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Microbial Contamination on Hospital Lift Buttons: A Metagenomic Perspective

Izzati Muhammad[1], Niza Shamsuddin[1], Raja Noor Zaliha Raja Abd Rahman[2], Norhidayah Kamarudin[3], Norsyuhada Alias[1,*]

[1] Department of Biomedical Science, Kulliyyah of Allied Health Sciences, International Islamic University Malaysia, Kuantan, Pahang, Malaysia
[2] Department of Microbiology, Enzyme and Microbial Technology Research Centre, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia, Serdang, Selangor, Malaysia
[3] Kulliyyah of Medicine, International Islamic University Malaysia, Kuantan, Pahang, Malaysia

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ABSTRACT

Lift buttons in the hospitals, recognised as high-touch fomites, contributed to the transmission of hospital-acquired infections (HAIs) due to frequent contact by individuals from diverse backgrounds and professions. Despite scheduled cleaning with dedicated chemicals, concerns remained regarding the persistence of microbial contamination on these surfaces, especially in Southeast Asia healthcare settings. This study aimed to explore the prevalence of microbial contamination and its diversity at a university teaching hospital (TH) in Pahang, Malaysia, during the COVID-19 pandemic. A purposive swab sampling approach was employed, with the sample collected three times at two-week intervals. Microbial prevalence and diversity were assessed using the standard plate count method and metagenomic analysis. Statistical analysis, including ANOVA and Bonferroni tests, were performed at a significance level of alpha value of less or equal to 0.05. The study revealed a significant prevalence of microbial contamination on interior and exterior lift buttons, reaching 44.4 %. An important difference was observed in the mean bacterial load between horizontal and vertical panel lift buttons, with horizontal panels contributing more to the overall microbial load ($p < 0.05$). Additionally, a significant relationship was found between the contamination levels of exterior lift button sets and the selected floors ($p < 0.05$). Metagenomic analysis identified Firmicutes as the dominant phylum, with *Bacillus* and *Meyerozyma* as the most prevalent genera. The KEGG pathway analysis emphasised the importance of ABC transporters and two-component pathways, with enriched vital genes involved in iron acquisition, energy utilisation, cell motility and drug resistance. These findings underscored the prevalence of microbial contamination on hospital lift buttons and their ability to adapt to challenging environmental conditions. Given the potential of lift buttons to harbour pathogenic microbes, it was imperative to implement effective infection control measures to minimise the risk of HAIs transmission. Future studies should broaden the scope of the research and explore diverse regional hospitals to understand the microbial contamination pattern on the lift buttons.

* *Corresponding author.*
E-mail address: norsyuhada_alias@iium.edu.my

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1. Introduction

Healthcare centres, such as hospitals, are considered environments prone to contamination from human activity, environmental factors and other living organisms. Various hospital areas, including the operation theatre, wards and lifts, have been identified as potential reservoirs for microbial growth [1-3]. Lifts, as essential infrastructure in hospitals, are frequently used by individuals from diverse backgrounds and professions. The human bodily fluids, including saliva, mucous, blood, sweat and respiratory droplets, were potential vectors that could carry contaminants, thus creating a risk of microbial contamination [4,5].

The contamination of these surfaces posed a significant concern, as it could contribute to the emergence of hospital-acquired infections (HAIs). The rise of HAIs poses a global health challenge due to affecting one in ten patients with increasing mortality rates, mainly when caused by antimicrobial resistance (AMR) pathogens [6]. Although frequent cleaning and sanitisation were employed in conjunction with this problem, some pathogens survived these processes [7]. The economic burden of HAIs is substantial, with increased treatment costs, prolonged treatment duration, and frequent physician visits contributing to higher expenditures for both patients and the country [8].

Numerous studies have linked communal surfaces within hospitals to the transmission of HAIs. *Staphylococcus aureus,* a well-known pathogen associated with HAIs, was discovered from hospital lift buttons in Iran [9]. Similarly, researchers in China had isolated *Acinetobacter baumannii*, another major contributor to HAIs, exhibiting carbapenem resistance [10]. Despite their natural habitats, *S. aureus,* usually associated with humans, and *A. baumannii,* commonly found in soil and water, have emerged as significant causes of HAIs. The presence of antimicrobial resistance genes within the hospital microbiome underscored the dire need to understand the complex microbial community structure and its potential impact on resident health.

While noteworthy research has been conducted on HAIs, a dearth of information remains regarding the role of fomites like lift buttons in their transmission, particularly within Southeast Asian healthcare settings. It was important to note that there was also a lack of comprehensive studies on microbial contamination in these areas, thus highlighting the need for a longitudinal study to assess changes on these surfaces over time. This study explored the prevalence of microbial contamination and the underlying genetic determinants on lift buttons at a university teaching hospital (TH) in Pahang, Malaysia. This location was selected due to Malaysia's ranking as the fourth-highest country in Southeast Asia for HAIs prevalence and its ideal population size [11,12]. The study aimed to understand microbes' prevalence, dominance patterns and survival strategies on these surfaces. Addressing these topics would provide a valuable perception of the current state of microbial contamination, giving insights into the steps to improve infection control measures in healthcare settings. In addition, this research represented a crucial initial step in elucidating the potential risks associated with lift button contamination and justifying evidence-based strategies to mitigate these risks.

2. Methodology

2.1 Study Setting

The TH, a healthcare institution serving as a tertiary referral centre in a coastal urban area of Pahang, boasted over 350 beds for inpatients. Comprising over 63 sub-clinics, departments and units, the hospital catered to a diverse patient population from urban and rural communities. Its

comprehensive range of healthcare services, with the support of 133 consultants and 70 sub-specialists, extended from primary care to advanced, specialised treatments and outpatient services.

The hospital participating in this study maintained a rigorous cleaning protocol throughout the COVID-19 pandemic. This protocol included daily cleaning, weekly decontamination and incident-specific decontamination. Daily cleaning involved two rounds, before and after patient visiting hour, with multipurpose detergent, where the cleaning staff would clean communal surfaces and wards. Weekly decontamination was conducted on the weekends, while incident-specific decontamination was implemented in response to specific events. Chlorine-based disinfectant, known for its broad-spectrum bactericidal properties, was used for weekly decontamination and incident-specific cleaning. The selection and concentration of chemicals and implementation of these practices followed the Ministry of Health Malaysia (MOH) guidelines for surface cleaning [13].

2.2 Sampling Procedure

This study aimed to assess the microbial contamination of hospital lift buttons under specific conditions. The lifts eligible for sampling were accessible to all patient floors, capable of accommodating standard hospital beds, and not involved in COVID-19-related transport. The areas locating the lifts were systematically selected based on documented contamination reports, including main entrances (ME), operation theatres (OT), intensive care units (ICU), paediatric wards (PW) and general wards (GW) [1,3].

The sampling method was adapted from [14]. It utilised a cotton swab moistened with 1 mL of 0.1 % peptone water (Merck, Germany) to swab a 14 cm^2 area for 10 seconds. The control samples were collected using the same procedure after disinfecting lift buttons with 70 % ethanol. The sample collection was repeated three times at two-week intervals during the COVID-19 Movement Control Order (March-April 2021), with 54 samples obtained from each collection, as observed in Figure 1 [15]. The samples were kept on ice until further analysis in the laboratory.

