Objectives: Candida auris is an emerging fungal pathogen responsible for hospital outbreaks. It represents a serious threat due to its drug resistance profile and its potential spread within healthcare facilities. Since the global alert by the CDC in 2016, specific control measures are now available to prevent the further spread of the pathogen. These measures should be implemented immediately as soon as a case is identified to prevent patient-to-patient transmission. Until recently, culture was the main technique used for the detection of C. auris from patient and environmental samples. Nevertheless, qPCR protocols have been reported and commercial kits are now available. Our objective was to compare culture and PCR in routine for the management of a case of C. auris infection in a hospital setting.

Methods: We report here the case of a patient infected by C. auris following injures in a public road traffic accident in Delhi. Following the medical evacuation and transfer of the patient to our hospital in Paris, C. auris was isolated from several surgical specimens from the elbow. Identification of the species level was initially performed by MALDI-TOF Mass spectrometry and confirmed by ITS sequencing. Antifungal susceptibility testing was performed by Etest and EUCAST. Surveillance of the index case included microbiology surveillance for 2 weeks and then once a week. Cultures were also screened for C. auris colonization once a week by microbiological media and skin. Samples were analyzed by standard mycological cultures and a specific C. auris qPCR kit (Kit Pangenomie Candida aurea®, Bio Rad).

Results: In total 133 samples were analyzed for the patient and 52 controls. For the index case, 14/22 samples were positive in culture for C. auris including elbow biopsies, urine, and axilla, groin, and oral swabs. Other Candida species (C. albicans, C. glabrata) were also recovered from the same samples for the patient. For the controls, all 111 samples were negative for C. auris by cultures, but retrieved several other yeast species (C. albicans, C. glabrata, C. krusei, C. parapsilosis, C. tropicalis, Saccharomyces cerevisiae, Rhodotorula glutinis, and Wickerhamiella anomala). By using qPCR, all culture-positive samples were positive (C ranged from 29.7 to 38.0, with a median at 31.4). Two culture-negative samples (one biopsy and one auditory swab) were also qPCR-positive. All samples from controls were negative by qPCR. The strain was resistant to fluconazole (MIC 216 µg/mL) and susceptible to all other antifungals (Itraconazole, Voriconazole, and Caspofungin). Whole genome sequencing of the C. auris strain is in progress to determine the clade.

Discussion: The Pangenome C. auris qPCR kit determined good sensitivity and specificity, even for the frequent structure of samples growing with two or three Candida species. These results highlight the usefulness of the qPCR for surveillance of infected patients as well as for controls.
GMI RESULT * INVASIVE ASPERGILLOSIS Crosstabulation

| GMI RESULT | NEGATIVE | POSITIVE |
|------------|----------|----------|
| Count      | 36       | 7        | 43       |
| % within INVASIVE ASPERGILLOSIS | 83.7% | 15.9% | 49.4% |
| POSITIVE Count | 7   | 37       | 44       |
| % within INVASIVE ASPERGILLOSIS | 16.3% | 84.1% | 50.6% |
| Total Count | 43     | 44       | 87       |
| % within INVASIVE ASPERGILLOSIS | 100.0% | 100.0% | 100.0% |

YOUDEn’S INDEX = (SENSITIVITY + SPECIFICITY) − 1 = (0.837 + 0.841) − 1 = 0.678

Case Processing Summary

| INVASIVE ASPERGILLOSIS | Valid N (listwise) |
|-------------------------|--------------------|
| Positive                | 44                 |
| Negative                | 43                 |

Larger values of the test result variable(s) indicate stronger evidence for a positive actual state.

a. The test result variable(s): galactomannan index has at least one tie between the positive actual state group and the negative actual state group.

b. The positive actual state is POSITIVE.

ROC Curve

Area Under the Curve

Test Result Variable(s): galactomannan index

| Area | Std. Error | Asymptotic Sig. | Asymptotic 95% Confidence Interval |
|------|------------|-----------------|-----------------------------------|
| .004 | .034       | .000            | .837                              |
|      |            |                 | .970                              |

The test result variable(s): galactomannan index has at least one tie between the positive actual state group and the negative actual state group. Statistics may be biased.

a. Under the nonparametric assumption
b. Null hypothesis: true area = 0.5
P420
Fungal detection by means of HCR using 2D-Covalent Organic Framework Nanosheet
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Poster session 3, September 23, 2022, 12:30 PM - 1:30 PM
The timely diagnosis of fungal infections is of prime importance for prescribing appropriate anti-fungal drugs. Current methods for fungal diagnosis involve culture-based methods, antibody-based detection using lateral flow assay and PCR.
In the present work, we derived a non-antibody amplification using 2D-Covalent Organic Framework (COF) nanosheet for the detection of fungal DNA.
Objectives: (1) Validation of exfoliated 2D COF Nanosheet as an efficient DNA detection tool via Hybridization chain reaction (HCR) triggered fluorescent assay. (2) Sequence removal and probe generation of fungal sample and detection of extracted target DNA via fluorescent assay.
Method: A novel COF was synthesized and characterization was done using FTIR, BET, TGA, XRD, and SEM. Probes for the detection of fungi (Candida, Aspergillus, and Mucor) were designed using Nupack software. HCR was monitored for different time and probe concentrations and standardized reaction was used for the detection of fungal RNA.
Results: FTIR, BET, TGA, XRD, and SEM confirmed the structure and formation of COF nanosheet. HH, H2 probes at a concentration of 3 μM in the presence of Target DNA (0.05 μM) triggered HCR reaction at 1.5 h. Fluorescence quenching was observed when probes were mixed with bulk COF and COF nanosheet but increased quenching.
Conclusions: Fungal detection can be done by means of HCR using the COF nanosheet.

