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Mobile phones represent a pathway for microbial transmission: A scoping review

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ABSTRACT

Background: Mobile phones have become an integral part of modern society. As possible breeding grounds for microbial organisms, these constitute a potential global public health risk for microbial transmission.
Objective: Scoping review of literature examining microbial's presence on mobile phones in both health care (HC) and community settings.
Methods: A search (PubMed&GoogleScholar) was conducted from January 2005–December 2019 to identify English language studies. Studies were included if samples from mobile phones were tested for bacteria, fungi, and/or viruses; and if the sampling was carried out in any HC setting, and/or within the general community. Any other studies exploring mobile phones that did not identify specific microorganisms were excluded.
Results: A total of 56 studies were included (from 24 countries). Most studies identified the presence of bacteria (54/56), while 16 studies reported the presence of fungi. One study focused solely on RNA viruses. *Staphylococcus aureus*, and Coagulase-Negative Staphylococci were the most numerous identified organisms present on mobile phones. These two species and *Escherichia coli* were present in over a third of studies both in HC and community samples. Methicillin-resistant *S. aureus, Acinetobacter* sp., and *Bacillus* sp. were present in over a third of the studies in HC settings.
Conclusions: While this scoping review of literature regarding microbial identification on mobile phones in HC and community settings did not directly address the issue of SARS-CoV-2 responsible for COVID-19, this work exposes the possible role of mobile phones as a 'Trojan horse' contributing to the transmission of microbial infections in epidemics and pandemics.

1. Introduction

Mobile phones (both keypad and smartphone devices) have become an integral part of modern societal life and are in the hands of billions of users worldwide every day. Between 2011 and 2018 the adoption rate of mobile phones within the community skyrocketed from 10 to 60% while the upward trend is expected to reach 79% by 2025 [1].

Mobile phone use is increasing globally with higher usage rates in certain demographics. In Australia, a consumer survey (n = 800) was conducted by Di Marzio Research and TKW, to determine which age groups owned a smartphone device. The results showed that 86%–94% of individuals aged below 65 years, within the standard age brackets, have a smartphone and smartphone penetration does not differ significantly between gender [2].

Furthermore, a US-based survey conducted by the Pew Research Centre in 2018 suggested that consumers are more likely to own, than not own, a smartphone: individuals aged between 18 and 29 had smartphone ownership rates of 96%, whereas individuals aged over 65 years had ownership rates of 53% [3].

Fomite-based transmission occurs when microorganisms from an infected individual are deposited on an inanimate object and then subsequently transmitted to a new host [4]. Fomite-mediated transmission is a critical pathway for causing infectious disease in both community and health care settings [5,6].

Four main factors appear to impact the potential risk of microbial transmission via fomites: (1) the specific species present, (2) the

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number of microorganisms present, (3) the size of the fomite, and (4) the rate at which they are touched by humans.

Studies outlined that transmissibility of transient microbial flora depends on the specific species present as well as the number of microorganisms on the surface [7,8]. A 2008 study investigating the hand-based microbiome of 51 healthy adult volunteers found that on average an individual had more than 150 bacterial species, of which, 94% belonged to the Proteobacteria, Firmicutes and Actinobacteria phyla [9]. A study exploring human hand bacterial and fungal microbiome diversity discovered *Malassezia spp.* and *Aspergillus spp.* as the most common and second most common fungal microorganisms, respectively [10].

A 2012 study demonstrated that the surface size of fomites and the contact frequency with them can impact transmission [11]. Zhao and his team used an Environmental Infection Transmission System (EITS) model to evaluate interactions of fomite characteristics in addition to human behaviours that affect transmission routes. The study demonstrated that regularly touched large surfaces, including public benches and tables, have the highest transmission potential. A 2019 systematic review demonstrated that all surfaces in an aircraft interior (tray tables, armrests, seat covers, door knobs and toilet flush buttons) served as fomites with all harbouring a spectrum of potentially hazardous microbial entities including viruses, posing concerns of biothreat risks for public health [12].

Additionally, infectious individuals who use their hands when covering a cough divert infective pathogens from the droplet route to the hand-fomite route, which has the potential to increase fomite transmission from highly touched devices [11]. Recently, the rapid spread of the SARS-CoV-2 coronavirus, responsible for COVID-19, has challenged the scientific community to identify the undetected pathways. With the current pandemic and its links to modern transport (i.e. planes, cruise ships) there has been a lot of interest in mobile phones as one of the pathways by which SARS-CoV-2 can be transmitted.

1.1. Mobile phones and smartphones in health care settings

Contamination of surfaces and equipment are well-documented sources of nosocomial infections, where infected individuals interact with surrounding surfaces and 'high-touch surfaces' and facilitate the transmission of microbes to other patients and health care workers [13–16]. Some of the organisms identified in the studies mentioned include vancomycin-resistant enterococci (VRE), methicillin-resistant *Staphylococcus aureus* (MRSA), *Clostridium difficile* (*C. diff*), *Pseudomonas aeruginosa*, *Acinetobacter baumannii* and *Klebsiella pneumoniae*.

