Table 3.

Proven and probable cases	n (total = 41)	%
Female sex	20	48.8%
Age	Median 56.2	IQR 21.8 years
Underlying disease		
ALL	5	12.2
AML	22	53.7
CML	3	7.3
Lymphoma	4	9.8
MDS	4	9.8
Other	3	7.3
Disease status		
De novo	13	31.7
Complete response	8	19.5
Relapse	11	26.8
Refractory	5	12.2
Partial	4	9.8
Previous HSCT	16	39.0
Neutropenic	32	78.0
T-lymphocyte inhibitors	15	36.6
Use of high dose steroids	18	43.9
Active GvHD	6	14.6
Proven IA	4	9.8
Probable IA	37	90.2
Aspergillus fumigatus cultured	8	19.5
EORTC response week 6		
Complete	4	9.8
Partial	16	3.9
Progression	1	2.4
Death	8	19.5
Unevaluable	8	19.5
Stable	4	9.8
Mould-active prophylaxis	0	0

P413

Screening and diagnosis of Candidemia in adult hematological malignancies of northern India

Gopa Banerjee[1], Shivangi Tripathi[1,2], Anil Kumar Tripathi[3], Shailendra Prasad Verma[3]
[1]King George's Medical University, Lucknow, India
[2]Department of Biosciences, Integral University, Lucknow, India
[3]Department of Clinical Hematology, King George's Medical University, Lucknow, India

Poster session 3, September 23, 2022, 12:30 PM - 1:30 PM

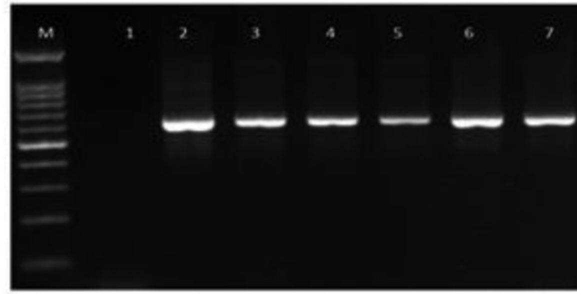
Candidemia is caused by *Candida* species which has become a common cause of fungal infection in the bloodstream infection throughout the world. In hematological malignancies, patients have a high rate of morbidity and mortality due to Candidemia.

Aim: To identify Candidemia in immunocompromised patients with the help of various conventional methods as well as automated methods for early detection and treatment.

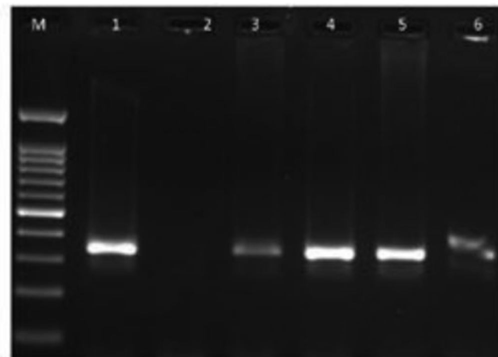
Material and Methods: This study was conducted from 2018 to 2021. In this study, we enrolled immunocompromised patients with hematological malignancies. For early diagnosis of Candidemia we did conventional method as well as PCR. Compare the conventional, automated, and PCR methods for diagnosis of Candidemia and was performed antifungal susceptibility testing for treatment in hematological patients.

Results: Total 187 patients were enrolled on the basis of febrile neutropenia. A total of 125/187 males (66.8%) and 62/187 females (33.2%) participated in the present study followed by age range from 10 to 77 years (mean = 33.16, standard deviation = 16.29). A total of 5 patients (2.6%) were positive from blood culture, and 9 patients (4.8%) were positive from PCR. In 4 patients of AML *C. tropicalis* was (3; 1.60%) and *C. auris* (1; 0.5%) followed by 1 patient with pancytopenia *C. tropicalis* (1; 0.5%). The sensitivity was done according to the Clinical Laboratory Standards Institute (CLSI) guideline M27-A3 reference document for *C. tropicalis* (4), and *C. auris* (1). A total of 4 isolates of *C. tropicalis* were sensitive to drug VRC (MIC range 0.125 μg/ml), AMP (MIC range 1 μg/ml), FLU (MIC range 1 μg/ml), CAS (MIC range 0.25 μg/ml) and 1 resistant pattern toward FLU (MIC range 4 μg/ml). *Candida auris* was resistant toward AMP (MIC range 2 μg/ml), FLU (MIC range 64 μg/ml), and sensitive toward CAS (MIC range 0.5 μg/mL). A total of 4 isolates of *C. tropicalis* was sensitive for drug VRC (80%), AMP (80%), FLU (60%), CAS (80%), and resistant pattern for FLU (20%). *Candida auris* was resistant toward AMP (20%), FLU (20%), and sensitive toward CAS (20%). In all, 9/187 patients' blood was positive for fungal infection, primer NL-1 and NL-4 were able to amplify the D1/D2 region of 28S r-DNA of large ribosomal subunit which target rDNA yielding Product of PCR give 600 bp related to all fungus. Primer P4501 and P4502 identify the *P*-450 lanosterol 14α-demethylase gene which is target *Candida* species genes single band of around 350 bp. Mannan antigen of *Candida* was performed by ELISA method for diagnosis of candidemia in hematological patients.

