Background. Treatment of invasive fungal infections with amphotericin B is a concern in kidney transplant patients due to fear of allograft loss. Reluctance to use amphotericin B may lead to suboptimal therapy and poor treatment outcomes. The risk of amphotericin B-related nephrotoxicity and allograft dysfunction has not been studied in kidney transplant patients. Our aim was to study the association between amphotericin B and acute kidney injury (AKI) as defined by the Acute Kidney Injury Network classification, allograft loss and patient mortality in kidney transplant recipients.

Methods. We used SPSS to conduct a descriptive analysis of a retrospective cohort of 30 adult kidney transplant recipients who were admitted to Virginia Commonwealth University Medical Center and received treatment with amphotericin B from 2005 to 2015.

Results. The median age in our cohort was 57. 40% were female, 60% were male. 60% had received a kidney transplant from a deceased donor; 13.3% from a living related donor; 13.3% from a living unrelated donor; and 13.3% had received a combined kidney–pancreas transplant. 63.3% of patients had received liposomal amphotericin B; 33.3% had received lipid-complex amphotericin B; 3.3% had received conventional amphotericin B. We found an association between cumulative amphotericin B doses above 5,000 mg and AKI, whereby 64.7% of patients exposed to less than 5,000 mg of amphotericin B developed AKI and 100% of patients exposed to more than 5,000 mg of amphotericin B developed AKI (P = 0.017). We did not find an association between cumulative amphotericin B doses above 5,000 mg and return to dialysis at 3 months and 12 months post-exposure (P = 0.436 and 0.288, respectively). We also did not find an association between such doses of amphotericin B and mortality at 30 and 90 days (P = 0.869 and 0.193, respectively).

Conclusion. In the first descriptive analysis of a retrospective cohort of kidney transplant patients exposed to amphotericin B, our results suggest that the risk of nephrotoxicity may be significantly increased when a cumulative dose of 5,000 milligrams is exceeded. Our results also suggest that amphotericin B doses associated with nephrotoxicity in kidney transplant patients may not have an effect on allograft survival and patient mortality.

Disclosures. **All authors:** No reported disclosures.

1139. Novel Formulation SUBA-Itraconazole Prophylaxis in Patients With Hematological Malignancy or Undergoing Allogeneic Stem Cell Transplantation: Follow-up Survival Data

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Background. Despite the advantageous spectrum of activity of itraconazole, it is rarely used as a prophylactic agent due to limited bioavailability and intolerance of the conventional formulation. After the development of a novel formulation SUBA-itraconazole* (SUper BioAvailability), we undertook a study to assess therapeutic levels, safety, tolerability, and IFI rates of this novel formulation when compared with the conventional itraconazole liquid in patients undergoing allogeneic hematopoietic stem cell transplantation or in hematological malignancy patients.

Methods. Following a single-centre, prospective study of SUBA–itraconazole 200 mg BID vs. conventional liquid itraconazole 200 mg BID, the SUBA–itraconazole group was assessed 1-year postallogeneic stem cell transplant for incidence of IFI and survival.

Results. A total of 57 patients (29 SUBA–itraconazole and 30 liquid-itraconazole) were assessed. Therapeutic concentrations were achieved significantly more quickly in the SUBA–itraconazole group; median of 6 days vs. 14 (P < 0.0001). At day 10, therapeutic concentrations were achieved in 69% of the SUBA–itraconazole group vs. 21% (P < 0.0001). The mean trough serum concentrations at steady state of SUBA–itraconazole were significantly higher, with less interpatient variability (1,577 ng/mL, CV 35%) vs. (1,218 ng/mL, CV 60%) (P < 0.001). There were 2 (7.5%) treatment failures in the SUBA–itraconazole group, both due to cessation of therapy for mucositis, compared with 7 (23.3%) treatment failures in the liquid-itraconazole group, due to subtherapeutic levels (five), mucositis (one), and gastrointestinal intolerance (one) (P = 0.096). There was one confirmed IFI in the SUBA–itraconazole treatment failure group defined by a blood culture that yielded yeast; however, this was after the cessation of SUBA–itraconazole for mucositis. No other probable/possible IFIs were observed. After 1 year postallogeneic stem cell transplant in the SUBA–itraconazole group, there were two deaths (10%) due to disease progression and no further IFIs were reported.

Conclusion. The use of the SUBA–itraconazole formulation was a safe and effective prophylactic agent. It was associated with more rapid attainment of therapeutic levels with less interpatient variability when compared with conventional liquid itraconazole.

Disclosures. **J. Lindsay**, Mayne Pharma: Consultant, Consulting fee.

1140. GATA2 Mutations Are Frequently Identified Among Patients With Myeloid Malignancies Who Develop Invasive Aspergillosis

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Background. Patients with myeloid malignancies are at risk of invasive aspergillosis (IA), a cause of significant morbidity and mortality. Identification of patients at higher risk for IA may help optimize prophylactic or preemptive treatment decisions. Molecular genetic testing used to risk-stratify and guide therapy for hematologic malignancies may also have applicability toward predicting infectious outcomes. The purpose of this study was to identify mutations that may increase risk for IA among patients with myeloid malignancies.