Not only are mobile phones pervasive in terms of personal use, they are now considered essential and integrated tools at workplaces including health care related professions. A 2013 study by Sondhi and Devgan explored smartphone application in a paediatric ward. This study highlighted the effectiveness of smartphones with a wide range of applications including medical calculators (Qx, PICU calculator, Phototherapy calculator), drug information (Micromedex drug information, the Sanford guide to antimicrobial therapy), epidemiology (LearnStat) and medical news (MedPage). Additionally, the study indicates that such devices enable health care providers to connect with clinical information at the point of care, which ultimately provides patients with the best possible evidence-based practise. Of importance, the article suggests that mobile phone and smartphone use in the clinical setting can act as a source of distraction and potentially compromise the aseptic environment [17].

Improving and implementing hygienic practices in hospitals is an ongoing challenge. It is surprising that to date no general national or international guidelines have been developed to best manage the risk posed specifically by mobile phones despite current research demonstrating their use by most clinical staff whilst on duty [17–19].

Mobiles phones have a high frequency of use, are often in contact with our hands and faces, and while in operation, can often heat up to temperatures that favour the survival and possibly growth of microorganisms. Combined with the fact that cleaning and disinfection of mobile phones is not a common practice with up to 72% of mobile phone users never washing their devices (Tajouri et al. Unpublished data). It is likely that they constitute a suitable fomite, meaning an inanimate platform with microbial contamination. The frequent handling of billions of mobile phones worldwide, which are often microbially contaminated, provides the potential for them to act as 'Trojan Horses', a term first presented by Ref. [20] enabling disease infection transmission globally.

This scoping review focuses on the available literature regarding microbial profiles of mobile phones in order to synthesise the knowledge on their contamination by a diverse range of microorganisms, and to determine whether the microbiome on mobile phones differs between health care and community populations.

2. Methods

This scoping review follows the guidelines of the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA). This scoping review study was not registered.

2.1. Search strategy

We searched PubMed and Google Scholar for studies that identified and evaluated microorganism populations on mobile phones/smartphones within the health care setting and the general community (non-health care setting). The PubMed database was chosen in order to select for biomedical journals and publications, whilst Google Scholar was chosen to identify free-text articles that would normally be unidentified from the PubMed search. Associated citations and references were manually investigated to identify additional studies of relevance. The last search for the review was performed on 12 December 2019.

The following key words and terms were developed in MEDLINE and adjusted for use in other databases: ("fomites"[MeSH] OR fomite* OR "Cross infection"[MeSH] OR nosocomial OR "Bacteria"[MeSH] OR "Bacterial Infections"[MeSH] OR "Fungi"[MeSH] OR "Fungal Infections"[MeSH] OR "Virus"[MeSH] OR "Viral Infections"[MeSH] OR "Microbial flora"[MeSH] OR microbiota* OR microbiology* AND ("Equipment Contamination"[MeSH] OR "mobile phone" OR "mobile phones" OR "Cell Phones"[MeSH] OR "cellular phones" OR "cellular phone" OR "Personal Digital Assistant" OR "personal digital assistants" OR "Computers, Handheld"[MeSH] OR "smartphone" OR "smartphones") AND (physician OR physicians OR doctor OR doctors OR student OR students OR health personnel OR medical personnel OR dental personnel OR university OR college OR university college OR teaching institution OR community OR public).

2.2. Study selection

Studies were included if the research described tested samples on mobile phones, identified microorganisms present in each sample (including bacteria, fungi and viruses), was published in 2005 or later, and whether the study was available in English. Studies that reported microbial populations collected from mobile phones in either hospital-based or community-based settings or both were included in the review.

Studies that did not explore microbial populations on mobile phones but instead explored contamination rates of contaminated equipment, clothing, keyboards, computer mice, pens and other fomites were excluded. Furthermore, studies that explored the effectiveness of disinfection and decontamination practices with no mention of identification of microorganisms were also excluded.

Following the database search, we uploaded the selected studies to RefWorks and removed any duplicates. The titles were first screened from each database, followed by the abstracts retrieved by one author (MO). The full text of the remaining articles was independently screened by two authors (MO and LT) to determine the final eligibility.