2.3 Standard Plate Count

An amount of 50 µL of the samples was evenly spread on nutrient agar plates and incubated at 37°C for 24-48 hours [16]. The calculation of bacteria prevalence and colony forming unit per millilitre (CFU/mL) followed the formula suggested by [17] and [18], respectively. The statistical analysis, including analysis of variance (ANOVA) and Bonferroni test, was conducted using (SPSS) software version 27.0, with statistical significance set at an alpha level of 0.05 or less.

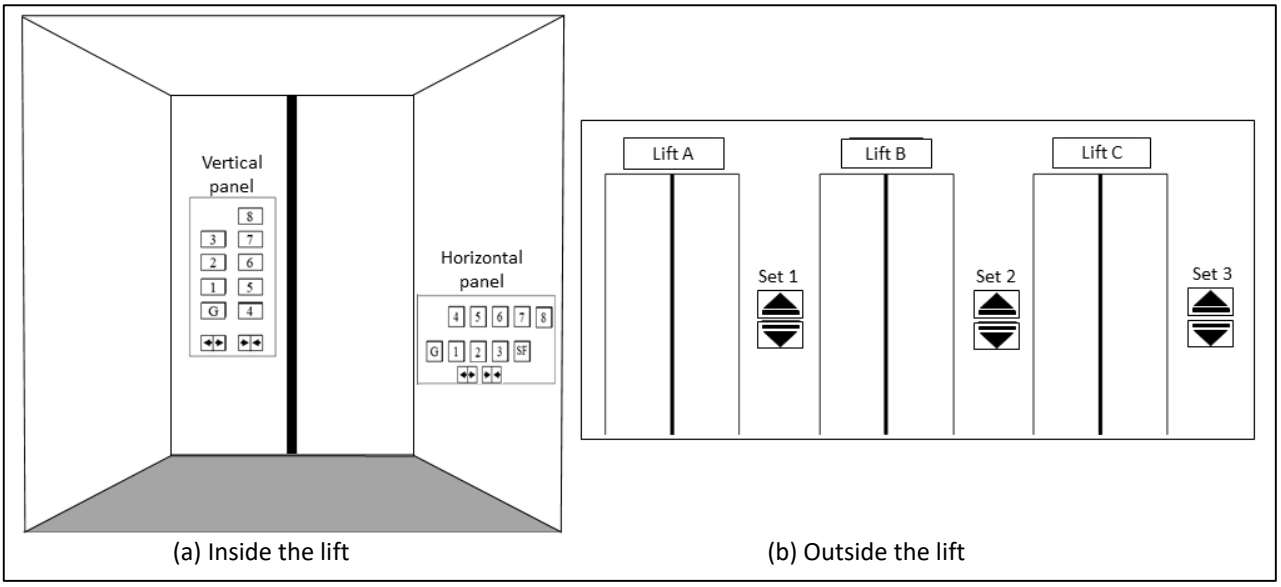

Fig. 1. Position of sampled lift buttons. (a) Lift interior and (b) Exterior lift buttons [15]

2.4 Metagenomic Analysis

Approximately 10 µL of each sample was pooled into a tube containing 10 mL tryptic soy broth (Merck, Germany) and incubated at 37°C with aeration of 200 rpm for 24-40 hours [19]. The sample was then pelleted down at 13,100 x *g* for 5 minutes, and the supernatant was removed. The analysis of the genomic DNA of the sample was performed using DNeasy® UltraClean® Microbial Kit (Qiagen, Germany) according to the provided manual. The extracted DNA was evaluated for its quality and quantity through gel electrophoresis of 1 % agarose gel (Vivantis, Malaysia) and spectrophotometer readings.

The DNA sample, with a concentration of 45 ng/µL, proceeded with the sequencing process using the Oxford Nanopore Technologies (ONT) MiNION flowcell (Oxford Nanopore, United Kingdom) for long reads. Guppy version 4.4.1 software was used to base-called the sequencing data in high accuracy mode. The reads were filtered to retain only those with a quality score of seven or higher and then were assembled into contigs using SPAdes with default parameters [20].

The analysis and annotation of the sequence were done by uploading the file in FASTQ format and its metadata to the Metagenomic Rapid Annotations using the Subsystems Technology (MG-RAST) server [21]. Similarity searches of the reads were employed against reference databases like RefSeq and KO with default settings to assign taxonomic identities. The abundance of each identified taxon was then calculated as a percentage based on the number of reads assigned to that taxon compared to the total number of reads obtained.

3. Results and Discussion

3.1 Implication of Microbial Load and Ecology on Lift Buttons to Human Health

The prevalence of microbes on the lift buttons was inevitable since the lifts were the leading vertical transportation in a hospital. A prevalence of 44.4 % was determined from the 54 sampled lift buttons of TH that yielded 104 bacterial growths. A total of 620 CFU/mL was isolated from the interior lift buttons, as seen in Table 1. The highest colony count was contributed by floor 3, followed by floor 5.

Table 1
Quantification of contaminants on lift buttons throughout various floors in a teaching hospital

Lift Details			Average colony forming unit per mL (CFU/mL ± SD)					
			Floor G	Floor 3	Floor 5	Floor 8	Floor 9	Total
Interior lift button	Lift A	Vertical panel	10 ± 14.1	40 ± 28.3	30 ± 42.4	20 ± 28.3	10 ± 14.1	260 ± 17.1
		Horizontal panel	0 ± 0.0	50 ± 70.7	30 ± 42.4	50 ± 14.1	20 ± 28.3	
	Lift B*	Vertical panel	10 ± 14.1	10 ± 14.1	0 ± 0.0	0 ± 0.0	0 ± 0.0	110 ± 12.0
		Horizontal panel	10 ± 14.1	10 ± 14.1	40 ± 0.0	10 ± 14.1	20 ± 0.0	
	Lift C	Vertical panel	10 ± 14.1	0 ± 0.0	10 ± 14.1	30 ± 42.4	0 ± 0.0	250 ± 35.0
		Horizontal panel	20 ± 28.3	10 ± 14.1	60 ± 28.3	110 ± 155.6	0 ± 0.0	
Exterior lift button*	Set 1	Up button	170 ± 212.1	230 ± 268.7	60 ± 84.9	10 ± 14.1	NA	970 ± 137.0
		Down button	NA	400 ± 565.7	30 ± 42.4	30 ± 42.4	40 ± 28.3	
	Set 2	Up button	20 ± 28.3	10 ± 14.1	10 ± 14.1	0 ± 0.0	NA	150 ± 37.6
		Down button	NA	0 ± 0.0	110 ± 127.3	0 ± 0.0	0 ± 0.0	
	Set 3	Up button	0 ± 0.0	0 ± 0.0	40 ± 56.6	10 ± 14.1	NA	330 ± 89.5
		Down button	NA	0 ± 0.0	260 ± 367.7	0 ± 0.0	20 ± 28.3	
Total			250 ± 53.8	760 ± 124.0	680 ± 70.4	270 ± 31.7	110 ± 13.9	2070 ± 72.8

Note: * = Significance difference ($p < 0.05$); SD = standard deviation; NA = data not available

The absence of pre-pandemic data on fomite contamination in Malaysian hospitals limited direct comparisons to pre-pandemic conditions. Consequently, the findings of this study were compared to those from hospitals in other countries. The microbial load in this study was lower than pre-pandemic research in Kenya and Nepal private and teaching hospitals, which demonstrated a prevalence of up to 66 % [22,23]. A study conducted in China hospital wards during the pandemic showed a bacterial prevalence of 56 % [24]. The reducing trend of microbial load from pre-pandemic to pandemic suggested significant improvement in addressing contaminants.

