PCA analysis revealed that the replicates of each protocol for the 4-time points analyzed were close to each other, related to the good quality of our experiments. The differential gene expression (DGE) showed significant \( P < 0.01 \) and Log2 fold change >1.5 differences at H10 which highlights the impact of the procedures on the TC process. The highest number of DGE were observed between H0 and H7 for the three protocols, where about two 410 DGE, two 168 DGE, and two 300 AA, O2, and EB, respectively. After analysis of the PCA plot showing the kinetics, EB and O2 are grouped while AA is not. That could be explained by the presence of PBS in O2 and EB protocols.

Conclusion: By running the three protocols in parallel, we showed here that the kinetics of TC generation differs between each other with a significant variation of the transcriptome. This is an important finding that paves the way to compare more deeply the transcriptome of C. neoformans during TC generation as the final goal is to identify the genes associated with TC generation.

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Scalp fungal microbiome and sebum composition in males with and without androgenetic alopecia
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Poster session 3, September 23, 2022, 12:30 PM - 1:30 PM

Objectives: Lipophilic Malassezia species are abundant in the scalp microbiome; we investigated the scalp microbiome and sebum composition of patients with androgenetic alopecia (AGA) and aimed to identify factors accelerating AGA progression.

Materials and Methods: Scalp scale samples (wax) were collected from 55 male Japanese patients with AGA and 63 healthy individuals. Fungal RNA genes were amplified by PCR and the amplicons were sequenced on the MiSeq platform. The extent of fungal colonization was determined by qPCR. We used gas chromatography/mass spectrometry to measure the sebum levels of free fatty acids, dihydroceramide, triglycerides, squalene, free cholesterol, cholesteryl esters, and wax.

Results and Discussion: Malassezia restricta predominated in all AGA (64.7%) and non-AGA age groups (44.6%). qPCR revealed that Malassezia colonization was more extensive in the AGA than non-AGA group, regardless of age; the Malassezia level was significantly higher in AGA subjects aged 10-19 than 30-49 years. The TC level was significantly higher in the AGA than non-AGA group \( (P < 0.01) \) but the free fatty acid, squalene, and free cholesteryl levels were significantly lower \( (P < 0.01) \).

Conclusion: Thus, the scalp fungal microbiome and sebum composition may influence AGA development.

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'Ye's not fungus, it's Nocardia'—an elementary diagnostic challenge for draining sinus on abdominal wall (rare): a case report
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Poster session 3, September 23, 2022, 12:30 PM - 1:30 PM

Introduction: A rare finding of abdominal wall clinical presentation of persistent progressive multifocal draining sinus with no granules caused by Nocardia brasiliensis.

Methods: History: A 22-year-old presented to the Dermatology OPD with complaints of swelling and tenderness and discharging masses with no granules around the periumbilical region in the lower abdominal area for three years. His initial fine needle aspiration cytology specimen report was inconclusive. He received anti-tuberculous treatment and a positive Mantoux test and family history from outside the hospital. Initially punch biopsy samples were sent for fungal processing to our laboratory which was inconclusive. Report pus aspirate and punch biopsy samples were subjected to conventional techniques. The sample was inoculated on Sabouraud’s Dextrose agar, Brain heart Infusion agar, and Lowenstein-Jensen media. Direct Smear was subjected to Gram stain and Modified Zehl-Nelson stain with 1% Sulfuric acid as decolorizer.

Results: 1. On Gram stain, Gram-positive filamentous bacilli against a background of pus cells in pus aspirate only (not in punch biopsy specimen).
   2. Modified Zehl-Nelson stain with 1% Sulfuric acid decoloriser performed on all three samples. Beaded acid-fast filamentous bacilli with plenty of pus cells in the background were seen in pus aspirate only (not in punch biopsy specimen).
   3. No fungal elements were observed on the 20% KOH mount.
   4. Clinicians were notified immediately with the provisional report of possible Actinomycetoma due to Nocardia sp.
   5. Growth observed within 9 days on SDA as well as LJ. It was a chalky white, dry colony to begin with that turned straw yellow in another week’s time. Smear from the colony showed Gram-positive filamentous bacilli which on Modified ZN Smear were acid-fast filamentous beaded bacilli. The isolate was identified as Nocardia species. This was further confirmed as Nocardia brasiliensis by MALDI-TOF.

On admission, the patient was initially started on im. Amikacin and then changed to Modified Kamen regime of double dose Ciprofloxacin and Gentamicin. His lesions started showing improvement over 2 weeks of in-patient treatment. He was discharged on oral treatment thereafter.