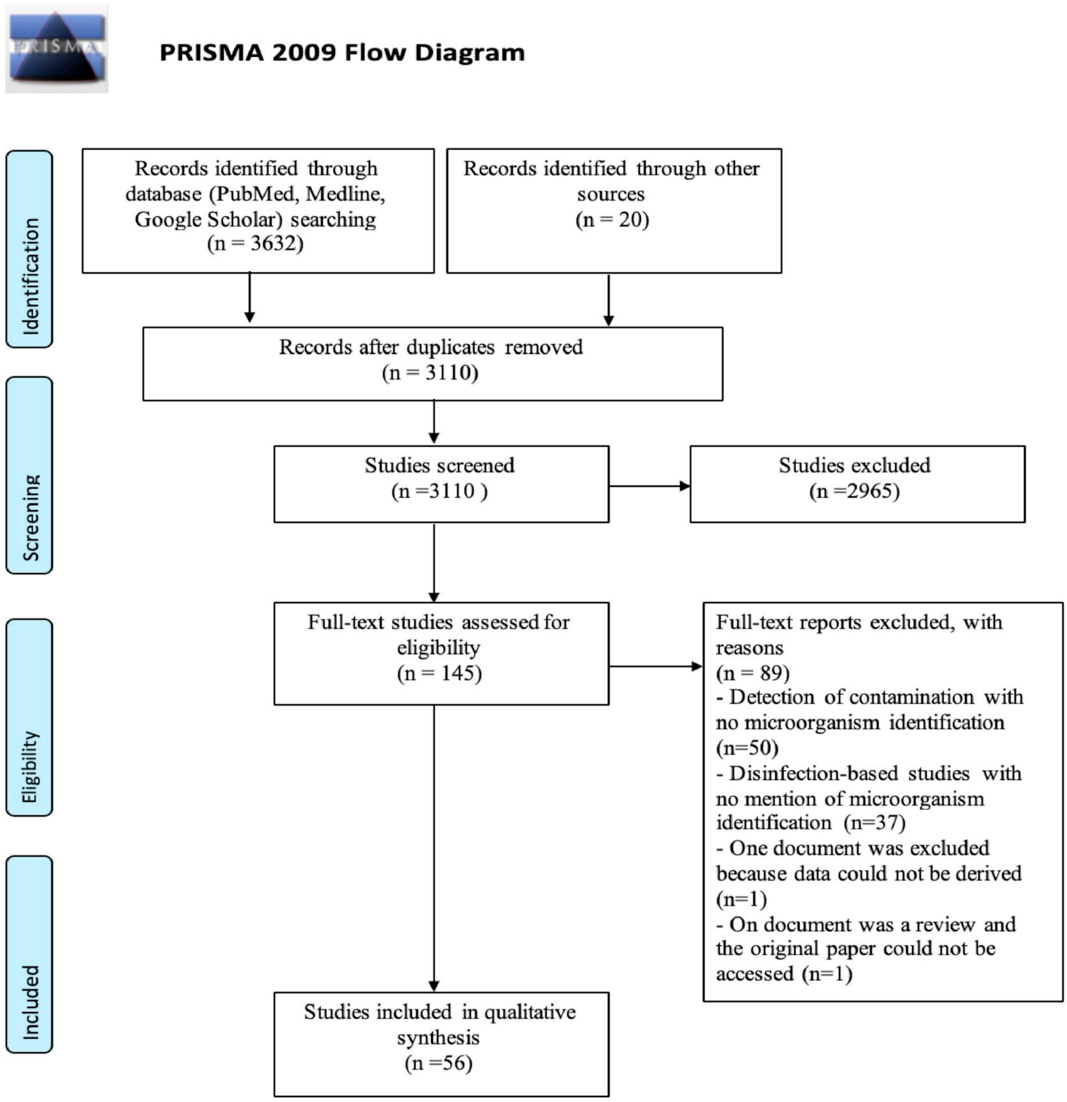

Fig. 1. PRISMA flow diagram of studies selected for full review.

2.3. Data extraction and quality assessment

One author (MO) extracted and compiled the data into a Microsoft Excel spreadsheet, and the data was independently put through quality assurance and quality checks by another two authors (MC and ABB). The compiled data included: author/year, country, target of the study, sample size (number of phones and/or swabs), setting (health care or community), microbial profiling techniques (spot test, biochemical tests, PCR, DNA sequencing), specificity of microbial profiling techniques (low, medium, high, very high), total number of isolates detected, and number of isolates detected for each species or taxonomic unit.

Some studies contained typographical errors in the background and discussion/conclusion sections. These studies were still included in the final review as there was no change to the data and figures presented. Two studies presented tables of results in which the values did not add up to the total. In these two cases, we included the studies considering the values presented for individual species as correct.

2.4. Analyses

We performed a qualitative analysis of the study characteristics and compiled the quantitative data for all studies included in this review to achieve a synthesis of the last 15 years of identification of microorganisms on mobile phones. Selected articles used in this systematic review were checked for their content by two additional co-authors (MC and AB) for quality control and quality assurance to prevent mistakes of information used in this review. Such quality assessment involved re-opening every publication and checking all input values listed in the review tables and so for every microbial species and asserting that results of each publication are complete.

We did not undertake statistical testing of the values achieved, as aims and methodologies between them were extremely varied and inconsistent. Nonetheless, we believe the results can inform a general pattern in health care and community settings worldwide.

3. Results

3.1. Study selection

Following the search, 3652 articles were retrieved from the literature, with 2684 articles from PubMed, 948 articles from Google Scholar and an additional 20 articles identified through a manual search. After duplicates were removed, the 3110 articles remaining were screened based on the inclusion criteria. Of these, 145 full-text articles were assessed for eligibility, of which 89 articles were excluded for not meeting the inclusion criteria. Finally, 56 articles met the criteria for full review and were included in the final analysis. Fig. 1 represents the PRISMA flow diagram outlining the selected studies that passed the criteria for full review.

3.2. Study characteristics

The systematic search identified 56 studies that were published between 2006 and 2019. This review includes studies representing 24 countries, with the most publications arising from India (19), followed by Egypt (5), and Nigeria (4).

Table 1 provides a qualitative overview of the studies included here. Ten studies were comparative between two or more population groups; 47 studies sampled the population of Heath Care Workers, and 18 studies sampled the population in the general community. The terminology of target organisms in the studies was mixed. Some studies targeted identification of ‘microorganisms’ or ‘pathogens’ or ‘microbial flora’ but only reported bacteria. It is unknown whether an attempt was made to detect other types or organisms. All but two publications (54 out of 56) targeted or reported on bacteria isolates; however, in multiple cases, only ‘clinically important’ or ‘pathogenic’ bacteria were presented in the results. One article focused solely on *Candida* species, 5 articles targeted fungi as well as bacteria, and another 10 articles reported on fungi despite targeting only bacteria. One article focused solely on viral RNA (Table 1).