One of the main changes during the pandemic was the cleaning and sanitisation routine. While the hospital adhered to the MOH guideline for cleaning and disinfection protocol [13], the details regarding the contact time of the disinfectant and the extent of surface coverage were not provided. Generally, the cleaning regularity usually followed the risk location, where moderate-risk areas required a daily cleaning while low-risk areas needed weekly cleaning [25]. However, the housekeeping schedule during the COVID-19 pandemic changed all areas to daily cleaning and decontamination during the weekend [2,15]. As a result, the stringent cleaning routine and other housekeeping measures during the pandemic helped reduce hospital bacterial load by approximately 10-20 % compared to pre-pandemic data. Innovative approaches could be taken to further reduce the risk of contamination by integrating a voice recognition system and enforcing self-cleaning lift buttons to minimise skin contact and accumulation of contaminants [26,27].

Although no statistically significant differences were observed in the mean bacterial load across different floors ($p > 0.05$), there was significance in the other panels of the lift buttons based on ANOVA analysis. Through confirmation with the post-hoc test, the horizontal panel in lift B contributed more to the lift buttons' microbial load than the vertical panel ($p < 0.05$). The horizontal panel lift button was placed in a specific location to facilitate disabled lift users [28]. With a limited number of lift users at one time during the pandemic, the higher usage of the horizontal panel in the lift reflected the subconscious behaviour of lift users.

The exterior lift buttons of TH exhibited a higher total CFU/mL than the interior lift buttons. Lift button set 1 had a higher microbial load than other sets, but the mean counts were insignificant. However, there was a significance in the means between the selected floors of exterior lift button with the lift button sets ($p < 0.05$). The lift buttons outside the lifts in this study were located on floors with relative departments, with some contributing a higher number of bacteria due to more visitors and patients [25]. However, the sterility of lift buttons in these locations should be addressed since a higher number of visitors and patients means a higher risk of getting HAIs.

3.2 Taxonomic Profiling of the Microbial Community on Lift Buttons

Metagenomic analysis of the TH sample yielded approximately 2,683,083 reads, representing an estimated 1,100 strain based on the rarefaction curve formed from the RefSeq database. The dominant domain identified was Bacteria. Figure 2 depicts each taxon's top strain with the highest abundance percentage.

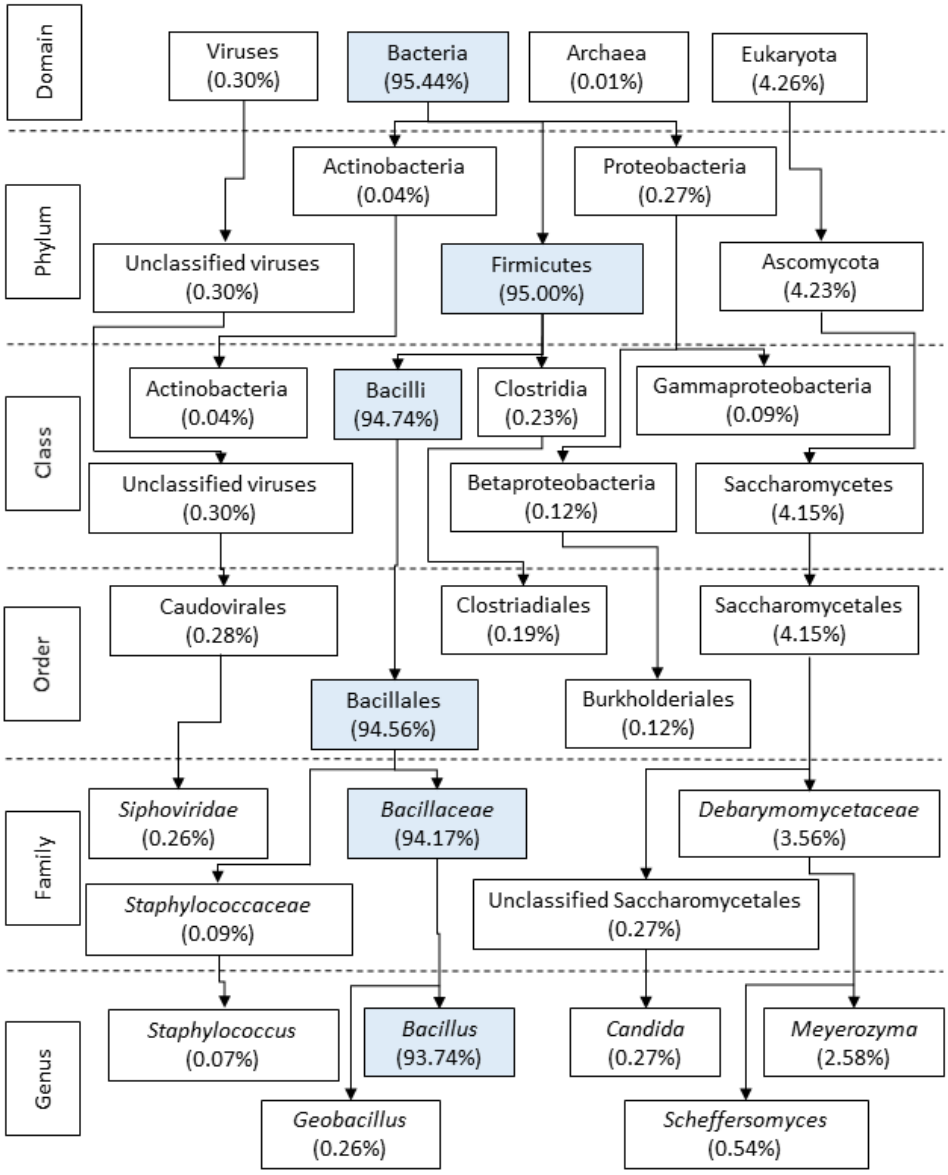

Fig. 2. Taxonomic abundance across various hierarchies in the TH metagenome, with the highest abundance highlighted in the blue box

Firmicutes was the most abundant at the phylum level, followed by Ascomycota and Proteobacteria. Bacilli was the predominant class, with Saccharomycetes as the second most abundant. Clostridia, Gammaproteobacteria, Betaproteobacteria and unclassified viruses constituted less than 0.74 % of the metagenome. Bacillales, an order within the Bacilli class, was the most prevalent order in the TH metagenome. *Bacillaceae* and *Debarymomycetaceae* were the most abundant families, with other families contributing less than 0.80 %. At the genus level, *Bacillus* dominated, accounting for nearly 94 % of the identified strain. *Meyerozyma* was the second most abundant genus, followed by *Scheffersomyces, Candida* and other less prevalent genera, as illustrated in Figure 3. Genera other than *Bacillus* and *Meyerozyma* total up to 2.74 %, with an average of 0.16 % for each genus. The one labelled as others (0.90 %) consisted of strains with an abundance of less than 0.03 %.