Conclusion:
1. Abdominal wall clinical presentation of persistent progressive multifocal draining sinus with no granules caused by N. brasiliensis is a rare clinical entity in Mycoses. The differential diagnosis includes other bacterial or fungal etiology or nocardiosis.
2. Delay in correct diagnosis led to the chronicity of the clinical presentation with inappropiate therapy.
3. For a chronic destructive debilitating infective mycetoma presentation, appropriate microbiological diagnosis become essential to have early correct antibiotic with proper sampling technique to guide the appropriate therapy as per the causative pathogen.
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Characterization of the virulence potential of Aspergillus species of section Semi in Galleria mellonella infection model
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Objective: Species belonging to the genus Aspergillus are among the most common causative agents of human and animal infections. Less than 40 species among all Aspergillus species are known to be associated with human infections, including allergic bronchopulmonary aspergillosis, chronic pulmonary aspergillosis, and invasive aspergillosis. And of these, Aspergillus section Fumigati is one of the major infection causes of death, followed by members of sections Mucor, Nigri, and Terrei. Aspergillus species in section Terrei are categorized into three species: Ambigui, Nivei, and Terrei. A. terreus aureus stricto is the first species described and the most common species found worldwide in different ecological habitats. However, there are several other species within the section Terrei, owning cryptic species which are not distinguished by conventional morphological analysis, even though they are genetically accepted by forming a distinctive phylogenetic clade. Despite definite species identification, there is still less known about the virulence potential of all species in this section, and it might be underestimated because of their lack of detection by conventional diagnostic methods. In this ongoing study, the virulence of Galleria mellonella model has been utilized to examine the intra- and interspecies virulence dependency of section Terrei. Methods: A total of 16 isolated Aspergillus species in section Terrei (n = 16) were tested, including A. terreus aureus stricto, A. ambigui ambigui, A. fumigatus fumigatus, A. flavus flavus, A. niger niger, A. clavatus, A. candidus, A. nivssus nivssus, A. terreus terreus, A. soclifera, A. nivssus nivssus, A. fumigatus fumigatus, A. flavus flavus, A. niger niger, A. clavatus, A. candidus, A. nivssus nivssus, A. terreus terreus, A. soclifera. Species were identified by sequencing gene regions of b-tubulin, calmodulin, and RNA Polymerase II subunit 2 (RP2). Briefly, groups of larvae (n = 50) were reared in wood shavings in the dark at 18°C for 24 h before the experiment. Three groups were included. Larvae infected with 107 conidial/larva, larvae injected with 20 µl sterile insect physiological saline, and untreated larvae. The survival rate was monitored for up to 144 h at 37°C.

Results: Medium survival rates revealed a species-dependent virulence pattern. Larvae associated with A. nivssus nivssus, A. soclifera soclifera (A. terreus Terrei) and A. streus, A. carneus, and A. nivssus nivssus exhibited high virulence potential by reducing the survivor rate in comparison with other species. In contrast, species belonging to the same Ambigii showed low virulence potential.

Conclusion: In conclusion, the virulence characteristics of section Terrei differ between species. Further studies are needed to analyze the species’ interactions, such as histopathology and immune response of G. mellonella.

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Candida auris: a growing threat to global health
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Background and Objective: The emerging pathogen, C. auris, has been associated with nosocomial outbreaks in recent times. The true scale of the problem is difficult to comprehend due to several issues with the identification of C. auris using both phenotypic and molecular techniques. Most commonly, these isolates have been misidentified as C. laurentii. Biofilm formation is strongly suggested given its association with innate care settings, especially in patients with CVG and long-term urinary catheters. Many isolates of C. auris have also shown raised MICs to multiple classes of antifungal agents, causing the possibility of pan-drug resistance.

Objective: To study the demographic characteristics, risk factors, and outcomes in patients with C. auris infection.

Methodology: This is a retrospective study from a tertiary care hospital (IPNATC, AMBS) including all patients from the time period of 2018-2022 that showed growth of C. auris in any site. C. auris was identified using conventional methods (gallocate growth on chromogenic medium, no pseudohyphae on gram-stain test, growth in presence of 10% NaCl) and VITEK-2. To reduce the misidentification and the inter-laboratory variability, the results were confirmed with MALDI-TOF. The risk factors and other patient information were taken from the HIS. Statistical analysis was performed.

Results: During the study period, a total of 31 patients had a C. auris infection. The most common age group was 20-40 years (n = 11,44%) with a predominance in males (n = 22,74%). A total of 57% of the infections were found in blood, which was the most common site of infection followed by urine (10%). The other sites were post-operative (n = 2), groin, tailbiops, and CVP (n = 1). Most of the cases were ICU patients (44%). All the patients with candidaemia due to C. auris (n = 17) had CVC, had surgery within the past 30 days, and were on broad-spectrum antibiotics. 73.1% (n = 12) had a history of immunosuppression and 18% (n = 4) had a history of prior antifungal therapy. Although 109% (n = 17) had the presence of an indwelling urinary catheter, none of them had candiduria due to C. auris. No patient with C. auris infection had neutropenia. The median LOS was 32.4 days. Most of the isolates were resistant to fluconazole (n = 27,93%), amphotericin B (n = 13,93%), voriconazole (n = 6,28%), caspofungin (n = 2,78%). A total of 47% (n = 12,48%) of isolates were sensitive to caspofungin and micafungin by VITEK-2 (Limitation of this study). In all, 24% (n = 7) of the patients died whereas 40% (n = 12) were discharged. A total of 75% patients had clearing of the questionable candidaemia when treated with caspofungin whereas only 25% patients had clearing of the candidaemia when treated with voriconazole.

Conclusion: Most cases of C. auris infections were found in critical patients with the most common presentation being candidemia. The risk factors are similar to any other Candida infection. C. auris is the leading antifungal-resistant fungus and poses an additional burden to the healthcare system. The fungus has a high crude-mortality rate and we are running out of treatment options. A comprehensive intervention program with ongoing surveillance and good AMR practice is the need of the hour to reduce the burden of this dangerous pathogen.