Poster Presentations

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Characterization of the virulence potential of Aspergillus species of section Sesi in Galleria mellonella infection model
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Objectives: 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 Nigri is one of the major infection causes of death, followed by members of sections Max, Nigri, and Terrei. Aspergillus species in section Terrei are categorized into winter, summer, and Terrei. A. terreus arises strictly in 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, arising cryptic species which are not distinguished by conventional morphological analysis, even though they are taxonomically accepted by forming a distinctive phlogistic clade. Despite definitive 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 in vivo Galleria mellonella model has been utilized to examine the intra- and interspecies virulence dependency of section Terrei.

Methods: A total of 14 accepted Aspergillus species in section Terrei (n = 14) were tested, including A. terreus var. strictus, A. camphoratus, A. horacekii, A. pseudoterreus, A. aflatropius, A. flavoconia, A. flavus, A. flavispora, A. carneus, A. stercorarius, A. terreus, A. clausii, A. hyalopezus, A. ficatarius, A. niger, A. niveus, A. rugosporus, A. brasiliensis, A. americana, A. flavus, A. niger, A. clausii, A. ficatarius, A. niveus, A. rugosporus, A. brasiliensis, A. americana, A. flavus, A. niger, A. clausii, A. ficatarius, A. niveus, A. rugosporus, A. brasiliensis, A. americana, A. flavus, A. niger, A. clausii, A. ficatarius, A. niveus, A. rugosporus, A. brasiliensis, A. americana, A. flavus, A. niger, A. clausii, A. ficatarius, A. niveus, A. rugosporus, and A. albabacladi. Species were identified by sequencing gene regions of b-tubulin, calmodulin, and rDNA Pol II. A total of 14 species were inoculated into the cuticle of Galleria mellonella larvae. Each strain was inoculated into the cuticle of Galleria mellonella larvae. The survival rate was monitored for up to 144 h at 37°C.

Results: Medium survival rates revealed a species-dependent virulence pattern. Lactovaccinum isolated from A. terreus, A. pseudoterreus (ivar Terrei) and A. stigmaster, A. carneus, and A. niger (ivar Niger) exhibited high virulence potential by infecting survival larvae in comparison with other species. In contrast, species belonging to the winter clade showed lower virulence potential.

Conclusions: In conclusion, the virulence characteristics of section Terrei differ between species. Further studies are needed to unravel the species' interactions, such as pathogenesis and immune response of G. mellonella.

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Candida auris: a growing threat to global health
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Objectives:
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. keurnielii. Biofilm formation is strongly suggested given its association with invasive care settings, especially in patients with CVCs 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.

Methodology: To study the dermatogenic characteristics, virulence factors, and outcomes in patients with C. auris infection.

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 = 23, 74%). A total of 74% of the infections were found in blood, which was the most common site of infection followed by sputum (10%). The other sites were pus-from-wound (n = 2), groin, tailbuds, and CVP tip (n = 1). Most of the cases were ICU patients (48%). All the patients with candidia due to C. auris (n = 17) 100% had CVC, had surgery within the past 30 days, and were on broad-spectrum antibiotics. Of these, 61% to 0.12 had a history of immunosuppression and 18% (n = 14) had a history of prior antifungal therapy. Although 100% (n = 31) had the presence of an indwelling urinary catheter, none of them had candida due to C. auris. No patient with C. auris infection had neutropaenia. The median LOS was 34.5 days. Most of the isolates were resistant to flucytosine (n = 13, 39%), amphotericin B (n = 13, 39%), voriconazole (n = 6, 18%), and caspofungin (n = 10, 71%). A total of 87% (n = 22, 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 71% patients had clearing of the present candidia when treated with caspofungin whereas only 25% patients had clearing of the candidia when treated with voriconazole.

Conclusions: Most cases of C. auris infections were found in critical patients with the most common presentation being candidaemia. The factors are similar to any other Candida infection. Caspofungin is leading the antifungal-resistant fungus and poses an additional burden to the healthcare system. The fungi 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 reverse the burden of this dangerous pathogens.

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Molecular identification and antifungal susceptibility of fungi causing sinusitis in arid climate region
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Objectives: Fungal sinusitis is a common problem worldwide with an increasing burden in arid climate regions. Clinical presentations of the disease range from allergic to acute invasive or chronic forms. In the present study, we aim to identify the etiology of fungal sinusitis in an arid climate region of Africa using molecular methods and to determine the antifungal susceptibility of the clinical isolates.
Methods: A total of 40 isolates collected from patients diagnosed with fungal sinusitis in Khetan один из называемых лабораторий в Кхетан.