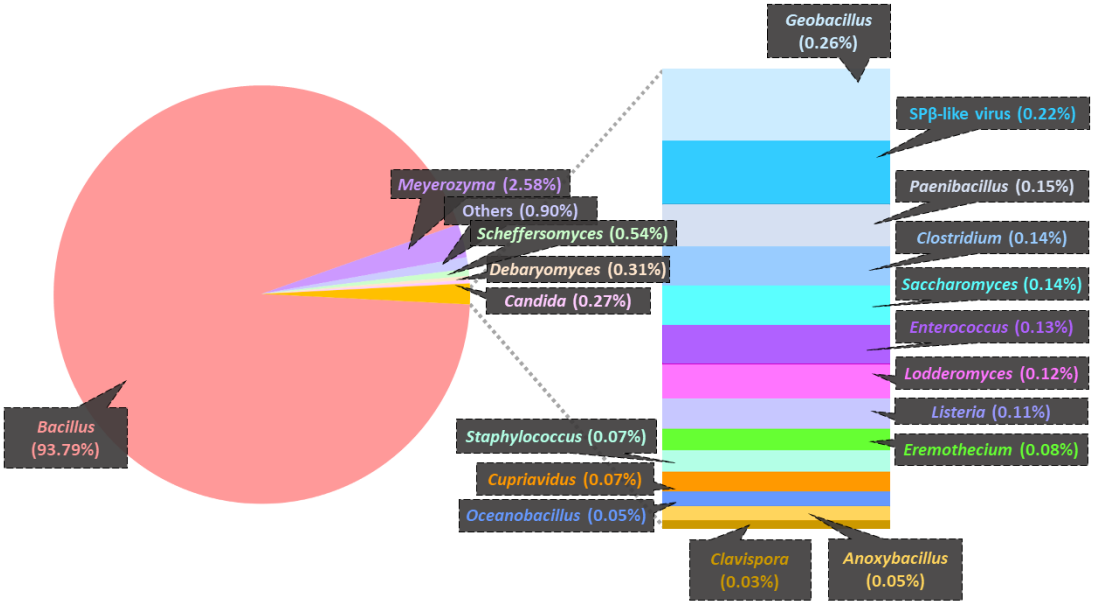

Fig. 3. Taxonomic data of the genus level in the TH metagenome

The presence of a diverse microbial community on lift buttons reflected the current state of this fomite. *Bacillus,* the most dominant genus in this sampling site and commonly originated from the soil and water, was found on lift buttons inside the hospital [29]. The distance of these two sources suggested an indirect transmission of *Bacillus* from outside the hospital into the building through a vector. However, the potential of this bacteria originating from humans existed since some researchers reported that *Bacillus* was identified as a normal human microflora [29]. Moreover, *Bacillus* was recognised as a prevalent bacteria on fomites, increasing the risk of it causing HAIs in immunodeficient people [30]. The ability of *Bacillus* to form endospores allowed it to survive against disinfectant and low-humidity environments [31].

The second predominant genus in TH, *Meyerozyma*, was previously identified from blood samples of patients with HAIs. The presence of *Meyerozyma* from lift buttons was speculated to be transmitted from infected human skin, mouth, throat and other cutaneous origin [32]. However, there was no report on the original reservoir of this fungi, making it difficult to pinpoint the trustworthy transmission source. Interestingly, *Scheffersomyces*, commonly used as xylose fermenters in the bioethanol industry, was isolated from the lift buttons [33]. This yeast usually occupies a xylose-rich habitat, like rotting wood and the presence of *Scheffersomyces* on the lift buttons could be due to reproductive-spore dissemination [34]. The appearance of diverse microbes on the lift buttons was concerning since it became a risk not limited to patients and visitors.

The microbial communities identified on the lift buttons in this study differed vastly from those reported in studies conducted in Kenya and Brazil [23,35]. These studies primarily isolated common hospital contaminants such as *Proteus* spp., *Streptococcus* spp., *Staphylococcus* spp. and *Escherichia coli* from fomites like staircase handrails and door handles [36,37]. The observed differences in microbial communities might be attributed to several factors, including variations in cleaning and disinfection protocols, environmental conditions, patient demographics and regional differences in microbial ecology. Additionally, the specific location of the lifts within the hospital, such as near patient rooms or public areas, might influence the types of microbes present. The data highlights the potential impact of specific hospital environments and activities on the microbial ecology of high-touch surfaces.

The presence of these microbes on the hospital lift buttons during the pandemic signified the effectiveness of the cleaning protocol conducted on the lift buttons. The use of chlorine-based disinfectants and multipurpose detergents was ineffective in managing the colonisation of these microbes in the hospital, as discussed by [7]. Although the ineffective cleaning routine might be due to the dirt or type of wiping cloth used [38], these microbes were still present on the lift buttons even during the stringent cleaning routine during the pandemic. The data showed the need to change the disinfectant's concentration and contact time and determine the compatibility of these disinfectant to be used on these surfaces [39].

3.3 Interpreting the Survival Mechanisms of Lift Buttons Microbiome

The KEGG pathway analysis, performed using the KO database, showed that the microbiome had several enriched metabolic pathways and functional capabilities. Most of the paths annotated by the analysed data were involved in the metabolism of the microbes, followed by the environment and genetic information processing, as displayed in Table 2. The table presented a subset of pathways the online analysis tool identified, focusing on those with the highest abundance. The total number of annotated pathways, as determined by the tool, was 940,540. Since other fields showed less pronounced results, this study did not highlight the result.

Table 2
Abundance of pathways identified through KEGG pathway analysis of the microbiome on hospital lift buttons

Functional protein			Percentage of
Field	Group	Pathway	abundance (%)
EIP	Membrane Transport	ABC transporters (PATH: ko02010)	9.8
EIP	Signal Transduction	Two-component system (PATH: ko02020)	6.9
GIP	Translation	Aminoacyl-tRNA biosynthesis (PATH: ko00970)	4.1
MET	Amino Acid Metabolism	Alanine, aspartate and glutamate metabolism (PATH: ko00250)	3.8
MET	Nucleotide Metabolism	Purine metabolism (PATH: ko00230)	3.3
MET	Amino acid metabolism	Glycine, serine and threonine metabolism (PATH: ko00260)	2.6
MET	Amino acid metabolism	Cysteine and methionine metabolism (PATH: ko00270)	2.2
EIP	Membrane transport	Phosphotransferase system (PATH: ko02060)	2.2
CEP	Cell motility	Bacterial chemotaxis (PATH: ko02030)	2.2
GIP	Replication and repair	DNA replication (PATH: ko03030)	2.1
MET	Amino acid metabolism	Valine, leucine and isoleucine degradation (PATH: ko00280)	2.0
GIP	Transcription	RNA polymerase (PATH: ko03020)	1.9
MET	Amino acid metabolism	Arginine and proline metabolism (PATH: ko00330)	1.7
MET	Energy metabolism	Oxidative phosphorylation (PATH: ko00190)	1.7
GIP	Translation	Ribosome (PATH: ko03010)	1.7

