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**Characterization of the virulence potential of *Aspergillus* species of section *Terrei* in *Galleria mellonella* infection model**

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

**Objectives:** Species belonging to the genus of *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 infectious causes of death, followed by members of sections *Fluvi*, *Nigri*, and *Terrei*. *Aspergillus* species in section *Terrei* are categorized into three series: *Ambigui*, *Nivei*, and *Terrei*. *A. terreus sensu 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*, stating cryptic species which are not distinguished by conventional morphological analysis, even though they are taxonomically accepted by forming a distinctive phylogenetic 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 distinction by conventional diagnostic methods. In this ongoing study, the *in vivo* *Galleria mellonella* model has been utilized to examine the inter-and/or intraspecies virulence dependency of section *Terrei*.

**Methods:** A total of 18 accepted *Aspergillus* species in section *Terrei* ( $n = 18$ ) were tested, including *A. terreus sensu stricto*, *A. citrinotereus*, *A. hortae*, *A. pseudotereus*, *A. alabamensis*, *A. aureotereus*, *A. floccosus*, *A. iranicus*, *A. recifensis*, *A. carneus*, *A. microcysticus*, *A. niveus*, *A. bicephalus*, *A. neandicus*, *A. neoffricanus*, *A. barbosa*, *A. ambiguus*, and *A. allahabadii*. Species were identified by sequencing gene regions of  $\beta$ -tubulin, calmodulin, and RNA Polymerase II Subunit 2 (RPB2). Briefly, groups of larvae ( $n = 30$ ) (0.3 to 0.4 g; SAGIP, Italy) were stored in wood shavings in the dark at 18°C for 24 h before the experiment. Three groups were included: larvae infected with 10<sup>7</sup> conidia/larva, larvae injected with 20  $\mu$ L sterile insect physiological saline, and untouched larvae. The survival rate was monitored for up to 144 h at 37°C.

**Results:** Median survival rates revealed a species-dependent virulence pattern. Larvae inoculated with *A. aureotereus*, *A. pseudotereus* (*Serie Terrei*) and *A. niveus*, *A. carneus*, and *A. iranicus* (*Serie Nivei*) exhibited high virulence potential by reflecting lower survival rates in comparison with other species. In contrast, species belonging to the series *Ambigui* showed low virulence potential.

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

## P385

***Candida auris*: a growing threat to global health**

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

**Background and 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. baumholfii*. Biofilm formation is strongly suggested given its association with intensive 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, raising 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 (JPNATC, AIIMS) 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 (pale-pink growth on chromogenic medium, no pseudophae on germ-tube test, growth in presence of 10% NaCl) and VITEK-2. To reduce the misidentification and the intertest 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 preponderance 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 urine (10%). The other sites were pus-from-wound ( $n = 2$ ), groin, nailbeds, and CVP tip ( $n = 1$ ). Most of the cases were ICU patients (86%). All the patients with candidemia due to *C. auris* ( $n = 17, 100\%$ ) had CVC, had surgery within the past 30 days, and were on broad-spectrum antibiotics and TPN. 71% ( $n = 12$ ) had a history of immunosuppression and 18% ( $n = 14$ ) had a history of prior antifungal therapy. Although 100% ( $n = 17$ ) 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 34.5 days. Most of the isolates were resistant to fluconazole ( $n = 13, 93\%$ ), amphotericin B ( $n = 13, 93\%$ ), voriconazole ( $n = 6, 55\%$ ), flucytosine ( $n = 10, 71\%$ ). A total of 87% ( $n = 12, 87\%$ ) of isolates were sensitive to caspofungin and micafungin by VITEK-2 (limitation of this study). In all, 28% ( $n = 7$ ) of the patients died whereas 40% ( $n = 10$ ) were discharged. A total of 75% patients had clearing of the persistent candidemia when treated with caspofungin whereas only 25% patients had clearing of the candidemia when treated with voriconazole.

**Conclusion:** Most cases of *C. auris* infection 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 antimicrobial-resistant fungi 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 practices is the need of the hour to reduce the burden of this dangerous pathogen.

## P386

**Molecular identification and antifungal susceptibility of fungi causing sinusitis in arid climate region**

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

**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.