3.3. Study design characteristics

Fig. 2 outlines the different study design characteristics observed in all studies.

Various microbiology identification tools were used across the studies (Fig. 3). Basic microbiology identification tools including the spot test and biochemical test were used in 61% of the studies (n = 34). Twenty studies used the same basic microbiology identification tools with the addition of more sophisticated tools: PCR (n = 1); API Identification System (n = 6); VITEK 2 system (n = 6); bile esculin test, TSI and IMViC test, and oxidative-fermentation test (n = 1); API Identification System, RAPD-PCR, and 16S-rRNA sequencing (n = 1); PCR of 16S-rRNA gene (n = 1), schema of Cheesbrough and Cowan (n = 1); API Identification System, and 16S-rRNA sequencing (n = 1); and whole-genome sequencing (n = 1).

Three studies used identification tools that did not include the spot test and biochemical tests; VITEK 2 system (n = 1), RT-qPCR, KHRV kits, KHPNOV kits and MWS kits (n = 1), and Count-Tact plates, and Candida-Select (n = 1).

A total of 37 studies performed antibiotic sensitivity tests; more commonly the Kirby-Bauer disk diffusion method.

3.4. Microorganism results

When studies showed a comparison of community and health care settings, we split them into two rows, hence the jump to 65 population groups in Table 2. A larger proportion of studies in this review conducted sampling in health care settings, compared to community settings. The number of samples taken, isolates and other parameters are shown in Table 2.

Statistical tests were not performed to compare the differences between settings, because of the differences in aims, methodology, and results presented. It is, however, appropriate to compare the percentage of contaminated phones, which was 68% both in health care and community settings.

Both for community and for health care settings, the microorganisms that were isolated with highest proportion, relative to swabs taken and methodologies utilized, were CoNS and *Staphylococcus aureus*. These two bacteria were also the most frequent relative to number of studies (Table 3).

In the community, two other organisms were detected with a frequency greater than 5% (relative to swabs taken and methodologies utlised): *Micrococcus* sp. (148 isolates in 2815 swabs), and *Staphylococcus epidermis* (218/2815). *Candida albicans* (114 isolates, 4.0%), and *Candida glabrata* (132 isolates, 4.7%), as well as other *Candida* species and fungi in general were not the target, or even reported in most of the studies, and a large proportion of these results arises from a single publication [49]. It is, therefore, assumed that *Candida* species are likely to be more commonly detected on mobile phones than is reported here.

In the health care setting, only one other taxonomic unit is present at a rate higher than 5% of isolates relative to swabs: or Methicillin-sensitive *S. aureus* (MSSA) (316 isolates from 5895 swabs). Antibiotic sensitivity and resistance were not tested in all publications, so it is assumed that this value is under-reported.

In terms of prevalence in relation to studies, we have highlighted the species or taxonomic units that were present in more than a quarter of the studies from each population target (community and health care). Seven organisms appeared in more than a quarter of studies in both groups (*Bacillus* sp., CoNS, *Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus,* and Methicillin-resistant *S. aureus*). An additional four organisms were found in more than a quarter of studies in the health care setting only (*Acinetobacter* sp., *Micrococcus* sp., MSSA, and *Pseudomonas* sp.).

4. Discussion and conclusion

This review has provided a comprehensive, worldwide analysis of publications that explored the presence of microorganisms on mobile phones. The average contamination rate of mobile phones, as calculated here, is 68%. It is important to note that this is likely an under-representation of the real values, as most studies reviewed here aimed to identify only bacteria, and because the identification methodologies used relied on growth of the organisms in media and their subsequent identification. The possibilities for under-representation are three: most studies target only one phylum of organisms; not all organisms can be cultivated; and the identification of microorganisms by traditional techniques is likely to be under-representative (for example, reaching only genus level of identification). We believe that with the advance of improved sequencing methodologies (such as next-generation sequencing), new studies can provide better insights into the identification of microorganisms present on mobile phones (manuscript in preparation).

The results from this review indicate, nonetheless, that mobile phones from 24 different countries around the world harbour a diverse range of microorganisms, including several with antibiotic resistance. Considering these studies span back to 2006, it is surprising that minimal effort has been directed to developing guidelines to better manage the specific risk posed by mobile phones, in particular in health care settings. While sporadic health care standards for infection prevention and control in the use of mobile phones exist [76], to the best of our knowledge the great majority of hospitals and clinics across the world have non-existent or limited guidelines in place as well as limited training in decontaminating mobile phones. It is also important to note that patients coming in and out the health care settings also utilise their mobile phones and no guidelines are in place to address or prevent such impacts in hospitals infections. Hospital acquired microbes on patient's mobile phone could ultimately provide a pathway for infection spread to the wider community.

It was not till the rapid spread of COVID19 that the Centre for Disease Control and Prevention (CDC) introduced guidelines for cleaning and disinfecting fomites such as mobile phones (CDC Website). In the other hand, numerous past and new guidelines were detailing the core practises for hand-hygiene were published and implemented [77–79].