Note: EIP = Environmental Information Processing; GIP = Genetic Information Processing; MET = Metabolism; CEP = Cellular Processes; PATH = the pathway number annotated by the database

The analysis identified 187 distinct metabolic pathways, categorised into 43 groups or subsystems. Amino acid metabolism was the most prevalent pathway, accounting for 17 % of the annotated subsystems. Among the identified pathways, the ATP synthase binding cassette (ABC) transporters pathway had the most abundant annotated genes, significantly outnumbering other pathways. Given their crucial role in microbial survival within the hospital environment, the ABC pathway and the two-component systems were further analysed.

The identified pathways encompassed multiple gene sets, each exhibiting varying levels of upregulation, downregulation or unchanged expression in response to diverse internal and external stimuli. Figure 4 illustrates the distribution of enriched gene sets within the ABC transporter pathway, where the abundance reflected the number of strains harbouring specific enriched genes.

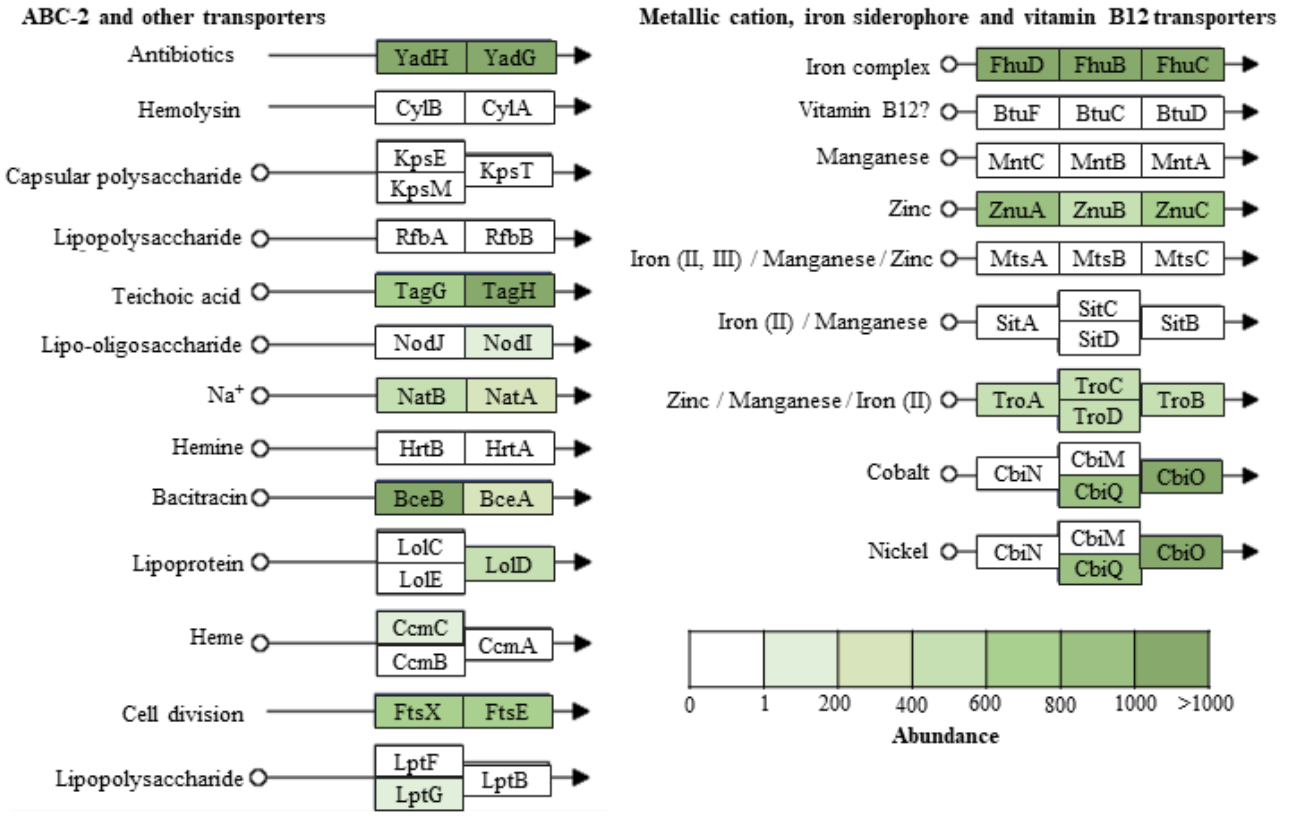

Fig. 4. Genes enriched in the ABC transporter pathway

Genes from the iron complex transport system, *fhuB, fhuD* and *fhuC*, were the most prevalent. The enrichment hierarchy was followed by *bceB, yadG, yadH* and *tagH* genes, which were involved in the antibiotics and other antimicrobial agents. The genes enriched in the iron complex, cobalt, nickel and zinc pathways were speculated to relate significantly with the microbe environment, where they were enriched to obtain iron from the environment for growth, survivability and pathogenicity [40]. Genes involved in antimicrobial agents were also enriched in the microbiome. The presence of enriched genes in the teichoic acid pathway suggested that it could be triggered by antibiotics such as bacitracin, a common tropical antibiotic ointment [41,42]. Given that the ointment could be bought without a prescription, the microbiome's response to the stimuli proved that the environment was polluted with related chemicals. Since some microbes, like *B. subtilis,* could become resistant to it, the use of over-the-counter antibiotics should be limited [43].

The two-component system comprised 11 families, with the CitB, OmpR and NarL families playing pivotal roles in the survival of the microbiome, as seen in Figure 5. The CitB family, for instance, demonstrated significant enrichment of genes involved in malate utilisation. Similarly, the NarL family exhibited an enrichment of the *narG*, which is crucial for nitrogen metabolism. The OmpR family, on the other hand, showed enrichment of genes associated with cell motility, enabling the microbiome to respond to changes in cell density.