Conclusion: This present observational study recognizes the main association of Candidemia with hematological malignancies. We try to develop PCR and automated methods in routine mycology laboratory to diagnose Candidemia in an early stage in hematological malignancies along with other immunocompromised patients for better treatment to cure the disease.



Picture 1. Lane M showing 100 bp DNA Ladder, lane 1 as a negative control, lane 2 showing 600 bp amplified PCR product of fungus DNA, Lane 3,4,5,6,7 showing 600 bp amplified PCR product of fungal DNA.



Picture 2. Lane M showing 100 bp DNA Ladder, lane 1 showing 350 bp amplified PCR product of Candida, Lane 2 showing as a negative control. Lane 3,4,5,6 showing 350 bp amplified PCR product of Candida.

P414

Diagnostic allele-specific PCR for the identification of *Candida auris* clades and common resistance mutations

Hans Carolus[1,2], Stef Jacobs[1], Celia Lobo Romero[1,2], Quinten Deparis[2,3], Christina A. Cuomo.[4], Jacques F. Meis[5,6], Patrick Van Dijck[1,2]
[1]Laboratory of Molecular Cell Biology, Department of Biology, Institute of Botany and Microbiology, KU Leuven, Leuven, Belgium
[2]VIB-KU Leuven Center for Microbiology, Leuven, Belgium
[3]Laboratory for Genetics and Genomics, Centre for Microbial and Plant Genetics, KU Leuven, Leuven, Belgium
[4]Broad Institute of MIT and Harvard, Cambridge, USA
[5]Department of Medical Microbiology and Infectious Diseases, Canisius-Wilhelmina Hospital, Nijmegen, The Netherlands
[6]Centre of Expertise in Mycology Radboudumc/CWZ, Nijmegen, The Netherlands

Poster session 3, September 23, 2022, 12:30 PM - 1:30 PM

Candida auris (*C. auris*) is an opportunistic pathogenic yeast that emerged worldwide during the past decade. This fungal pathogen poses a significant public health threat due to common multidrug resistance (MDR), alarming hospital outbreaks, and frequent misidentification. Genomic analyses have identified five distinct clades that are linked to five geographic areas of origin and characterized by differences in several phenotypic traits such as virulence and drug resistance.

Typing of *C. auris* strains and the identification of clades can be a powerful tool in molecular epidemiology and might be of clinical importance by estimating outbreak and MDR potential. As *C. auris* has caused global outbreaks, including in low-income countries, typing *C. auris* strains quickly and inexpensively is highly valuable. We report five allele-specific multiplex polymerase chain reaction (AS-multiplex PCR) assays for the identification of *C. auris* and each of the five described clades of *C. auris* based on conserved mutations in the internal transcribed spacer (ITS) rDNA region and a clade-specific gene cluster. Additionally, we developed AS-PCR assays for the identification of SNPs in FKS1 and ERG11 that are commonly linked to echinocandin and azole resistance respectively.

This PCR method provides a fast, cheap, sequencing-free diagnostic tool for the identification of *C. auris*, *C. auris* clades, and common resistance mutations.

P415

High positive and rapid detection of clinical urine samples of fungal infection based on modified calcium fluorescence

Biao Chen, Dongmei Shi
Jining No. 1 People's Hospital, Jining, China

Poster session 3, September 23, 2022, 12:30 PM - 1:30 PM

Successful management of urinary fungal infection depends upon the detection positive and efficiency. The aim of this study was to evaluate the detection positive and efficiency of modified calcium fluorescent white (m-CFW) staining in direct detection of *Candida* spp. in urine samples of patients with suspected fungal infection. We collected 100 clinical urine samples from different departments and analyzed the detection positive rate of the methods of culture, KOH, sequence, and modified CFW. The results indicated that the positive rate of the methods was 12%, 8%, 14%, and 15%, respectively. The positive rate of modified CFW staining was significantly higher than that of ordinary microscopic examination and fungal culture ($P < .05$). Modified CFW in the detection of fungi in urine can significantly improve the positive rate of fungi in clinical urine samples and shorten the detection time. It has a certain reference value for clinical diagnosis and medication.