrant consideration. Since instructors and laboratory technicians worked in both facilities, cross-contamination between laboratories seems unlikely as the sole explanation. Potential contributing factors include: (1) Differences in ventilation between laboratories, which could influence environmental bioaerosol deposition; (2) Variation in student hand hygiene practices; (3) Differences in cleaning frequency or protocols, if any; and (4) Varying usage intensity. Laboratory B, composed of older computers, was potentially receiving more frequent use, leading to greater accumulation of human-derived organisms.

The higher prevalence of fungi in Laboratory A (3 isolates vs. 1) may reflect environmental factors such as elevated humidity levels that favor spore germination and fungal growth[24]. Future studies should include environmental monitoring of temperature, humidity and air quality to better characterize factors influencing microbial colonization patterns.

Computer mice warrant distinct attention in contamination research because their patterns of use and contact surfaces differ from keyboards. Unlike keyboards where contact is distributed across multiple keys, mouse use concentrates hand contact on a small, repeatedly touched surface, increasing the likelihood of sustained microbial deposition and transfer[13]. The mouse is also manipulated continuously during computer interaction, often with the same hand that may have contacted other surfaces, food, or personal items, making it a more dynamic vector for organism spread. Additionally, mice are less frequently disinfected than keyboards, partly because users and cleaning staff may overlook them or assume they pose a lower risk[8]. These factors make the computer mouse a particularly important target for environmental hygiene research and intervention planning.

Although this study isolated only non-pathogenic or opportunistically pathogenic organisms, their persistence on frequently touched surfaces highlights important hygiene considerations for shared computing environments. Computer mice can serve as fomites, inanimate objects capable of harboring and transmitting infectious agents, particularly in settings where users may have compromised immune function or open wounds[2].

We recommend implementing the following practices to reduce microbial contamination in computer laboratories:

- **User-initiated cleaning:** Students should clean computer mice with 70% isopropanol wipes or other EPA-approved disinfectants before and after each use
- **Institutional protocols:** Laboratory personnel should implement regular disinfection schedules, particularly for high-traffic periods
- **Hand hygiene enforcement:** Posting hand hygiene reminders and providing hand sanitizer stations near computer workstations can reduce microbial transfer from contaminated hands to shared devices[25].
- **Periodic monitoring:** Conducting routine microbiological surveillance can help assess the effectiveness of cleaning protocols and identify potential pathogen reservoirs

Several limitations should be noted. First, sampling occurred at a single time point two weeks into the semester, which may not represent peak contamination levels. Second, only aerobic cultivation at 37°C was employed, potentially missing anaerobic or psychrophilic organisms. Third, fungal isolates were not identified to the species level. Finally, the study did not assess actual infection transmission or clinical relevance of the organisms detected. Future research should include longitudinal sampling, comprehensive pathogen screening (including viruses) and correlation with actual infection rates in the student population.

CONCLUSION

This study demonstrates that computer mice in college laboratories harbor diverse microbial communities, predominantly Gram-positive cocci and bacilli of human and environmental origin. The distinct microbial profiles between laboratories suggest that contamination patterns are influenced by multiple factors including cleaning practices, usage patterns and environmental conditions. While the organisms detected pose minimal risk to healthy individuals, they underscore the potential for shared computer equipment to serve as fomites in academic settings. Implementation of routine disinfection protocols and promotion of hand hygiene can significantly reduce microbial loads on these high-touch surfaces and minimize potential health risks to users.

SIGNIFICANCE STATEMENT

This study demonstrates that computer mice in college laboratories function as digital fomites, harboring diverse microorganisms originating from human contact and the surrounding environment. Variations in microbial composition between laboratories highlight the impact of usage patterns and hygiene practices on contamination levels. These findings emphasize the importance of integrating routine disinfection of shared digital devices into environmental hygiene and infection control protocols within academic settings.

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