



Original Research Article

Microbial Density on Electronic Devices

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ABSTRACT

Keywords

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Tablet

Electronic devices are common accessories in modern society. Because different devices contact body parts and their residing microorganisms differently, each device is characterized by a unique contamination profile. We investigated the influence that device size and function have on microorganism density. Human participants each used an tablet, smart phone and media player for 20 minutes. We predicted that microbial density would differ among devices due to contact with different body part surfaces. We found no significant differences among devices but significant differences between participant groups. These findings could affect guidelines for using devices in health care settings.

Introduction

As technology continues to affect daily activities in modern society, electronic devices have become common accessories. Different device types are distinguished by their different sizes and functions and consequently exposed to distinct arrays of infectious body parts. Despite their frequent usage, devices rarely undergo routine cleaning (Ramesh *et al.*, 2008).

They therefore gradually may become reservoirs for potentially pathogenic microorganisms (Brady *et al.*, 2009). Given that each device is exposed to a unique contamination sources and microbial communities, function should dictate residing microorganisms.

Microbial diversity on human bodies

Human bodies host a large variety of bacterial species. Although microorganism populations generally are stable, they are affected by factors such as climate (geographic as well as metabolic), age, ethnicity and health (including medication) (Roth and James, 1988). Objects exposed to infectious body parts constitute sources for contamination (Brady *et al.*, 2009; Ekkrakene and Igeleke, 2007; Jeske *et al.*, 2007; Roth and James, 1988). Two highly infectious areas are hands and mouths (Fierer *et al.*, 2010; Fierer *et al.*, 2008; Grice *et al.*, 2010). Different regions thereon are characterized by different microbial communities. For examples, some microorganisms reside only in specific areas within oral cavities (Aas *et al.*, 2005) and microbial composition differs

between dominant and nondominant hands (Fierer *et al.*, 2008).

Research on fixed and mobile telephones in healthcare settings provide evidence for an increase in contamination after usage (Brady *et al.*, 2009; Jeske *et al.*, 2007). This is concerning because mobile telephones are used frequently by health care workers in close proximity to patients. Research on personal and public electronic devices has shown that user number is proportional to microorganism abundance (Anderson and Palombo, 2009; Ekraene and Igeleke, 2007). Shared devices therefore generally constitute greater infection sources.

Although research on telephones in healthcare settings has been conducted, scant research has been conducted on other electronic devices. Media players and tablets differ in size and function. We used an tablet as a representative for media players, an smart phone as a representative for mobile telephones, and an media player as a representative for tablets. The tablet was similar in size to the smart phone and similar in function to the media player, so the tablet served as a useful reference. Considering that smart phones are exposed to unique contamination sources (i.e., mouths) – in addition to contamination sources common with mobile and media players (i.e., hands), we predicted that the smart phone would contain greater microbial densities than would the tablet and media player.

Materials and Methods

Control

We performed two control tests, to evaluate effectiveness for a cleaning agent and determine if contamination was inherent in our experimental design. The first control test followed experimental procedures

(described subsequently) except that moistened swabs were streaked directly onto plates without swabbing devices. The second control test followed experimental procedures except that devices were swabbed after they had been cleaned using 70% ethanol. Control tests were performed in the same environment as the main experiment.

Main experiment

Seventeen undergraduate students at McMaster University were recruited in an unbiased manner as participants. Participants each were instructed to complete a questionnaire and visit three stations. The order in which participants visited the three stations was determined pseudorandomly before the experiment and assigned individually upon arrival. Participants were seated at each station for 20 minutes, constituting a run. Each run involved using one electronic device: tablet touch (8 Gb) 4th Generation, smart phone 4 (16 Gb), and media player 2 (64 Gb). During each run, participants were asked to use the device as they would routinely. A list detailing activities to perform with each device was provided to ensure that all participants used the devices similarly.

To reduce data-collection bias, labels containing an identifying number on three different colored tags were created (i.e., blue for tablet, yellow for smart phone, red for media player). During data collection, participants were assigned pseudorandomly to an identifying number unknown to volunteer assistants. Each identifying number was associated with the data from one participant (with color coding identifying devices). Numbers were revealed only after all data had been collected.

Surfaces were swabbed from the front and

back on devices, as swabbing is an effective method for surveying bacterial counts (Fierer *et al.*, 2010; Fierer *et al.*, 2008; Hamady *et al.*, 2008). Equal-sized areas were sampled from each device (i.e., several relatively small quadrilaterals spread over the media player surface were swabbed – their surface areas collectively were approximately equal to the individual surface areas for the tablet and smart phone). Size can influence which body parts and specific areas thereon contact devices. An tablet or smart phone can be held easily with one hand, whereas an media player requires two hands or one hand and contact with another body part (e.g., hip), for instance. Size effects therefore might be revealed with microbial density measurements.

