Syndrome	Number of Patients	Treatment	Outcome at 30 days
Catheter Associated UTI (CAUTI)	5	Caspofungin (2 patients– Pyelonephritis with sepsis). One patient with Fluconazole (no sepsis) 2 patients were managed with change of Foley catheter and observation only (only one spike of fever)	All patients were cured
Central Line Associated BSI (CLABSI)	3	Caspofungin for all 3 patients	All 3 patients died
Surgical Site Infection (SSI)	9	3 prosthetic joint infections & 2 Sternal Osteomyelitis – 2 weeks of Caspofungin followed by 6-8 weeks of Voriconazole. 4 patients with superficial SSI – wound debridement and local antiseptics only.	One patient died (not attributable to Candida infection – progressive malignancy
Others – Peritonitis	1	Post-OP peritonitis treated with Caspofungin	Died

All these infections originated in the surgical ICU. This outbreak of Candida auris in the Surgical ICU was terminated after horizontal infection control measures like hand hygiene, equipment disinfection and environmental cleaning were enhanced and the surface/equipment disinfectant used was revised from Quaternary Ammonium Compounds to Peroxide based compounds.

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267. Fungal Culture Diagnostic Stewardship: An Avenue for Antimicrobial Stewardship in the Immunocompromised Host

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Background. Bronchoalveolar lavage (BAL) is a widely used procedure in the diagnosis of pneumonia in critically ill and immunocompromised hosts. Fungal smears and cultures are commonly performed on these samples. We evaluated the yield of various fungi, including but not limited to *Candida species, Aspergillus species, Penicillium species*, isolated from BAL specimens at our institution to determine the yield of this test and its impact on decision making.

Methods. We identified adult immunocompromised patients who underwent "Bronchoscopy with Immunocompromised Host Protocol (ICH)," which consists of an exhaustive list of diagnostic tests for various pathogenic organisms, over a one year period from January 1, 2017 to December 31, 2017. We reviewed if positive fungal cultures led to a change in management and if this was appropriate.

Results. 582 patients underwent bronchoscopy with ICH protocol. There were 285/582 (48.9%) positive fungal cultures of which 177 (62%) grew *Candida species*. The most common species was *Candida albicans* (142/177, 80%). 53(18%) were *Aspergillus species* of which *Aspergillus fumigatus* was the most common (26/53). 16/285 (5.6%) patients underwent intervention based on the results, 14(87.5%) of which were appropriate. 176/177 (99.4%) patients with *Candida species* in BAL cultures were not treated.10/53 (18. 8%) patients with *Aspergillus species* in BAL cultures were treated of which 80% were appropriate interventions based on proven/probable invasive fungal infections criteria as were rest of the 6/16 patients with other fungal organisms (Table 4). Patients with *Aspergillus species* in BAL cultures are 8 times more likely to have an intervention (OR: 8. 7, $P = < 0.0001$) while patients with *Candida species* in BAL cultures are not likely to be intervened upon (OR: 0. 26, $P = 0.0098$) (Table 3).

Conclusion. Although *Candida species* is commonly isolated in BAL cultures its clinical significance is minimal in the absence of disseminated disease even in immunosuppressed hosts. Evaluating the way that *Candida* cultures are communicated for respiratory specimens, along with diagnostic stewardship may be a route for antimicrobial stewardship. Consulting ID service early on is essential in assessing the significance of fungal culture data thereby resulting in appropriate changes in management.

	Intervention done(n=16)	No Intervention done (n=269)	p-value
Age (median, interquartile range)	68 (60-72)	63 (54-70)	0.1232
Diabetes Mellitus	3(18.75%)	60(95.24%)	1.00
ANC	5.385	5.23	0.92
Malignancy	11(68.75%)	134(49.81%)	0.19
Transplant	6(37.5%)	83(30.86%)	0.57
Immunosuppressive medication	15(93.75%)	220(81.78%)	0.32
Steroids	11(68.75%)	157(58.36%)	0.42
Targeted therapy	5(31.25%)	76(28.25%)	0.8
Chemotherapy	5(31.25%)	79(29.37%)	0.8
BAL aspergillus antigen	7(43.75%)	9(56.25)	<0.0001
Serum aspergillus antigen	2(12.50%)	1(0.37%)	0.008
Serum β-D glucan	3(18.75%)	7(2%)	0.001
Proven/ probable fungal infection	13(81.25%)	0	<0.0001
Infectious Diseases consultation	15(93.75%)	153(56.88%)	0.003