Methods. We identified patients cared for at Dana-Farber/Brigham and Women's Cancer Center between March 1, 2015 and January 31, 2018 who were diagnosed with probable or proven IA during the treatment of myeloid malignancies including acute myeloid leukemia (AML) or myelodysplastic syndrome (MDS). We reviewed pathogenic mutations detected by the Rapid Heme Panel (RHP), a clinical targeted next-generation sequencing panel of 95 recurrently mutated genes in hematologic malignancies.

Results. Twenty-four patients with myeloid malignancy (AML 20, MDS 4) were diagnosed with IA, 20 of whom (AML 17, MDS 3) had undergone genetic testing with the *RHP* at the time of their cancer diagnosis. We found that three of 20 patients (15%) had a pathogenic mutation in *GATA2*. All were missense mutations within the functional zinc-finger domains, including one resulting in an R398W amino acid change, one of the spectrum of germline mutations known to cause the primary immunodeficiency MonoMAC. Patients with *GATA2* mutations in our cohort were ages 35–68 and variant allele fraction ranged from 16.3% to 49.7%, raising the possibility that both inherited and acquired *GATA2* dysfunction could incur a similar infectious risk.

Conclusion. Mutations in *GATA2*, a gene associated with MonoMAC syndrome, were common among patients with myeloid malignancy who developed IA. These data suggest that personalized genetic analyses of patients with underlying hematologic malignancy may also be useful for assessment of infectious risk.

Disclosures. **All authors:** No reported disclosures.

1141. Microbial Assessment of Healthcare-Associated Pathogens on Various Environmental Sites in Patient Rooms After Terminal Room Disinfection

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Background. Hospital room environmental surfaces can be contaminated with healthcare-associated pathogens even if terminal room cleaning/disinfection is implemented. We examined the microbiological burden on hospital room environmental sites after standard or enhanced terminal room disinfection.

Methods. Microbial data from the Benefits of Enhanced Terminal Room Disinfection Study were utilized. All patient rooms were randomly assigned to standard disinfection (Quaternary ammonium [Quat]) or an enhanced disinfection (Quat/ultraviolet light [UV-C], Bleach, or Bleach/UV-C). Microbiological samples were obtained using Rodac plates (25 cm^2/plate) from 8 of 10 hospital room sites, including bed rail, over-bed table, supply/medicine cart, chair, side counter, linen hamper lid, sink, toilet seat, shower floor, and bathroom floor. The number of colony forming units (CFU) of four target epidemiologically important pathogens (EIP), including multidrug-resistant *Acinetobacter*, *Clostridium difficile*, methicillin-resistant *Staphylococcus aureus*, and vancomycin-resistant enterococci, was counted. A total of 3,680 samples from 736 environmental sites in all 92 patient rooms (21 standard rooms and 71 enhanced rooms) were analyzed.

Results. Overall, the frequency of all environmental sites positive for EIP was 11% (84/736) in all rooms, 21% (36/168) in standard rooms, and 8% (48/568) in enhanced rooms (P < 0.001) (Figure 1). Environmental sites, other than the toilet seat, in standard rooms were likely to be more frequently contaminated with EIP than in enhanced rooms (P = 0.013 for overbed table, P = 0.010 for bed rail, and P > 0.05 for other sites each). Mean CFU of EIP per room was 19.2 in all rooms, 60.8 in standard rooms, and 6.9 in enhanced rooms (P = 0.006) (Figure 2). All sites in standard rooms tended to have higher mean counts than in enhanced rooms (P = 0.001 for overbed table, P = 0.001 for bed rail, P = 0.012 for side counter, and P > 0.05 for other sites each).

Conclusion. Our results demonstrate that an enhanced terminal room disinfection reduced microbial burden of healthcare-associated pathogens on environmental sites better than standard room disinfection. Environmental hygiene of touchable surfaces after terminal room cleaning using Quat needs to be improved.

Fig. 1. Frequency of environmental sites positive for epidemiologically-important pathogens after terminal room disinfection

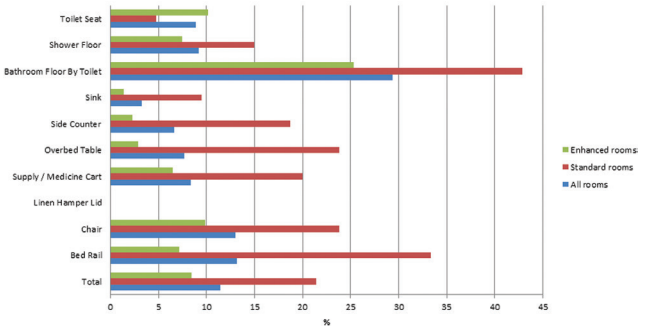
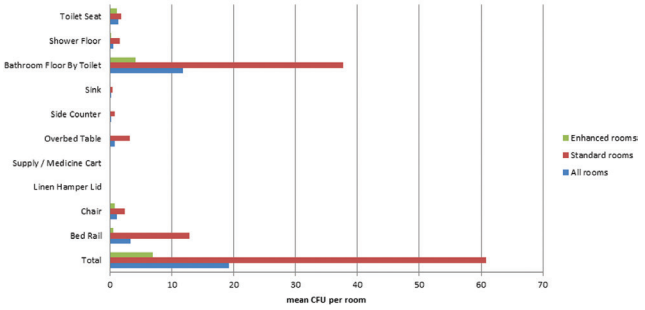


Fig. 2. Epidemiologically-important pathogens by environmental site after teminal room disinfection



Disclosures. **W. Rutala**, PDI: Consultant and Speaker's Bureau, Consulting fee and Speaker honorarium. **D. Weber**, PDI: Consultant, Consulting fee.

