the temperature, humidity and pressure minute by minute. **Conclusion:** OR traffic increases the particle count particularly the small size. Other physical aspects of the OR environment were tightly controlled. The ability to automatically monitor OR parameters could be extremely helpful for assuring patient safety as well as reviewing OR factors in SSI cases.

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Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Environmental Cleaning
Filtered handheld far-ultraviolet disinfection device in reducing environmental pathogens from high-touch clinical surfaces
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Background: Healthcare-acquired infections (HAIs) continue to be a major challenge. In fact, an increased risk of HAIs has been linked to high-touch surfaces contaminated with multidrug-resistant organisms (MDROs), and enhanced environmental disinfection is linked to reduced HAI rates. Recently, more focus has been placed on emerging disinfection technologies, such as UV light-producing portable device that emits light at a wavelength of 222 nm, which has previously demonstrated germicidal capabilities at short contact times. In this study, we aim i) to evaluate the efficacy of a filtered far-UV-C handheld device (FFUHH) to reduce bacterial loads on high-touch surfaces in clinical workrooms in a cancer center, and ii) to isolate, identify and establish a genetic relationship between these environmental clinically significant pathogens and the ones recovered from patients. **Methods:** Samples were collected weekly on a rotating schedule over a 24-week period from five high-touch items (dictation device, mouse, armchair, desk, and keyboard) in multiple clinical work rooms on hematologic malignancy and stem cell transplant units. Contact plates for colony count and swabs were collected pre- and post-intervention with the FFUHH on standardized adjacent areas respectively for each surface. The swabs were enriched and cultured on selective media to isolate clinically significant pathogens. Whole genome sequencing (WGS) was then performed on environmental pathogens validated by MALDI-TOF as well as clinical samples collected from patients in the same unit around the time of environmental sample collection. **Results:** A total of 440 plates, 220 pre- and 220 post-interventions, were collected and analyzed. The highest mean colony count pre-treatment was detected from the armchairs and the lowest for the keyboards. The mean reduction of colony forming units (CFUs) ranged between 53% for the keyboard and 83% for the mouse. The reduction was statistically significant across all surfaces with P values < 0.05, except for the keyboard (Figure 1). We isolated many pathogens of the human microbiota identified by MALDI-TOF such as Micrococcus luteus, S. capitis as well as methicillin-resistant S. epidermidis, S. haemolyticus and S. hominis. We also identified several Candida parapsilosis, Pseudomonas stutzeri, one Listeria grayi and one Acinetobacter baumanni. Finally, WSG allowed us to further characterize an environmental multi-drug resistant S. epidermidis ST5 strain associated with patient bacteremia, and ST16 strains detected on surfaces both pre- and post-FFUHH treatment. **Conclusion:** The FFUHH effectively reduced the microbial burden on high-touch surfaces in clinical workrooms on hematologic malignancy and stem cell units.

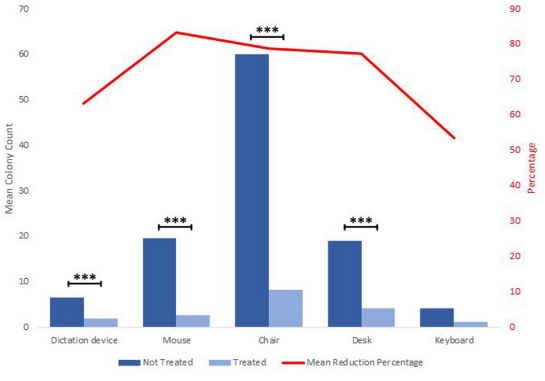

Figure 1: Efficacy of the UV treatment. Columns indicate mean CFUs before and after treatment with the FFUV handheld device for each tested surface. Mean reduction percentages were calculated by comparing not treated and treated values for each surface respectively. Statistical analysis was performed, and P values calculated using Wilcoxon matched pairs signed rank test. (***) indicate statistically significant results with a P value <0.000.

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Subject Category: Environmental Contamination
Environmental Fungal Contamination Characterization of Three Inpatient Units Utilizing Optimized Detection Methods
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Background: Environmental sampling and detection methods for fungi in healthcare settings are not well-established. We previously refined methods for fungal sampling and detection in a controlled laboratory environment and aimed to validate them in a real-world healthcare setting. **Methods:** We performed a microbiological analysis of air and surfaces in three inpatient units at a tertiary care center. Surface samples were obtained with foam sponges from 3 locations in patient rooms (Patient bedrails, bathroom floor, HVAC export) and 5 locations in units (HVAC exports 3x, clean linen storage, soiled linen storage). Air samples were taken with an active air sampler directly below HVAC exports. Sponges were processed using the stomacher technique. Samples underwent DNA extraction followed by qPCR with FungiQuant primers targeting the 18S rRNA gene. Amplicons from positive samples were sequenced (NextSeq 1000, 300bp PE) and SmartGene databases were used to interpret sequence data. For comparison to culture methods, samples were also plated onto Sabouraud and HardyCHROM Candida + auris medias. Fungal growth underwent DNA extraction, 18S PCR and Sanger sequencing for genus and species identification. **Results:** A total of 85 samples were obtained, from 15 patient rooms and three units resulting in 61 surface and 24 air samples. Patients in study rooms had a median age of 53, 9 (60%) were male, and no patients had an invasive fungal infection during their hospital encounter. 44 (53%) and 39 (46%) samples were positive for fungi via qPCR and culture, respectively. Of the 44 positive qPCR samples, microbiome analyses identified at least one fungi to the species, genus and family levels in 43 (98%), 28 (64%), 18 (41%) samples, respectively (Table 1). 114 total isolates were identified of which the most common were Mallassezia restricta (30 [26%]), Malassezia globose (29 [25%]), and Pennicillium paradoxum (4 [4%]). 39 genera were identified of which the most common were Mucor (19 [49%]) and Candida (8 [21%]). Of the 39 culture positive samples, 90 total isolates were recovered. The most common species were Paradendryphiella arenariae (19 [21%]), Aspergillus niger (12 [13%]) and Penicillium commune (12 [13%]). **Conclusion:** These results demonstrate the presence of diverse fungal