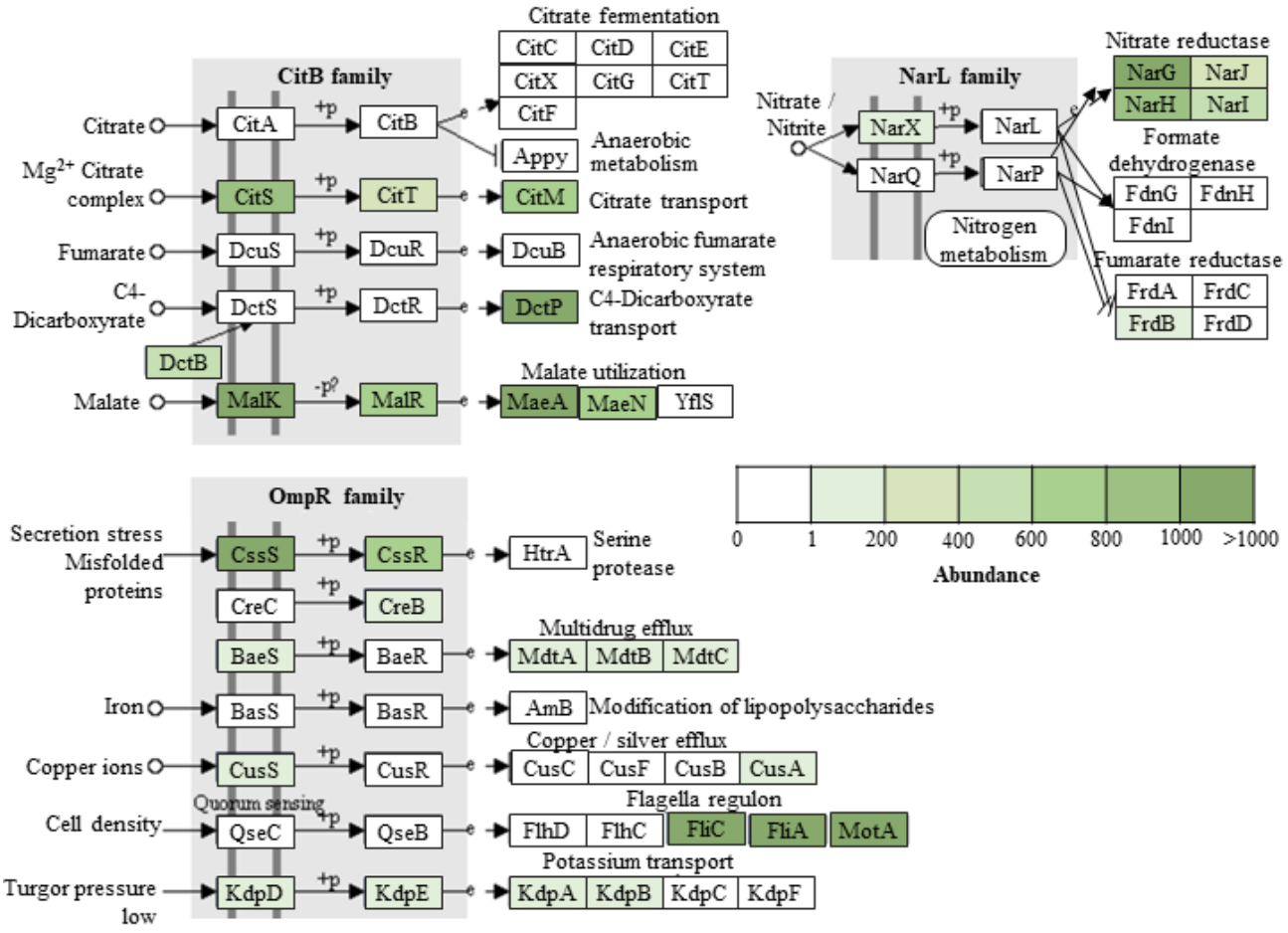

Fig. 5. Genes enriched in the two-component system pathway

Microbes obtain their essential energy requirement from the environment. In a glucose-lack environment, the microbes demonstrated adaptability by enriching genes involved in malate and nitrogen utilisation. *B. subtilis* could obtain malate from decomposing organic matter and chemical compounds. At the same time, nitrogen was taken directly from the soil and eventually used to produce energy for their survivability [44,45]. In addition, the enrichment of genes involved in cell motility demonstrated the potential growth of the microbes even on the lift buttons. The survival tenacity of the microbes was something to be concerned about since the accumulation of these microbes could increase the risk of transmission.

It was important to note that this study was conducted in a single hospital in a specific region, limiting the generalizability of the findings. The sample size was relatively small, which might have influenced the statistical power of the analysis. Additionally, the study focused on a specific period during the COVID-19 pandemic, which might have affected the microbial community and diversity. Furthermore, the lack of detailed information on the cleaning protocols and disinfectant use could

limit the results' interpretation. Further studies could address these limitations by expanding the geographical scope, increasing the sample size and incorporating a more comprehensive assessment of cleaning and disinfection practices.

4. Conclusion

In conclusion, the lift buttons in TH exhibited intriguing findings that illuminated the diversity of microbial contamination and the hospital ecosystem's adaptable mechanisms. A prominent prevalence of microbial contamination was observed on the lift buttons, reaching up to 44.4 %, with the exterior lift buttons contributing 1,450 CFU/mL to the total microbial load. Remarkably, there was a substantial difference in contaminant prevalence observed between the horizontal and vertical panel lift buttons, with the horizontal panel being more contaminated than the other panel ($p < 0.05$). Moreover, this study showed a significant relationship between the contaminated exterior lift button sets and the selected floors ($p < 0.05$). The metagenomic analysis revealed a diverse microbial community on lift buttons, with Firmicutes as the dominant phylum. *Bacillus* and *Meyerozyma* were the most prevalent at the genus level, highlighting their ability to persist despite cleaning efforts.

The KEGG pathway analysis provided insights into these microbes' metabolic capabilities and survival mechanisms. The ABC transporter pathway showed enrichment of genes involved in iron complex transport and antimicrobial resistance. At the same time, the two-component system exhibited enrichment of genes associated with energy acquisition and cell motility. Both pathways suggested the response-ability of the microbial community to external stimuli for its survivability.

While this study was conducted in a single hospital in a specific region, limiting the generalizability of the data, it provided valuable insights into the microbial ecology and its survival adaption on the hospital lift buttons. The comprehensive metagenomic analysis employed in this study allowed for a detailed characterisation of the microbial community, including identifying critical bacterial taxa and functional pathways. Despite the limitations, this study represented a significant contribution to the understanding of HAIs and highlighted the importance of effective infection control measures. Future studies could broaden the scope by including more hospitals from various regions and settings, providing a more comprehensive understanding of microbial contamination patterns on lift buttons. In addition, research on determining the impact of different cleaning agents on microbial survival should also be considered since this would help gain insights into optimising the hygiene practices of frequently touched surfaces.

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References

[1] Menezes, Ralciane de Paula, Lara de Andrade Marques, Felipe Flávio Silva, Nagela Bernadelli Sousa Silva, Priscila Guerino Vilela Alves, Meliza Arantes de Souza Bessa, Lúcio Borges de Araújo, Mário Paulo Amante Penatti, Reginaldo dos Santos Pedroso, and Denise Von Dolinger de Brito Röder. "Inanimate surfaces and air contamination with multidrug resistant species of *Staphylococcus* in the neonatal intensive care unit environment." *Microorganisms* 10, no. 3 (2022): 567. https://doi.org/10.3390/microorganisms10030567

[2] Muhammad, Izzati, Niza Samsudin, Raja Noor Zaliha Raja Abd Rahman, Norhidayah Kamarudin, and Norsyuhada Alias. "Metagenomic analysis of contaminated lift buttons reveals prevalent pathogens with antimicrobial resistance genes: A study in a public hospital in Pahang, Malaysia." *International Journal of Allied Health Sciences* 8, no. 2 (2024): 3086-3098.