1142. Use of DNA Markers to Assess the Potential for Pathogen Transmission from Physicians' White Coats

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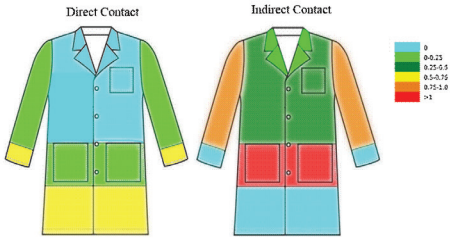
Background. Physicians' white coats are often contaminated, but seldom cleaned. A "bare below the elbows" dress code policy has been advocated as a strategy to reduce the risk for transmission of healthcare-associated pathogens by white coats. However, transfer of contamination by clothing has not been demonstrated in clinical settings and it is not known if long sleeves are the major source of transfer.

Methods. We observed physicians during routine patient encounters and characterized the frequency of direct and indirect contact between white coats and the patient or environmental surfaces. To assess transfer from white coats in clinical settings, we applied one cauliflower mosaic virus DNA marker to the sleeve cuffs and another to the coat pockets of physicians prior to routine patient encounters. Polymerase chain reaction was used to determine whether DNA markers from the clothing sites were transferred to patients or environmental surfaces.

Results. Ninety percent of observed patient encounters included one or more direct or indirect contacts between a physician's white coat and a patient or the environment. Direct contact occurred on average 1.7 times per encounter and indirect contact (i.e., physicians' hands contacting the coat prior to touching the patient or environment) occurred on average 2.3 times per encounter. The figure shows the frequency and distribution of sites of direct and indirect contact with white coats. Of 11 patient encounters with DNA-contaminated white coats, five (45%) resulted in transfer of one or both DNA markers; there were three transfers from sleeve cuffs and three from coat pockets.

Conclusion. Contaminated white coats may be an under-appreciated source for transmission of healthcare-associated pathogens. Our results provide support for the bare below the elbows policy, but also highlight the potential for indirect transfer of pathogens from other sites on white coats.

Figure. Frequency and distribution of sites of direct and indirect contact between physicians' white coats and patients or the environment



Disclosures. **All authors:** No reported disclosures.

1143. Epidemiologic Characteristics of Outbreaks Associated With the Healthcare Environment

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Background. The healthcare environment serves as a reservoir or a source for outbreaks. Single outbreaks via an environmental reservoir have often been described in healthcare settings, while the trend of these multiple outbreaks has not been understood well. Here, we investigated the epidemiologic features of outbreaks associated with the healthcare environment.

Methods. Structured data on environmental sources from Outbreak Database based on information from articles published worldwide were extracted. A total of 317 articles of outbreaks associated with the healthcare environment (e.g., environmental surfaces, patent care items, water and water-related appliances, and air and ventilation systems) in 48 countries during 1965–2016 were analyzed.

Results. Of the 317 outbreaks reviewed, 295 (93%) were monophasic. One hundred sixty-one outbreaks (51%) occurred in an ICU setting. The 6,317 infected patients and 338 healthcare personnel were involved in 317 healthcare-associated outbreaks via the environment. Two hundred fifty-one patients (4%) died of an infection. Two hundred sixty-five outbreaks (84%) caused at least one infection among patients involved, including 112 pneumonias (35%) and 104 bloodstream infections (33%) (Figure 1). Bacteria ($N = 244$, 77%) were the most frequent pathogen, followed by fungi ($N = 49$, 15%) and mycobacteria ($N = 15$, 5%) (Figure 2). Of the bacteria, nonfermenting Gram-negative bacilli ($N = 100$, 41%) was the most common, followed by *Legionella* ($N = 56$, 23%), *Enterobacteriaceae* ($N = 35$, 14%), and multidrug-resistant organisms ($N = 31$, 13%). One hundred thirty-six outbreaks (43%) were obviously transmitted by contact, followed by inhalation and invasive technique. Genotyping was performed in 66% of outbreaks ($N = 209$). Key control measures included modification of care/equipment ($N = 181$, 57%) and improved disinfection/sterilization ($N = 170$, 54%). Forty-seven (15%) and 5 (2%) outbreaks led to closure of the affected location and restriction of workload, respectively (Figure 3).

Conclusion. This study characterized epidemiologically outbreaks associated with healthcare environment, demonstrating the environmental role in healthcare-associated outbreaks. Analysis of structured data on multiple outbreaks can help develop infection prevention strategies in healthcare facilities.

Fig. 1. Infection types of outbreaks associated with the hospital environment