copies/mL) or negative viral load. Sustained EBV DNAemia was defined as EBV DNA copies/mL). While uncommon, development of sustained EBV DNAemia was associated with hematological malignancies. The identified ESBL risk factors create an opportunity to decrease delay in optimal therapy through risk stratification during initial antibiotic selection.

**Results.** A total of 28 patients with ESBL-E BSIs and 60 patients with non-ESBL-E BSIs were included. The 30-day mortality rate with ESBL-E BSIs was 25% compared to 15% with non-ESBL-E BSIs (P = .373). In-hospital mortality, 30-day infection recurrence, intensive care unit (ICU) admission, and length of stay after culture were not significantly different. However, time to optimal therapy was longer in the ESBL-E group (median = 14.9 vs 1.9 h; P < .001). Multivariate logistic regression analysis showed an association of 30-day mortality with ICU admission (OR 3.05; 95% CI, 1.01-9.23; P = .049) and prior intravenous antibiotic use (OR 2.96; 95% CI, 0.96-9.09; P = .033) and secondary clinical outcomes as appropriate. Risk factors associated with 30-day mortality and EBV production were assessed as secondary outcomes using logistic regression models.

**Results.** All had prolonged (median = 24 days, range = 9-210) and profound immunosuppression from chemotherapy and/or stem cell transplantation for acute myeloid leukemia (n = 3) or lymphoma (n = 2) at the time of culture positivity. Four were severely neutropenic (median = 0.08/mm³, range = 0.01-0.26). Median patient age was 62 years (range = 58-73). S. capitata was isolated from blood (n = 3), urine (n = 2), and liver (n = 2) samples. Whole genome sequencing of these isolates was performed to confirm the presence of an outbreak. All patients received empirical treatment with intravenous caspofungin before culture-guided therapy with intravenous liposomal amphotericin B +/- oral fluconazole. Two of the five patients died although both had advanced refractory malignancies. Whole environmental sampling of fridges/freezers, drains, and vents in patient rooms and clean areas for handling or storage of food and medication failed to identify a clear point source despite isolation of multiple environmental organisms. No further cases have emerged after intensification of the cleaning regimen in these areas.

**Conclusion.** Our experience highlights the emerging threat of drug-resistant yeasts particularly in the immunocompromised. Management of such outbreaks requires a multidisciplinary approach incorporating antifungal stewardship, infection control, and environmental microbiology, alongside close clinical liaison between hematologists-oncologists and infection specialists.

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

936. Risk Factors and Clinical Outcomes for Extended-Spectrum Beta-Lactamase Producing Enterobacteriaceae Blood Stream Infections in Patients with Hematologic Malignancies

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**Session:** P-53. Infections in Immunocompromised Individuals

**Background.** Hematologic malignancy patients have high rates of antibiotic exposure, and increasing resistance is a major concern, particularly with extended-spectrum beta-lactamases (ESBL) in Enterobacteriaceae blood stream infections (BSIs). Identifying risk factors for ESBL-producing Enterobacteriaceae (ESBL-E) BSIs may facilitate faster appropriate antibiotic use and decrease mortality.

**Methods.** This was a retrospective study of patients with hematologic malignancies (leukemia or lymphoma, Ewing’s sarcoma or Kaposi’s sarcoma). Bloodstream isolates of Enterobacteriaceae were screened with the ChromID ESBL strip (bioMérieux). Risk factors for ESBL-E BSIs were identified using univariate and multivariate analyses.

**Results.** A total of 28 patients with ESBL-E BSIs and 60 patients with non-ESBL-E BSIs were included. The 30-day mortality rate with ESBL-E BSIs was 25% compared to 15% with non-ESBL-E BSIs (P = .373). In-hospital mortality, 30-day infection recurrence, intensive care unit (ICU) admission, and length of stay after culture were not significantly different. However, time to optimal therapy was longer in the ESBL-E group (median = 14.9 vs 1.9 h; P < .001). Multivariate logistic regression analysis showed an association of 30-day mortality with ICU admission (OR 3.05; 95% CI, 1.01-9.23; P = .049) and prior intravenous antibiotic use (OR 2.96; 95% CI, 0.96-9.09; P = .033) and secondary clinical outcomes as appropriate. Risk factors associated with 30-day mortality and EBV production were assessed as secondary outcomes using logistic regression models.

**Results.** All had prolonged (median = 24 days, range = 9-210) and profound immunosuppression from chemotherapy and/or stem cell transplantation for acute myeloid leukemia (n = 3) or lymphoma (n = 2) at the time of culture positivity. Four were severely neutropenic (median = 0.08/mm³, range = 0.01-0.26). Median patient age was 62 years (range = 58-73). S. capitata was isolated from blood (n = 3), urine (n = 2), and liver (n = 2) samples. Whole genome sequencing of these isolates was performed to confirm the presence of an outbreak. All patients received empirical treatment with intravenous caspofungin before culture-guided therapy with intravenous liposomal amphotericin B +/- oral fluconazole. Two of the five patients died although both had advanced refractory malignancies. Whole environmental sampling of fridges/freezers, drains, and vents in patient rooms and clean areas for handling or storage of food and medication failed to identify a clear point source despite isolation of multiple environmental organisms. No further cases have emerged after intensification of the cleaning regimen in these areas.

