A randomized, double blind phase III proof-of-concept superiority trial of favipiravir 200 mg or 300 mg weekly dose versus itraconazole 400 mg daily, all time arms in combination with surgery, in patients with eumycetoma in Sudan—Top line results

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S5.4

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S5.4.d

Comparing the diagnostic performance of the commonly used eumycetoma diagnostic tests using sequencing of the internally transcribed spacer region as the gold standard

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4.7 Mycology Clinical Trial on favipiravir treatment in eumycetoma—Top Line Results, September 22nd, 2022, 10:30 AM - 12:00 PM

Objectives: Mycetoma is a neglected tropical disease caused by 70 different infective agents. Identifying the causative organism to the species level is essential for appropriate patient management. Ultrasound, histopathology, cultures, and species-specific PCR can be used for the species-specific identification of organisms. The aim of this study was to compare the diagnostic performance of these commonly used assays using sequencing of 18S rDNA as the gold standard.

Methods: This describes cross-sectional study was conducted at the Mycology Research Center, University of Khartoum, Sudan. It included 222 patients suspected of fungal mycetoma caused by Mucorales. Samples were collected from the standard-of-care microbiology laboratory for species-specific PCR. In 60 patients, at least one diagnostic of the tests failed to identify M. mycetomatis. A total of five patients had no evidence of eumycetoma, and for three, only the ultrasonics was indicated. Mycetoma: Two species-specific PCRs were the most sensitive diagnostic methods, followed by histopathology and ultrasound. Mycetoma was the least specific as it allowed differentiation between eumycetoma and eumycetoma. The result was that 99.9% for ultrasound, 3.74% for PCR, 8.5 days for histopathology, and 21 days for gene culture.

Conclusion: Currently, PCR directly on DNA isolated from grains in the most rapid and reliable diagnostic test to identify M. mycetomatis eumycetoma.

S5.4.d.1

Antifungal resistance

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S5.1 Antifungal resistance, September 22nd, 2022, 10:00 AM - 11:00 PM

Resistance to clinical antifungals in Aspergillus fumigatus has become an increasing threat in healthcare worldwide over the past two decades. Factors that contribute to the continuing trend are manifold, among others resistance emergence in environmental fungal strains through selection pressure due to fungicidal use in agriculture and farming. resistant clones are dispersed around the world through global travel and shipping routes, as well as prophylactic and long-term administration of antifungal agents in patients with chronic fungal disease causing selection pressure. Physicians face particular challenges in their patients with invasive aspergillosis, given the unpredictable consequences of using a subtherapeutic or suboptimal regimen, with emerging resistance adding another layer of therapeutic complexity. We are beginning to gain an understanding of the clinical implications of the different patterns of resistance. For instance, some fungal isolates have shown that resistance to A. fumigatus to clinical antifungal agents significantly hampers the successful treatment of patients.

This presentation aims to highlight the difficulties associated with antifungal resistance in A. fumigatus with a focus on hematological oncological patients.

S5.1d

Mechanisms of azole antifungal resistance in clinical isolates of Candida tropicalis

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S1.1 Antifungal resistance, September 22nd, 2022, 10:00 AM - 11:00 PM

Objectives: To study the pattern of resistance in C. tropicalis and its impact on therapeutic outcome. To study the role of biofilm and its impact on the clinical outcome. To study the role of resistance in the clinical outcome.

Methods: A total of 30 azole-resistant (R) and 10 azole-susceptible (S) C. tropicalis were included in this study. All the isolates were subjected to complete gene sequencing of azole target genes including ERG11 to analyze the drug resistance pattern. The subcutaneous infection models were used to compare the clinical outcomes.

Results: All the isolates showed a complete gene sequence of azole target genes including ERG11. The subcutaneous infection model showed no significant difference in the clinical outcomes.