[3] Olise, C. C., and I. Simon-Oke. "Fomites: Possible vehicle of nosocomial infections." *Journal of Public Health and Nutrition* 1, no. 1 (2018). https://doi.org/10.35841/public-health-nutrition.1.1.11-16

[4] Hendricks, Sriwathi Angeline, and Bhuwaneswaran Vijayam. "the interplay between oral, nasal, lungs and gut microbiome ecology in Coronavirus Disease 2019 (COVID-19) infection." *Semarak International Journal of Public Health and Primary Care* 1, no. 1 (2024): 16-36. https://doi.org/10.37934/scbtrj.1.1.1839
[5] Gooch, Christopher M., and Roopma Wadhwa. "Body fluid exposures." (2020).
[6] Drysdale, Carla. "WHO launches first ever global report on infection prevention and control." World Health Organization, 2022.
[7] Okamoto, Akira, Saki Otsuji, Miho Kamako, Ikumi Inoue, Kokoro Tasaka, and Juntaro Kato. "*Bacillus cereus* group exhibits more resistant to chlorhexidine rather than *Bacillus subtilis* group." *Open Journal of Medical Microbiology* 10, no. 3 (2020): 139-152. https://doi.org/10.4236/ojmm.2020.103012
[8] Orlando, S., M. Cicala, C. De Santo, C. Mosconi, F. Ciccacci, L. Guarente, M. Carestia *et al.* "The financial burden of healthcare-associated infections: A propensity score analysis in an Italian healthcare setting." *Infection Prevention in Practice* (2024): 100406. https://doi.org/10.1016/j.infpip.2024.100406
[9] Abbasian, Sara, Narges Nodeh Farahani, Zahra Mir, Faranak Alinejad, Mehri Haeili, Mustafa Dahmardehei, Mehdi Mirzaii, Seyed Sajjad Khoramrooz, Mohammmad Javad Nasiri, and Davood Darban-Sarokhalil. "Genotypic characterisation of *Staphylococcus aureus* isolated from a burn centre by using *agr, spa* and SCC*mec* typing methods." *New Microbes and New Infections* 26 (2018): 15-19. https://doi.org/10.1016/j.nmni.2018.08.001
[10] Liu, Wen J., Li Fu, Mei Huang, Jing P. Zhang, Yang Wu, Ying S. Zhou, Jing Zeng, and Guang X. Wang. "Frequency of antiseptic resistance genes and reduced susceptibility to biocides in carbapenem-resistant *Acinetobacter baumannii*." *Journal of Medical Microbiology* 66, no. 1 (2017): 13-17. https://doi.org/10.1099/jmm.0.000403
[11] Goh, Lucky Poh Wah, Hartinie Marbawi, Shu Meng Goh, Abdul Kahar bin Abdul Asis, and Jualang Azlan Gansau. "The prevalence of hospital-acquired infections in Southeast Asia (1990-2022)." *The Journal of Infection in Developing Countries* 17, no. 02 (2023): 139-146. https://doi.org/10.3855/jidc.17135
[12] Department of Statistics Malaysia. "[2022] Vital Statistics." OpenDOSM. 2023.
[13] Ministry of Health Malaysia. "COVID-19 Management Guidelines in Malaysia No.5/2020 (Annex 36)." 2021.
[14] Carrascosa, Conrado, Esther Sanjuán, Rafael Millán, Sara Martín, Pedro Saavedra, António Raposo, Cristóbal del Rosario-Quintana, and José Raduán Jaber. "Is the use of supermarket trolleys microbiologically safe? Study of microbiological contamination." *Journal of Applied Animal Research* 47, no. 1 (2019): 17-23. https://doi.org/10.1080/09712119.2018.1555091
[15] Muhammad, Izzati. "Prevalence of contaminants on the hospitals' lift buttons leads to an investigation on antimicrobial resistance coagulase-negative *Staphylococcus* spp. " Master diss., International Islamic University Malaysia, 2023.
[16] Osman, Faridah, Mohd Nizam Lani, Nik Hafizah Nik Ubaidillah, Mohd Yahya Fadzli Jusoh, Roshita Ibrahim, and Vira Putri Yarlina. "Effects of acidic ingredients on the microbial quality, sensory acceptance and shelf life of chilli shrimp paste." *International Journal of Advanced Research in Food Science and Agriculture Technology* 2, no. 1 (2024): 40-53. https://doi.org/10.37934/fsat.2.1.4053
[17] Bakon, Sophia Karen, Zuraifah Asrah Mohamad, Mohd Azerulazree Jamilan, Hazimah Hashim, Mohamed Yazid Kuman, Rafiza Shaharudin, Norazah Ahmad, and Nor Asiah Muhamad. "Prevalence of antibiotic-resistant pathogenic bacteria and level of antibiotic residues in hospital effluents in Selangor, Malaysia: Protocol for a cross-sectional study." *JMIR Research Protocols* 12, no. 1 (2023): e39022. https://doi.org/10.2196/39022
[18] Appeh, Osita Gabriel, Tochukwu Frank Egwuatu, Onwubiko Emmanuel Nwankwo, and Adure Christabel Ibe. "Bacterial contamination of microphones used in places of worship in Umuahia, Abia State, Nigeria." *Suan Sunandha Science and Technology Journal* 6, no. 2 (2019): 16-23.
[19] Sandle, Tim. "A case study in environmental monitoring: Reviewing incubation times upon recovery of microorganisms." BioProcess International. 2023.
[20] Wei, Siew Shing, Choo Mei Yen, Ian PG Marshall, Hazrulrizawati Abd Hamid, Shamrulazhar Shamzir Kamal, Dennis Sandris Nielsen, and Hajar Fauzan Ahmad. "Gut microbiome and metabolome of sea cucumber (*Stichopus ocellatus*) as putative markers for monitoring the marine sediment pollution in Pahang, Malaysia." *Marine Pollution Bulletin* 182 (2022): 114022. https://doi.org/10.1016/j.marpolbul.2022.114022
[21] Meyer, Folker, Daniel Paarmann, Mark D'Souza, Robert Olson, Elizabeth M. Glass, Michael Kubal, Tobias Paczian *et al.* "The metagenomics RAST server–a public resource for the automatic phylogenetic and functional analysis of metagenomes." *BMC Bioinformatics* 9 (2008): 1-8. https://doi.org/10.1186/1471-2105-9-386
[22] Bhatta, Dharm Raj, Deependra Hamal, Rajani Shrestha, Supram Hosuru Subramanya, Nisha Baral, Rajesh Kumar Singh, Niranjan Nayak, and Shishir Gokhale. "Bacterial contamination of frequently touched objects in a tertiary care hospital of Pokhara, Nepal: How safe are our hands?" *Antimicrobial Resistance & Infection Control* 7 (2018): 1-6. https://doi.org/10.1186/s13756-018-0385-2

[23] Susan, Muthoni Maina, K. Nyerere Andrew, and Wangari Ngugi Caroline. "Isolation of bacterial diversity present in medical waste and health care settings in hospitals in Kenya." *African Journal of Microbiology Research* 12, no. 26 (2018): 606-615. https://doi.org/10.5897/AJMR2018.8876

[24] Qin, Mingyang, Ping Chen, Baoguo Deng, Ruowen He, Yiping Wu, Yanxian Yang, Wenbin Deng *et al.* "The emergence of a multidrug-resistant and pathogenic ST42 lineage of *Staphylococcus haemolyticus* from a hospital in China." *Microbiology Spectrum* 10, no. 3 (2022): e02342-21. https://doi.org/10.1128/spectrum.02342-21

[25] Center for Disease Control and Prevention. "Environmental Cleaning Procedures." Healthcare-associated Infections (HAIs). 2024.