**Conclusion.** Our experience highlights the emerging threat of drug-resistant yeasts particularly in the immunocompromised. Management of such outbreaks requires a multidisciplinary approach incorporating antifungal stewardship, infection control, and environmental microbiology, alongside close clinical liaison between hematologists-oncologists and infection specialists.

**Disclosures.** All Authors: No reported disclosures.
prediction model for use at one month post-HT with the ability to predict serious infection in the first year.

**Methods.** A retrospective cohort study of all HT recipients at a single center between 2000 and 2018 was performed, excluding dual-organ recipients, those who died within one month of HT, and those with insufficient data. The composite endpoint included cytomegalovirus infection (CMV), herpes simplex (HSV) or varicella zoster virus infection (VZV), blood stream infection (BSI), and invasive fungal infection (IFI). The follow-up period extended from 1 month to 1 year post-HT. A least absolute shrinkage and selection operator (LASSO) regression model was fit using 13 candidate variables. A C-statistic, calibration curve, and Brier score were used to assess model performance.

**Results.** 375 patients were analyzed; 93 outcomes occurred (65 CMV, 3 HSV, 2 VZV, 28 BSI, and 15 IFI). 12 of 13 variables remained in the final model: year of transplant, age at transplant, ischemic cardiomyopathy, diabetes, immune-mediating disease, need for renal replacement therapy in first month, CMV risk status (high, intermediate, low) derived from donor-recipient serology, use of basiliximab induction, use of cytolytic agent in first month, use of rituximab in first month, rejection treated with high-dose steroids in first month, lymphocyte count under 0.75 x10⁹ cells/µL at 1 month, and inpatient status at 1 month. The C-statistic was 0.82 and Brier score 0.142. The calibration curve is shown in Figure 1.

Figure 1. Calibration plot

Actual versus predicted probability of infection by 1 year. Gray line = ideal Dotted line = smoothed non-parametric calibration curve

**Conclusion.** This model synthesizes multiple highly-relevant clinical and laboratory parameters, available at 1 month post-HT, into a unified, objective, and clinically-useful prediction tool for the occurrence of serious infection in the first post-transplant year. Good discrimination and calibration are demonstrated. External validation is required before generalized use.

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938. Azole Resistant Aspergillus Species in Lung Transplant Recipients: A 10 Year Experience
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**Session:** P-53. Infections in Immunocompromised Individuals

**Background.** Invasive aspergillosis (IA) causes significant morbidity and mortality in lung transplant (LTX) recipients. Antifungal resistance in Aspergillus species is on the rise globally with specific concern in Europe related to the TR34/L98H mutation in the cyp51A enzyme that induces pan-azole resistance. Azole exposure is a known risk factor for development of resistant Aspergillus, but this is less well described in LTx population.

**Methods.** We reviewed the electronic medical records of LTx patients with respiratory cultures positive for Aspergillus species known to be inherently resistant or any Aspergillus species tested to be resistant to one or more triazole from 2010 to 2019. For available isolates, Sanger sequencing was performed on cyp51A with primers targeting the promoter region and 3 known hotspot areas.

**Results.** Twenty eight patients met inclusion criteria and 2.7% (28/1026) Aspergillus isolates wereazole-resistant during study period (Figure 1). Median time from LTx to resistant Aspergillus growth was 196 days (range 14 - 3146). There was a cluster of positive cultures within 1-year post-Tx period (13/28). Azole exposure varied, from 7 to 2443 days (median 128). There was no change in incidence over the study period. The most common species was Aspergillus calidoustus (Figure 2). Twenty cases were deemed colonization, vs 5 probable IFI and 3 proven IFI. Mortality of IFI with resistant Aspergillus was 38% (3/8), higher than azole-susceptible IA (p=0.05). Twelve isolates were available for sequencing; none carried TR34/L98H mutation. There was wide variation in mutations, ranging from 1 to 12 point mutations in the cyp51A enzyme, many of whom SNPs previously described as engendering an azole resistant phenotype (Figure 3).

**Aspergillus-free Survival by Resistant and Susceptible Isolates**

2.7% (28/1026) Aspergillus isolates in the study period were azole-resistant

Development of azole-resistant aspergillus colonization/infection was rare relative to common occurrence of colonization/infection with susceptible isolates in the lung transplant recipient population

Azole Resistant Aspergillus Species Isolated from Lung Transplant Recipients

**Aspergillus species**

The most commonly isolated species were A. calidoustus and ustus. Only 4/28 isolates were A. fumigatus.

Azole Resistant Aspergillus Genotypic Analysis

Sequenced isolates showed wide variability in point mutations. M220V, G54, and G418 were the only mutations observed more than once. 3 isolates were wild type.

**Conclusion.** Azole resistant Aspergillus infections remain an uncommon problem in LTx. The majority of isolates were deemed colonization, but mortality was high when IFI was present. Most isolates had mutations within the hot spot regions of cyp51A known to induce azole resistance. There were no TR34/L98H mutants found in our patient population.

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