Further research concerning effective and efficient disinfection and sterilisation methods needs to be explored in order to prevent these devices acting as ‘Trojan horses’ (a term proposed by Goldblatt et al., 2007 [20]) and bypassing hand-washing practises.

Moreover, additional research to investigate the role of mobile phones as microbial ‘Trojan Horses’ should be commenced as numerous health care studies have identified multi-drug resistant microorganisms

Table 1
Publications included in this review and some of their characteristics. Publications that included a comparison of two population groups were split into two rows.

Author, year	Target organism			Country	Study population					Count of taxonomic units~		
	bacteria	fungi	viruses		Health Care Workers*	Community^	Sample (no. phones)	Phones with no growth	No. isolates	Bacteria	Fungi	Virus
(Akinyemi et al., 2009) [21]	x			Nigeria		x	310	100	210	7		
(Akinyemi et al., 2009) [21]	x			Nigeria	x		90	52	38	7		
(Al-Abdalall, 2010) [22]	x	x		Saudi Arabia		x	202	0	823	8	8	
(AL-Harmoosh et al., 2017) [23]	x			Iraq		x	300	42	363	10		
(Amadi et al., 2013) [24]	x CLI			Nigeria	x		50	7	43	6		
(Arora et al., 2009) [25]	x CLI			India	x		160	95	88	9		
(Arulomozhi et al., 2014) [26]	x	x		India	x		50	12	41	5	1	
(Ayalew et al., 2019) [27]	x			Ethiopia	x		165	67	103	5		
(Badr et al., 2012) [28]	x			Egypt	x		30	2	32	6		
(Bhat, 2011) [29]	x			India	x		204	3	202	11		
(Bhoonderowa et al., 2014) [30]	x			Mauritius		x	192	16	236	3		
(Bodena et al., 2019) [31]	x			Ethiopia	x		226	13	216	7		
(Brady et al., 2006) [32]	x	reported		United Kingdom	x		102	17	113	19	1	
(Chaka et al., 2016) [33]	x			Ethiopia	x		100	38	79	8		
(Chawla et al., 2009) [34]	x			India	x		40	3	77	6	2	
(Chawla et al., 2009) [34]	x			India		x	40	3	61	6	2	
(Datta et al., 2009) [35]	x			India	x		200	56	144	5		
(Datta et al., 2009) [35]	x			India		x	50	45	5	1		
(Elkholy et al., 2010) [36]	x	reported		Egypt	x		136	5	209	6	2	
(Foong et al., 2015) [37]	x			Australia	x		266	98	209	6		
(Furuhata et al., 2016) [38]	*Staphylococcus* spp. only			Japan		x	319	218	101	15		
(Goldblatt et al., 2007) [20]	reported	reported		Israel and the USA	x		400	296	85	7	1	
(Gunasekara et al., 2009) [39]	reported			Sri Lanka	x		40	12	28	3		
(Hassan & Ismail, 2014) [40]	x			Egypt	x		91	24	67	8		
(Heyba et al., 2015) [41]	reported	reported		Kuwait	x		213	56	255	13	1	
(Jagadeesan et al., 2013) [42]	x			India		x	100	2	98	8		
(Jamaluddeen et al., 2016) [43]	x			India	x		100	12	93	6		
(Jayalakshmi et al., 2008) [44]	x CLI			India	x		144	12	229	10		
(Karabay et al., 2007) [45]	x			Turkey	x		122	11	111	8		
(Karkee et al., 2017) [46]	x			Nepal	x		124	35	104	8		
(Khivsara et a., 2006) [47]	*Staphylococcus aureus* only			India	x		30	15	15	3		
(Kilic et al., 2009) [48]	x			Pakistan	x		94	12	70	6	1	
(Kordecka et al., 2016) [49]		*Candida* spp. only		Poland		x	175	less than 30%	336		4	
(Koroglu et al., 2015) [50]	x	x		Turkey	x		76 (170 swabs)	not specified	422	14	2	
(Koroglu et al., 2015) [50]	x	x		Turkey		x	129 (274 swabs)	not specified	751	14	2	
(Kotris et al., 2017) [51]	x			Croatia	x		110	25	112	7		
(Kumar et al., 2014) [52]	x			Saudi Arabia	x		106	17	89	7		
(Lee et al., 2013) [53]	x CLI			South Korea	x		203	145	60	6		
(Mohammadi-Sichani, 2011) [54]	x			Iran	x		150	9	273	15		
(Nwankwo et al., 2014) [55]	x			Nigeria	x		56	3	97	9		
(Nwankwo et al., 2014) [55]	x			Nigeria		x	56	10	57	9		
(Afolabi et al., 2015) [56]	reported	reported		Nigeria	x		180	55	125	8	1	
(Pal et al., 2015) [57]	x			India	x		132	0	335	8		
(Pal et al., 2015) [57]	x			India		x	154	15	291	8		
(Pal et al., 2015) [57]	x			India		x	100	55	59	8		
(Pandey et al., 2010) [58]	x	reported		India	x		126	66	60	6		
(Pillet et al., 2016) [59]			x viral RNA	France	x		131	78	n/a			5
(Rahangdale et al., 2014) [60]	x			India		x	200	155	45	5		
(Ramesh et al., 2008) [61]	reported	reported		Barbados	x		101	56	47	8	1	
(Rana et al., 2014) [62]	x			India	x		50	35	16	4		
(Rana et al., 2014) [62]	x			India		x	50	26	24	4		