[26] Ruzaidi, Ayuni Mardhiah, and Norsyuhada Alias. "Knowledge, attitude and practice of IIUM Kuantan students on the transmission of microorganisms via lift buttons." *Semarak Current Biomedical Technology Research Journal* 2, no. 1 (2024): 1-15.

[27] Meenatchi, D., R. Aishwarya, and A. Shahina. "A voice recognising elevator system." In *Proceedings of the International Conference on Soft Computing Systems: ICSCS 2015, Volume 1*, pp. 179-187. Springer India, 2016. https://doi.org/10.1007/978-81-322-2671-0_17

[28] Kloepple, Sarah. "ADA Elevators: What are the requirements?" Buildings. 2009.

[29] Baindara, Piyush, and Bilal Aslam. "*Bacillus* spp.-Transmission, pathogenesis, host-pathogen interaction, prevention and treatment." *Frontiers in Microbiology* 14 (2023): 1307723. https://doi.org/10.3389/fmicb.2023.1307723

[30] Soundhararajan, Ranjani, and Hemalatha Srinivasan. "Multidrug-resistant *Bacillus* species isolated from hospital soil environment is controlled by nanobiotics incorporated nanoformulation." *Environmental Research* 246 (2024): 118122. https://doi.org/10.1016/j.envres.2024.118122

[31] Ulrich, Nikea, Katja Nagler, Michael Laue, Charles S. Cockell, Peter Setlow, and Ralf Moeller. "Experimental studies addressing the longevity of *Bacillus subtilis* spores–The first data from a 500-year experiment." *PloS one* 13, no. 12 (2018): e0208425. https://doi.org/10.1371/journal.pone.0208425

[32] Chaves, Alessandra Leal Silva, Luciana Trilles, Gabriela Machado Alves, Maria Helena Galdino Figueiredo-Carvalho, Fábio Brito-Santos, Rowena Alves Coelho, Ianick S. Martins, and Rodrigo Almeida-Paes. "A case-series of bloodstream infections caused by the *Meyerozyma guilliermondii* species complex at a reference center of oncology in Brazil." *Medical Mycology* 59, no. 3 (2021): 235-243. https://doi.org/10.1093/mmy/myaa044

[33] Lopes, Mariana R., Thiago M. Batista, Glória R. Franco, Lucas R. Ribeiro, Ana RO Santos, Carolina Furtado, Rennan G. Moreira *et al.* "*Scheffersomyces stambukii* f.a., sp. nov., a d-xylose-fermenting species isolated from rotting wood." *International Journal of Systematic and Evolutionary Microbiology* 68, no. 7 (2018): 2306-2312. https://doi.org/10.1099/ijsem.0.002834

[34] Jia, Ran-Ran, Shi-Long Lv, Chun-Yue Chai, and Feng-Li Hui. "Three new *Scheffersomyces* species associated with insects and rotting wood in China." *MycoKeys* 71 (2020): 87. https://doi.org/10.3897/mycokeys.71.56168

[35] Pereira da Fonseca, Tairacan Augusto, Rodrigo Pessôa, Alvina Clara Felix, and Sabri Saeed Sanabani. "Diversity of bacterial communities on four frequently used surfaces in a large Brazilian teaching hospital." *International Journal of Environmental Research and Public Health* 13, no. 2 (2016): 152. https://doi.org/10.3390/ijerph13020152

[36] Abougrara, Ghada, Ghada Algeblaue, Enas Almabrouk, and Ebtisam Almahdi. "Isolation and identification of pathogenic bacteria from hospital door handles/knobs." *Khalij-Libya Journal of Dental and Medical Research* (2024): 1-6. https://doi.org/10.47705/kjdmr.248101

[37] Mulongo, Tony, Kingsley Kamvuma, Christopher N. Phiri, John A. Mulemena, and Warren Chanda. "Elevators and staircase handrails as potential sources of nosocomial pathogens at Ndola Teaching Hospital, Zambia." *Infection* 4 (2021): 8.

[38] Gallandat, Karin, Riley C. Kolus, Timothy R. Julian, and Daniele S. Lantagne. "A systematic review of chlorine-based surface disinfection efficacy to inform recommendations for low-resource outbreak settings." *American Journal of Infection Control* 49, no. 1 (2021): 90-103. https://doi.org/10.1016/j.ajic.2020.05.014

[39] Artasensi, Angelica, Sarah Mazzotta, and Laura Fumagalli. "Back to basics: Choosing the appropriate surface disinfectant." *Antibiotics* 10, no. 6 (2021): 613. https://doi.org/10.3390/antibiotics10060613

[40] Seyoum, Yohannes, Kaleab Baye, and Christèle Humblot. "Iron homeostasis in host and gut bacteria–A complex interrelationship." *Gut Microbes* 13, no. 1 (2021): 1874855. https://doi.org/10.1080/19490976.2021.1874855

[41] Wu, Xia, Jing Han, Guoli Gong, Mattheos AG Koffas, and Jian Zha. "Wall teichoic acids: Physiology and applications." *FEMS Microbiology Reviews* 45, no. 4 (2021): fuaa064. https://doi.org/10.1093/femsre/fuaa064

[42] Nguyen, Rosalee, Niloufar R. Khanna, Anthony O. Safadi, and Yan Sun. "Bacitracin topical." In *StatPearls [Internet]*. StatPearls Publishing, 2022.

[43] Radeck, Jara, Susanne Gebhard, Peter Shevlin Orchard, Marion Kirchner, Stephanie Bauer, Thorsten Mascher, and Georg Fritz. "Anatomy of the bacitracin resistance network in *Bacillus subtilis*." *Molecular Microbiology* 100, no. 4 (2016): 607-620. https://doi.org/10.1111/mmi.13336

[44] Khan, Atif, and Subba Rao Toleti. "Molecular evolution of xenobiotic-degrading genes and mobile genetic elements in soil bacteria." In *Microbial Diversity in the Genomic Era*, pp. 731-746. Academic Press, 2024. https://doi.org/10.1016/B978-0-443-13320-6.00010-X

[45] Meyer, Frederik M., and Jörg Stülke. "Malate metabolism in *Bacillus subtilis*: Distinct roles for three classes of malate-oxidising enzymes." *FEMS Microbiology Letters* 339, no. 1 (2013): 17-22. https://doi.org/10.1111/1574-6968.12041