To confirm the presence of fungal elements in tissue, histology was performed for all samples. Cultured isolates were then identified by sequencing the internal transcribed spacer (ITS), β-tubulin, and calmodulin gene regions. Antifungal susceptibility was tested using the protocol of the European Committee on Antimicrobial Susceptibility Testing (EUCAST).

Results: Sequencing of the three genes identified the following species: Aspergillus flavus (n = 48), A. chroomeus (n = 1), A. sawadae (n = 2), A. restrictus (n = 2), A. flavus (n = 1). Trichophyton auwahi (n = 1), and Paunamut diastelopsis (n = 1).

Conclusion: The fungi associated with sinusitis are of high diversity; the 40 isolates were found to belong to 8 different species. With the exception of cryptic species, a large concordance was found between molecular and phenotypic identification methods. Aspergillus is the most commonly reported genus with A. flavus as the most prevalent species.

Figure 1. Flow chart of specimens analyzed during the validation of the IMMY lateral flow assay for detection of anti-Sporothrix antibodies.

P390 A lateral flow assay for the immunodiagnosis of human cat-transmitted Sporotrichosis

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Objective: Sporotrichosis is a neglected zoonotic (animal-borne) mycosis caused by different species of Sporothrix spp. Since the 1990s, cat-transmitted sporotrichosis (CTS) by Sporothrix brasiliensis has emerged as an important zoonosis in Brazil, being a public health issue. The disease continues to spread in the country and neighboring countries. Therefore, the aim of the study is to validate a fast and accurate test for Lateral Flow Assay (LFA) for serodiagnosis of CTS using sera from human patients.

Methods: The anti-Sporothrix LFA was developed and provided by IMMY (Oklahoma, USA), and obtained using GAC purification of culture filtrate, composed by a 50:50 mix of A. brasiliensis (ATCC: 15251), and S. brasiliensis (ATCC: MYA 4024). The control line was a goat anti-human IgG conjugate. The gold conjugate was a blend of proteins G and λ. The strip was a conjugate pad, introduction membrane, and an absorbent pad. A prospective cross-sectional study was performed with 100 human sera specimens divided into three groups: Group 1: n = 100—patients with a proven or probable diagnosis of CTS based on the CDC/Clinical and Laboratory Standards Institute (CLSI) criteria; Group 2: n = 100—patients with other mycoses (zoonoses, oropharyngeal infections confirmed in the laboratory by direct examination and/or culture and/or serological tests); Group 3: n = 100—asymptomatic volunteers (Fig. 1). Specimens were collected between November 2018 and March 2021 at the Mycology Laboratory of the Clinical Hospital Complex of the Federal University of Paraná, Curitiba, Brazil. The sera were diluted 1:441 with specimen diluent, 100 µL of the dilution dispensed into a flat bottom well, unstraw strip, and incubated at room temperature (20±2°C) for 30 min. A visual read of the strips was done; this was read performed by two operators, within 10 min after the time of incubation. This study was approved by the Research Ethics Committee under registration CAAE 12319819.4.0000.5000. Data analysis was performed using MedCalc software.

Results: Using the IMMY’s anti-Sporothrix antibody detection LFA, we observed a global accuracy of 83% (95% confidence interval CI 80%-86%), a specificity of 82% (95% CI: 76%-87%), positive predictive value of 68% (95% CI: 42%-72%), negative predictive value of 90% (95% CI: 83%-95%), and an accuracy of 82% (77%-86%). The results by clinical form and cross-reaction analyses can be seen in Table 1.

Conclusion: These findings suggest that IMMY’s anti-Sporothrix antibody detection LFA prototype is promising, can be a useful diagnostic test for the diagnosis of CTS in human specimens, and can be used for the qualitative detection of serum antibodies against Sporothrix spp. Like other rapid tests, this LFA is faster and simpler to perform in comparison with other conventional laboratory assays for the diagnosis of sporotrichosis. This test can improve the earliest diagnosis of probable disease. Rapid detection of CTS reduces the morbidity of the disease, and consequently the time of therapy. It could have an impact on the control of the outbreak.