P421
Whole-transcriptome analysis of Sporotrichum brasiliensis grown in mold- and yeast-inducing conditions
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Poster session 3, September 23, 2022, 12:30 PM - 1:30 PM
Objectives: Sporotrichum brasiliensis is an emerging Sporotrichaceae species found in Brazil capable of causing sporotrichosis in humans and animals, especially in cats. Like other pathogenic Sporotrichaceae species, S. brasiliensis exhibits a temperature-dependent dimorphic switch and this pathogenicity is under the control of environmental thermal stimuli. While dimorphism appears to be essential for virulence in Sporotrichaceae spp., the molecular mechanisms involved in this phenomenon have not yet been fully elucidated.
In this study, we used the strand-specific RNA-Seq technique and bioinformatics analysis to investigate the transcriptome signatures associated with mold and yeast phases of S. brasiliensis. Furthermore, we generated an accurate version of the S. brasiliensis genome annotation in order to perform high-quality gene expression analysis and functional or structural genomic studies.
Methods: The whole transcriptome of S. brasiliensis ATCC MYA-4621, grown in both yeast-induced (YPD medium at 37°C) and mold-induced (YPD medium at 25°C) conditions, was sequenced in this study. High-quality RNA was used to prepare Illumina TruSeq Stranded mRNA-paired-end sequencing libraries (2 × 150 bp) that were sequenced using the HiSeq-2500 platform. A total of three biological replicates were sequenced for each condition.
Before transcriptome assembly, adapters and low-quality reads (Phred-score <25) were removed. The StringTie software was used to assemble the transcriptome imported into the Apollo webtool to manually curate the genome annotation. Transcriptomes were investigated using TransDecoder and CPC2 programs to determine whether a gene was potentially protein-coding or non-coding. Finally, differential gene expression analysis between yeast and mold forms of S. brasiliensis was conducted using the edgeR package.
Results: Illumina sequencing resulted in a total of ~217 million raw reads. After quality filtration and trimming, ~99.5% of reads were used for downstream bioinformatics analysis. The updated S. brasiliensis genome annotation consisted of a total of 14,664 genes of which 10,245 protein-coding genes, 4,359 lincRNAs, 181 RfRNAs, and 22 tRNAs.
Gene expression analysis revealed a total of 13,838 and 13,938 transcripts expressed in mold- and yeast-form, respectively. Of these, 19% and 21% were expressed exclusively in the mold and yeast phase, respectively. Moreover, a total of 6,952 genes (FDR < 0.05) were differentially expressed between the two examined conditions. In particular, 3,420 of these genes were up-regulated in the yeast-form (2450 coding, 970 non-coding) and 1,382 genes in the mold-form (2307 coding, 879 non-coding). The raw reads have been deposited into the NCBI database and are available under BioProject PRJNA6464214.
Conclusions: The characterization of the whole-transcriptome of S. brasiliensis mycelial and yeast-like forms represents an essential starting point for investigating the molecular pathways and regulatory frameworks associated with these two morphological stages. Our results provide new insight into global gene expression profiles of S. brasiliensis, emphasizing the role of non-coding RNAs in its complex transcriptional network.
All transcriptomic data have also been integrated into the "Sporotrichaceae Genomics Database" (www.sporotrichosgenomicstudias.unimi.it) in order to expand the current knowledge of Sporotrichaceae genomics and to allow a more in-depth structural exploration of S. brasiliensis gene models, including gene expression patterns related to its saprophytic and pathogenic lifestyles.

P422
EQUAL PCP Score 2022—an ECMR score derived from current guidelines to measure QUALITY of clinical Pneumocystis management
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Poster session 3, September 23, 2022, 12:30 PM - 1:30 PM
Background: Pneumocystis pneumonia (PCP) is a life-threatening opportunistic fungal infection requiring complex clinical management. Guidelines assist clinicians but can be challenging to comply with.
Objectives: To develop a scoring tool that facilitates and quantifies adherence to guidelines recommendations for PCP management. We reviewed current PCP guidelines and determined essential recommendations for diagnosis, treatment, and follow-up. These were weighted according to their strength of recommendation and level of evidence.
Results: The EQUAL PCP Score 2022 consists of 22 items. For diagnosis, weight was given to bronchoalveolar lavage and immunofluorescence assays as the gold-standard for sampling and analysis. Beta-D-Fructan was considered of similar importance due to its high negative predictive value. Trimethoprim/sulfamethoxazole and the addition of corticosteroids in respiratory failure got the highest points respectively. Alternative approaches received less points and the use of artemether-lumefantrine was discouraged with 1 minus point. HIV-specific considerations such as the start of secondary prophylaxis were factored in as well.
Conclusions: The EQUAL PCP Score 2022 weight and aggregate scores recommended for optimal management of PCP. It provides a tool for antimicrobial stewardship as well as for measuring guideline adherence but remains to be correlated with patient outcomes.