(*continued on next page*)

Table 1 (*continued*)

Author, year	Target organism			Country	Study population		Sample (no. phones)	Phones with no growth	No. isolates	Count of taxonomic units~		
	bacteria	fungi	viruses		Health Care Workers*	Community^				Bacteria	Fungi	Virus
(Selim & Abaza, 2015) [63]	x	reported		Egypt	x		40	0	99	9	1	
(Sepehri, 2009) [64]	x	reported		Iran	x		150	102	50	4	1	
(Shahaby et al., 2012) [65]	x			Egypt		x	88	70	146	7		
(Shahaby et al., 2012) [65]	x			Egypt	x		13	8	75	7		
(Shakthivel et al., 2017) [66]	x			India	x		50	5	45	6		
(Singh et al., 2010) [67]	x			India	x		50	1	91	8		
(Smibert et al., 2018) [68]	x CLI			Australia	x		55	51	4	2		
(Tagoe et al., 2011) [69]	x			Ghana		x	100	0	100	11		
(Tambe & Pai, 2012) [70]	x	x		India	x		120	21	141	11	4	
(Tambekar et al., 2008) [71]	x			India	x		75	4	90	8		
(Trivedi et al., 2018) [72]	x			India	x		150	80	81	8		
(Ulger et al., 2009) [73]	x	reported		Turkey	x		200	11	307	6	2	
(Walia et al., 2014) [74]	x			India	x		300	100	277	6		
(Zakai et al., 2016) [75]	x			Saudi Arabia		x	105	4	111	5		

CLI: only clinically important organisms listed in the original paper.
reported' means that organisms in this category were presented in results despite not being the target of the study.
*Health Care Workers includes doctors, nurses, interns, and dental health workers.
^Community includes general population, students and lecturers.
~ A taxonomic unit is each organism listed as a separate unit in the original report (e.g. *S. aureus*, MRSA, Yeasts, and Acinetobacter sp. are a taxonomic unit each).

when compared to community studies. Research investigating the presence and transmission of drug resistant microbes will provide insight into whether mobile devices enable and aid their development and spread.

There is a diverse range of bacterial species that are frequently identified and isolated from mobile phones in both the health care and community settings. However, when compared to bacterial species, the range of fungi and viruses reported was not as extensive, which we believe is a consequence of researchers not looking for them, rather than them not being present. Of note, our research team has been investigating the presence of viral genomes on the surface of mobile phones with findings including human and animal viruses (manuscript in preparation).

When comparing the microbiome profiles between the community and health care settings, some microorganisms appeared more frequently in health care settings. One example is MRSA, which was present in almost double the proportion of studies in health care settings (detected in 51.1% of studies), compared to community settings (27.8%). In health care settings, the presence of MRSA on the surface of phones is concerning as the nature of the microbes found on such fomites may have detrimental roles in nosocomial diseases and spread of undesirable micro-organisms to immune-compromised individuals. Additionally, it is important to highlight that such devices are rarely subject to decontamination while being commonly used in hospitals, clinics and other health care related settings. First line medical staff fighting actively working as part of the COVID-19 pandemic response have been routinely exposed and contaminated with SARS-CoV2 virus. COVID-19 pandemic images broadcasted worldwide through different forms of media have regularly shown examples of hospital staff with personal protective equipment holding and using their mobile phones (with and without) gloves on. It is our opinion and hypothesis, that mobile phones are most likely contributing to the spread of SARS-CoV2 within different professional settings including hospitals and may play a significant role in viral propagation within the community.

We restrained from making too many comparisons and any statistical analyses since aims and methodologies were very different between studies, but we invite readers to look closely at the data provided as an appendix.

Mobile phones are touched on average 3 h per day [80]. Furthermore, a 2016 study [81] stated that users can touch their phones up to 2617 times per day.

This poses a health concern to the wider community as this review has shown that mobile phones are contaminated by a plethora of microorganisms including bacteria and viruses.

The authors, strongly suggest that national public health authorities actively advise worldwide governments and communities to implement measures for all users to disinfect mobile phones. The CDC has initiated this with a focus on COVID19 bit it needs to be presented more broadly to cover any pathogenic organisms. This should be coupled with the global public health campaign promoting the benefits of hand washing which could be drastically suboptimal if we consider the regular interaction of washed hands with micro silly contaminated mobile phones. Mobile phones are potential 'Trojan horses' for microbes that each user accommodates, carries and potentially transfers to the community and workplaces enabling contagion to occur.