Table 1: Groups with and without intervention based on age, comorbidities, supportive laboratory criteria, and Infectious Diseases consultation. ANC=Absolute Neutrophil Count

BAL fungal culture	Intervention done(n=16)	No Intervention done (n=269)	p-value
Aspergillus species	10(62.50%)	43(15.99%)	<0.0001
Candida species	5(31.25%)	171(63.75%)	0.0098
Penicillium species	1(6.25%)	47(17.47%)	0.48
Cryptococcal species	2(13.33%)	0	0.0028
Fusarium species	1(6.25%)	2(0.74%)	0.15
Mucorales	1(6.25%)	3(1.12%)	0.20

Table 2: Groups with and without intervention based on the type of fungal organisms isolated in BAL fungal cultures. 5 patients with *Candida species* who had an intervention were treated for other fungal organisms that grew with it rather than for *Candida* per se.

	Intervention done(n=16)	No Intervention done (n=269)	p-value
All types of leukemia	4(25%)	36(13.38%)	0.254
All types of lymphoma	3(18.75%)	30(11.15%)	0.41
Multiple myeloma	0	12(4.46%)	1.00
Other malignancies	4(25%)	52(19.33%)	0.52
Allogenic SCT	2(12.5%)	24(8.92%)	0.64
Autologous SCT	0	11(4.09%)	1.00
Solid organ transplant	4(25%)	45(16.73%)	0.49

Table 3: Groups with and without intervention based on the type of malignancy and transplant. SCT= Stem Cell Transplant

Fungal Organism Isolated on BAL Fungal Culture	Intervention done (n=16)/Appropriate intervention(n=14)
SCEDOSPORIUM BOYDII COMPLEX	1/1
HISTOPLASMA CAPSULATUM	1/1
FILAMENTOUS FUNGUS (BASIDIOMYCETE)	1/1
CRYPTOCOCCUS NEOFORMANS	2/2
FUSARIUM sp	1/1
ASPERGILLUS SPECIES	10/8

Table 4: Fungi with intervention based on culture positivity.

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268. Fungal NGS: Identification of Etiological Agents of Invasive Fungal Infection by High-throughput Sequencing

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Background. Invasive fungal infections (IFI) cause severe symptoms that affect immunocompromised and transplant patient populations. Antifungal therapies vary depending on the pathogenic species, and delays in diagnosis can lead to graft loss and an increase in morbidity and mortality. Therefore, rapid identification of fungi causing IFI is critical for informing antifungal therapy. Such actionable genus/species information can be obtained quickly via Next-generation Sequencing (NGS). In this study, an NGS assay was developed to identify fungal species responsible for IFI, allowing for selection of effective antifungal therapies.

Methods. Internal transcribed spacer (ITS) regions 1 and 2 were used for fungal identification. Primers were taken from published research and/or designed/modified by assessment in fungal sequence alignments. A DNA sequence database was compiled and a reference-assisted assembly approach utilizing % sequence ID and % coverage was developed for species identification. End-point PCR was conducted on DNA extracted from 19 pathogenic fungal species, and mixed communities (MC) for preliminary sensitivity and inclusivity. Sensitivity was assessed using dilutions of template DNA into the PCR reaction.

Results. NGS data of 14 individual species and 4 MC passed quality control checks. Using only ITS1 and ITS2, species identification was expected for 10 of 14 individuals. We observed species identification in 9 individual samples, and 13 were identified within the top 5 results. All individuals were identified to genus. In MC analyses, combinations of 3, 4, 6, and 10 fungal species resolved 100% of the genera present, but failed to resolve species adequately with only 2 loci evaluated. Unexpectedly, 3 tested Aspergillus spp. were correctly identified with this limited data in both single and MC samples. The lower limit of detection was assessed at 5,000 genomic equivalents/mL of eluate.

Conclusion. The inclusivity and sensitivity demonstrated here of an NGS approach for identification of etiological agents of IFI support this assay's potential utility as an aid in the treatment of IFI in at-risk patient groups. This assay allows for rapid identification (<4 days) of fungal species to aid clinicians in improving case outcomes.

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