After samples had been collected following procedures similar to Fierer *et al.* (2010, 2008), devices were cleaned with 70% ethanol. Samples were plated directly onto 100 mm Tryptic Soy Agar plates with Lecithin and Tween-20. Plates were stored temporarily in a refrigerator after each run and later incubated for 24 hours at 34 °C. One experimenter (SK) and one volunteer assistant counted bacterial colonies. Plates for which count discretion exceeded lowest microbial density counts by 5% were recounted. If count discretion remained greater than 5% in a recount, an average was calculated over all four counts. Results were processed using the statistical software IBM SPSS.

Result and Discussion

Control tests

Control tests suggest that the cleaning agent was effective and no contaminants were introduced from the experimental design, similar to previous studies (Brady *et al.*, 2009).

Main experiment

The tablet samples contained the highest average bacterial density (94 Colony Forming Units, CFU), followed by smart phone (48 CFU) and media player (27 CFU). A repeated measures ANOVA was performed on bacterial colony density among devices. No significant difference was observed ($p = 0.075$), suggesting that neither size nor function significantly determined resident microbial communities.

Call time. The fundamental functional difference that distinguishes the smart phone from the other two electronic devices is the capability to place telephone calls. Speaking can contaminate a surface positioned 30 cm away from the speaker (Philips *et al.*, 1992). Telephone call time was recorded, and the abundance data were analyzed in a one-way ANOVA with call time as covariate. No significant effect was observed between telephone call length and microbial density. Many participants allotted a small time period to placing telephone calls, which might have contributed to the observed insignificant result.

Gender. Gender for each participant was self-declared on the questionnaire. Among the 17 participants, 6 were female and 11 were male. No significant effect on microbial density was observed among devices by gender (Figure 1). This nonsignificant gender effect is consistent with previous studies (Fierer *et al.*, 2008; Ramesh *et al.*, 2008). Males, however, showed a greater variation compared to females in microbial density (standard deviation for males: tablet = 220 CFU, smart phone = 127 CFU and media player = 74 CFU, standard deviation for females: tablet = 34 CFU, smart phone = 25 CFU and media player = 5 CFU).

Figure.1 Bacterial colony number (CFU) on electronic devices after 20 minutes use (means represented by bar heights; standard deviations represented by whiskers). Gender differences were insignificant, but variation among males was greater than was variation among females

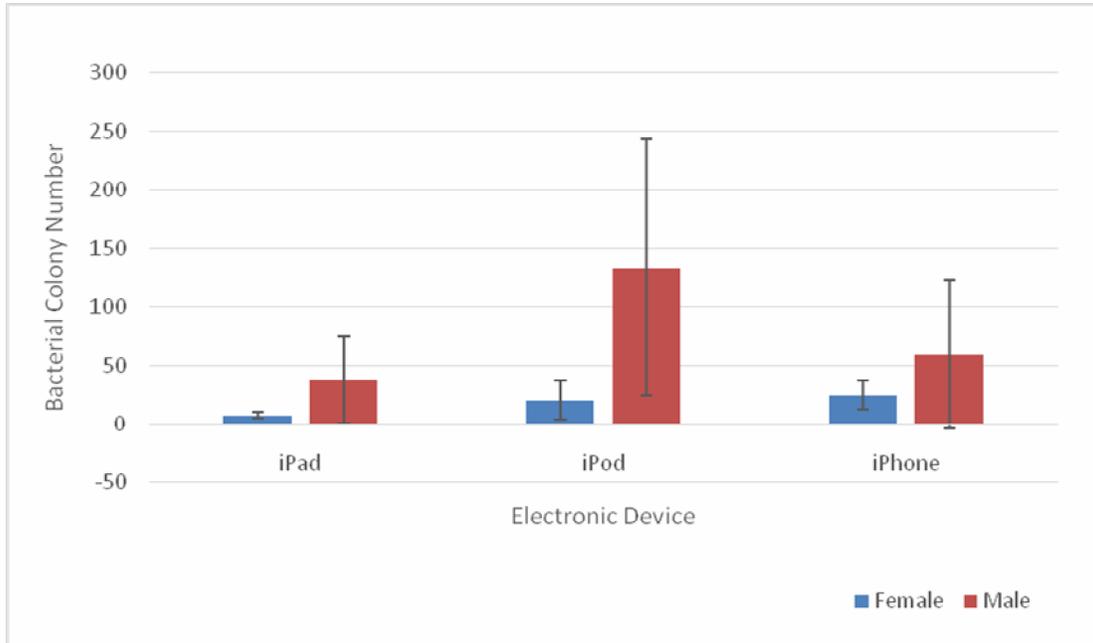
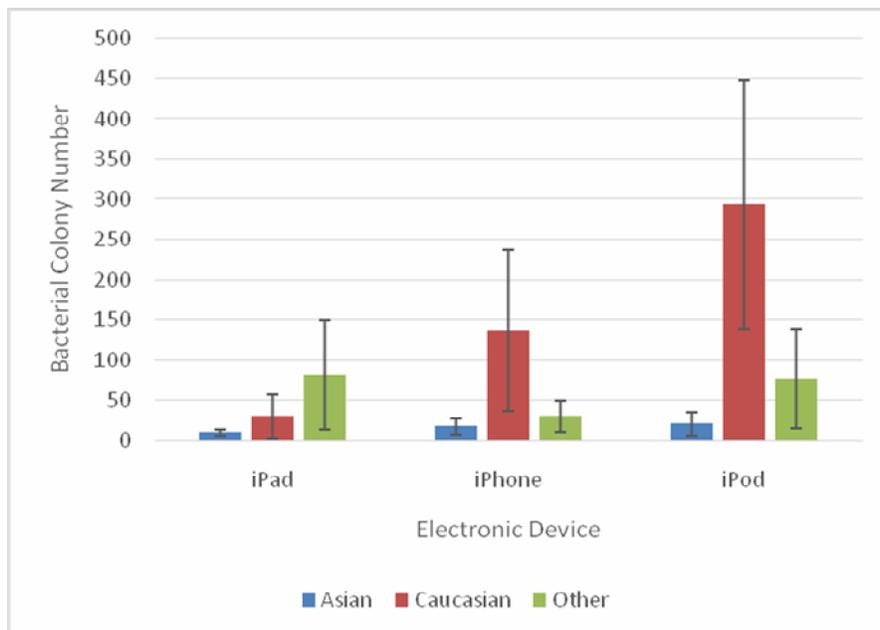