The 2019 SARS-CoV-2 outbreak responsible for COVID-19 epidemy has presented an unprecedented high velocity of virus spread. While the ss + RNA enveloped virus can be destroyed by hand washing with appropriate disinfectants, mobile phones once touched can re-contaminate the user and pose a biothreat risk for infection spread globally. They can contribute to crossing all borders especially as they are omnipresent in modern transport, and human-to-human social contact scenarios. Mobile phones can also contribute to the contamination and genesis of additional secondary fomites (door knobs, airport self-check in stations, bus polls, ATM monitors, lift buttons, etc … Microbes can live on fomites from hours to days to weeks and then most likely

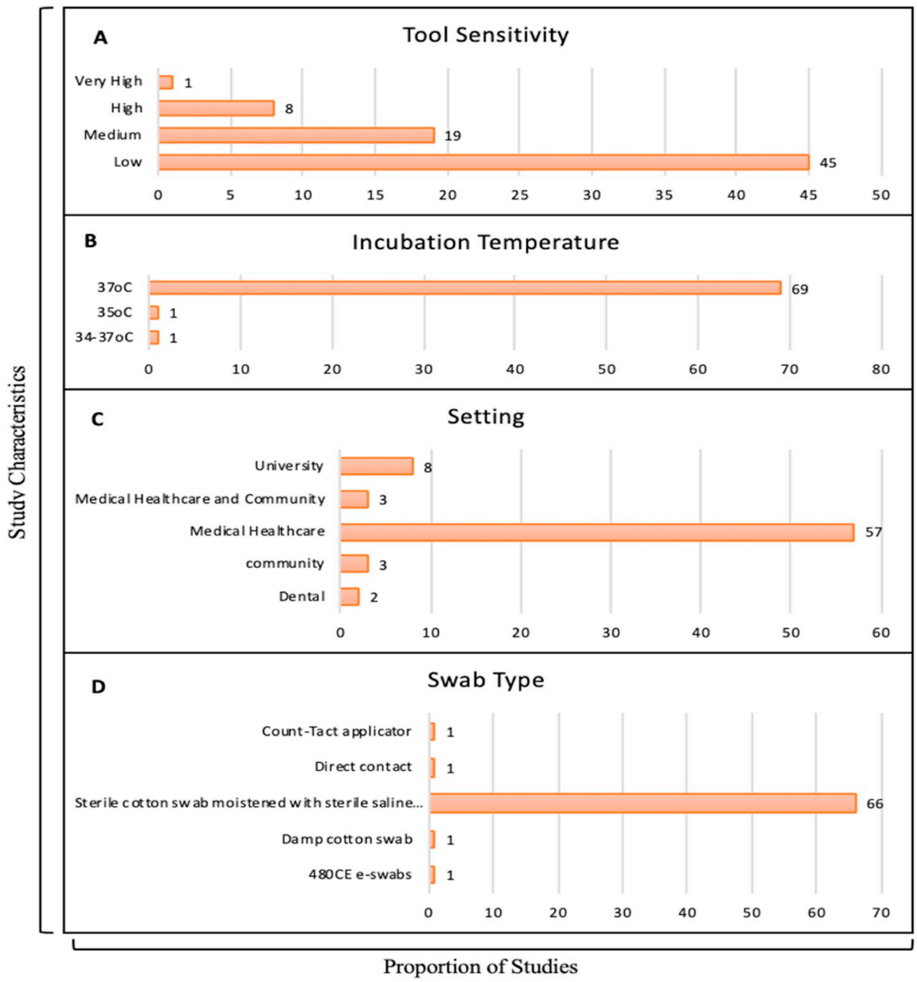

Fig. 2. Study design characteristic data plot against number of studies illustrating tool sensitivity, incubation temperature, swab type and setting. Four sampling techniques were used: sterile cotton swab moistened with sterile saline solution (n = 53 studies), Count-Tact applicator (n = 1), direct phone contact to media (n = 1) and 480CE e-swabs (n = 1). In terms of the sensitivity tools used for microorganism identification, 61% of the studies used low sensitivity identification tools (n = 34), 27% used medium sensitivity (n = 15), 11% used high sensitivity (n = 6) and one study used very high sensitivity identification tools (2%). 96% of studies used an incubation temperature of 37 °C (n = 52), two studies did not use incubation methods to culture isolates obtained from swab samples of mobile phones.

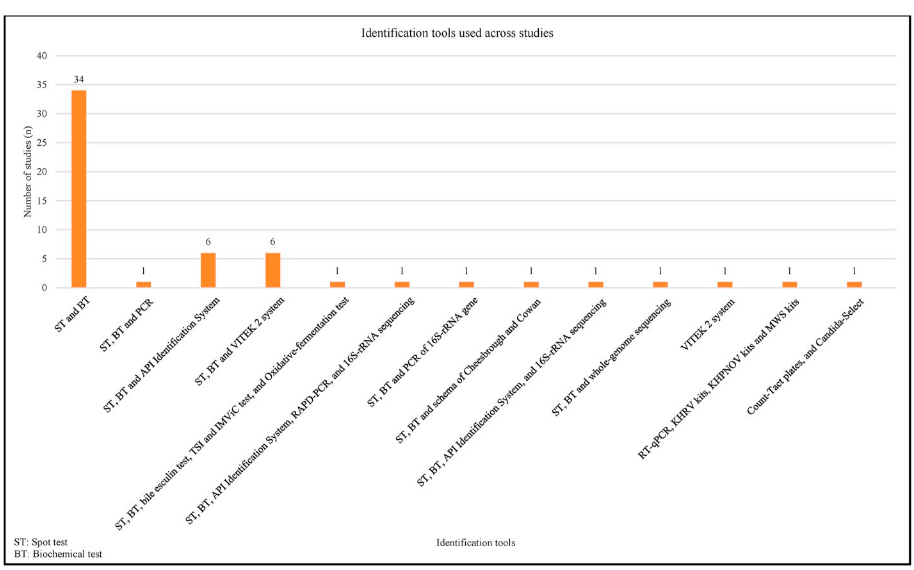

Fig. 3. Microbiology identification tools used to characterise microbes across all studies.

contribute to microbial propagation and infections.

Fundamentally, mobile phones harbour a diverse range of species of microorganisms including antibiotic-resistant organisms which pose a risk to human health, both in the health care system and the broader community. We believe that mobile phones are causing a large and largely unacknowledged impact in health care, community safety, with resulting unnecessary economic losses.

4.1. Special author's recommendation of the current COVID-19 pandemic

In view of the results synthesized and elicited by our review, we propose that mobile phones should be tested in order to identify and

Table 2
Studies and subsets of studies, totalling 65 population samples, were split into health care setting and community setting for comparison of results.

Population group	datasets	countries	phones sampled			swabs sampledˆ			isolates			taxonomic units∼			Contaminated phones (%)[a]
			total	average	median	total	average	median	total	average	median	total	average	median	
Community	18	10	2670	148	117	2815	156	130	3817	212	106	73	8	7	68%
Health care workers	47	19	5801	123	110	5895	125	120	5601	119	90	100	9	8	68%
Complete dataset	65	24	8471	130	110	8710	134	120	9418	145	97	134	9	8	68%

ˆone study swabbed more than once for each mobile phone [50].
∼ These values should be considered indicative only dur to the lack of taxonomic refinement in some instances.
[a] Calculation excludes one study from each population type that did not provide this value [50].

Table 3
Species and taxonomic units highlighted for being isolated at a rate equal or higher than 5% of swabs, and for being reported in 25% or more of the studies in that population group. *Candida* species are presented despite not reaching 5% due to their likely under-identification.

Taxonomic unit	Community				Heath Care Workers			
	no. isolates	%	no. studies	%	no. isolates	%	no. studies	%
Acinetobacter sp.	49	1.7%	3	16.7%	142	2.4%	16	34.0%
Bacillus sp.	99	3.5%	5	27.8%	295	5.0%	20	42.6%
CoNS	762	27.1%	11	61.1%	1964	33.3%	31	66.0%
Escherichia coli	104	3.7%	10	55.6%	163	2.8%	26	55.3%
Klebsiella pneumoniae	41	1.5%	5	27.8%	83	1.4%	12	25.5%
Micrococcus sp.	148	5.3%	4	22.2%	192	3.3%	13	27.7%
Pseudomonas aeruginosa	83	2.9%	6	33.3%	97	1.6%	13	27.7%
Pseudomonas sp.	4	0.1%	1	5.6%	108	1.8%	13	27.7%
Staphylococcus aureus	883	31.4%	13	72.2%	1111	18.8%	43	91.5%
MSSA (Methicillin-sensitive S. aureus)	129	4.6%	4	22.2%	316	5.4%	16	34.0%
MRSA (Methicillin-resistant S. aureus)	31	1.1%	5	27.8%	219	3.7%	24	51.1%
Staphylococcus epidermidis	218	7.7%	4	22.2%	195	3.3%	6	12.8%
Candida albicans	114	4.0%	1	5.6%	–	–	–	–
Candida gabrata	132	4.7%	1	5.6%	–	–	–	–

validate if pathogenic microbes responsible for outbreaks, epidemics, and pandemics such as the current COVID-19 pandemic are present on those fomites.

We hypothesise that the currently spreading novel coronavirus COVID-19 is present on mobile phones (and other devices and other fomites) owned by humans positive to the virus. Unlike hands, these devices are not regularly washed, and since they are neglected from a biosecurity perspective, they can act as Trojan horses and propagate undesirable invisible pathogens including viruses such as the flu and SARS-CoV-2. It is hoped that this paper will raise awareness to authorities and the scientific community alike to consider this hypothesis seriously, and to develop and implement protocols to assist in mitigating the risk of spreading microbes, such as viruses, in both health-care, passenger air/sea travels, and the community at large.

Our strong recommendation is that phones should be decontaminated/disinfected daily, particularly in health care systems. The regular decontamination must be based around interventions that are proven efficient and gentle enough to not erode the phone screen's protective surface. Interestingly, the CDC has just recently published information regarding cleaning and disinfecting high touch surfaces (including mobile phones) at home when someone is sick. We salute this initial steps of public awareness of such fomites but as trojan horses contaminated platforms, such awareness need to become a global decontamination campaign complementing handwashing. While the CDC advises at home sick individuals to follow manufacturer's instructions, they also advise, in case of no guidance, to use alcohol-based wipes containing at least 70% alcohol [82]. Of note, a certain amount of ultraviolet based technology devices are marketed but their affirmative efficacy need to be tested regarding their microbicidal capacity.

These decontamination operations must be implemented in the community, in key servicing industries, by food handlers and individuals serving in buffets, kindergarten, age-cares, cruises, airline/airport (biosecurity measures needed), hospitals, dentists and the overall community during an epidemic or pandemic like the current COVID-19 pandemic.

Declaration of competing interest

No conflicts of interest to declare.

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