Figure.2 Bacterial colony number (CFU) on electronic devices after 20 minutes use by users from different ethnic backgrounds (means represented by bar heights; standard deviations represented by whiskers; the “other” group comprised one African participant, one Middle Eastern participant and one participant with undeclared ethnicity). Ethnicity differences were significant



Significant differences for between-subject effects ($p = 0.043$) were present, suggesting that samples taken from the same individual were characterized by high relatedness across the three devices. These findings are similar to those found by Fierer *et al.* (2008) on the use of cutaneous microbial communities in forensic identification. Being able to perform forensic identification even after a device has come into contact with a different body part would increase the versatility for swabbing as a forensic tool. Large between-subject variance also might have contributed to the observed insignificant results.

Last hand sanitization. Seven participants stated on their questionnaire that they had sanitized their hands within 4 hours prior to the experiment. Similar to the study by Fierer *et al.* (2008), no significant difference in bacteria colony density was found between these and the other participants. Bacterial communities possibly were able to reestablish and return to previous levels between sanitization and experimentation (Fierer *et al.*, 2008).

Ethnicity: Ethnicity was self-declared on the questionnaire. Among the 17 participants, ten reported Asian ethnicity, four Caucasian, one African, one Middle Eastern and one participant included no information. Statistical analysis revealed a significant ethnicity effect on bacteria colony density (Figure 2). Additional, *post hoc* analysis with paired t-tests and a Bonferroni correction revealed no significant difference in microbial density on surfaces between Asian and Caucasian participants. Caucasians, however, showed greater variation for every device (standard deviations: tablet = 308 CFU, smart phone = 200 CFU, media player = 56 CFU) compared to Asians (tablet = 30 CFU, smart

phone = 22 CFU, media player = 7 CFU). The significant overall ethnicity effect may be attributed ultimately to differences in anatomy by combining three observations: (1) Asians are characterized by fewer apocrine glands compared to Caucasians (Bang *et al.*, 1996); (2) human perspiration has been known to be a suitable environment for microbial growth (Braks *et al.*, 2000); and (3) moist surfaces allow for greater bacterial transfer than do dry surfaces (Sattar *et al.*, 2001). The variable bacterial load in Caucasians may have resulted from greater sweat production promoting more cutaneous bacterial growth and its transfer onto other surfaces.

Prospectus: Future research should include identifying resident microorganisms. High levels for *Bacillus cereus*, *Proteus mirabilis*, and *Staphylococcus epidermidis* are expected; other residing microorganisms might include *Klebsiella pneumoniae*, *Staphylococcus aureus*, *Escherichia coli* and species in the genera *Citrobacter* and *Pseudomonas* (Ramesh *et al.*, 2008; Tagoe *et al.*, 2011).

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