P372
Designing transcript isoform switching and utilization in mature biofilm of Candida glabrata through a global transcriptomic approach
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Poster session 3, September 23, 2022, 12:10 PM - 1:30 PM

Objectives: Eukaryotic cellular systems utilize alternative transcript isoforms generated via an isoform-switching mechanism to thwart various stress conditions. To the best of our knowledge, transcript isoform switching and differential transcript isoform usage (DTE) in Candida glabrata have not been studied. Therefore, the present study was designed to delineate differential transcript isoform expression (DTE) and transcript isoform switching followed by DTEU and the functional impact of transcripts in a mature biofilm of C. glabrata (clinical isolate, NCUP 100077) through an RNA sequencing approach. Results: DTE analysis generated 97378 transcript isoforms from the C. glabrata genome (5295 genes in total), and DTEU investigations revealed that transcript isoforms of 292 genes were specifically utilized in the formation of mature biofilms via the isoform-switching process. Gene Ontology/pathway analysis and protein-protein interactions further substantiated the functional attributes of mature transcript isoforms selectively used by C. glabrata in biofilm formation and survival.

Conclusion: The present study elucidates that specific transcript isoforms utilized in mature biofilms of C. glabrata could be used as potential targets for the development of novel antifungal therapeutics.

P373
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Objectives: Candida tropicalis is a common cause of nosocomial candidaemia and candidiasis. The role of biofilm formation in resistance and antimicrobial resistance in C. tropicalis remains understudied. We aimed to evaluate the biofilm-formation capacity of C. tropicalis isolates exhibiting resistance, borderline resistance, and sensitivity to echinocandins. Methods: The echinocandin resistant, borderline resistant, and susceptible isolates of C. tropicalis were collected based on their minimum inhibitory concentration (MIC) values according to Clinical and Laboratory Standard Institute (CLSI) broth microdilution guidelines. The isolates were subjected to FK517 gene sequencing. To estimate biofilm production, echinocandin resistant (n = 2), borderline resistant (n = 5), and susceptible isolates (n = 5) were seeded at the cell concentration of 1 × 10^7 cells/mL in RPMI-1640 with 0.141 M MOPS in polyvinyl 96-well microtiter plates and incubated for 24 and 48 h at 37°C. The biofilm was quantified by crystal violet fluorescence-based spectrophotometric method and XTT (2,3-Bis-(2-methoxy-4-nitro-5-sulphophenyl)-2H-tetrazolium-5-carboxanilide) reduction assay. Statistical analysis was performed using one-way ANOVA with Bonferroni’s post-hoc test for multiple comparisons among the groups.

Results: FK517 sequencing analysis revealed 50% mutations in H3Y1 in both resistant isolates while isolates exhibiting borderline MIC in echinocandins carried wild-type FK517 gene. Biofilm formation in borderline echinocandin-resistant C. tropicalis isolates was significantly (P < 0.001) higher compared to resistant and susceptible isolates. However, no significant difference in biofilm formation was noted among resistant and susceptible isolates.

Conclusion: This study suggests differential biofilm-formation capacity among C. tropicalis isolates with reduced susceptibility to echinocandins. However, this warrants further studies before any definitive inference can be made.

P374
Fungal coinfection in patients with SARS-CoV-2: Atertiary care hospital study
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Background: There is a high risk of developing fungal co-infections in patients infected with SARS-CoV-2, few studies have been conducted on the incidence and risk of these secondary infections. The incidence of Candida infection due to different Candida species is increasing in COVID patients.

Methods: This retrospective study comprised a total of 23 patients with upper respiratory infections investigated in the Department of Microbiology of University College of Medical Science (UCMS) and Guru Teg Bahadur Hospital (GTBH), Delhi from April 2021 to June 2021. Identification was done using DNA sequencing.

Results: Of the 23 cases, identification by DNA sequencing, C. albicans was present in 34.78%, C. tropicalis in 30.43%, Pichia kudriavzevii in 26.09%, C. parapsilosis in 4.35%, and C. auris 4.35%.

Conclusion: C. albicans is the leading pathogen in our patients, along with the rise in the incidence of P. kudriavzevii which is usually an environmental contaminant. Regular surveillance and infection control practices are future ventures to reduce the burden of infection.

P377
Study of the prevalence of candidemia and its antifungal susceptibility pattern in a tertiary care hospital
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Objectives: Study of the prevalence of candidaemia and its resistance pattern in a tertiary care hospital.

Methods: • Retrospective observational study
• Study period—January 1, 2020-December 31, 2021
• Blood culture bottles (aerobic and anaerobic) were received in the laboratory
1) Incubated in BacT Alert 3D (BioMérieux) for 5 days.
2) After flagging positive, a dipper gram stain was prepared from the culture bottle and informed to the clinician. Culture plating was done on Blood agar and Mac Conkey agar which were incubated for 18-24 h at 37°C.
3) After 24 h, growth was obtained on the culture plate and identification was done by using MALDI-TOF MS (Biomérieux) and Susceptibility Testing was done using VITEK 2 Compact (Biomérieux).

Results: • During the study period, 18 235 blood culture bottles were received, and 1652 blood culture bottles were flagged positive. The most common organisms causing bloodstream infection belonged to B. bavariensis spp. • Candida spp. 4% was found to be the ninth most common organism causing bloodstream infection.
• Among Candida spp most common isolate was C. tropicalis 42% followed by C. parapsilosis 21%, C. albicans 21%, and C. auris 12%, and the least isolated species was C. glabrata 4%.
• Minimum number of Candida spp were isolated from intensive care units.
• Susceptibility testing was given by VITEK 2 compact for all Candida spp except for C. glabrata.
• The isolated Candida spp showed the least susceptibility to fluconazole (resistant range 8-30.6%) as compared to micafungin, caspofungin, fluconazole, and amphotericin B (R 13.9%, 13.9%, 22.2%, and 3.6%, respectively).
• Candida glabrata showed less sensitivity toward caspofungin as compared to other antifungals.

Conclusion: Candida spp. are a part of the normal flora of healthy hosts, but they are also found to be a major cause of invasive fungal infections which is now found to be one of the leading causes of mortality in hospitalised patients. The emergence of unusual and relatively unknown Candida species as nosocomial pathogens with increasing treatment failure, emphasises the need to isolate and identify all species and to start early definitive treatment according to the susceptibility patterns reported to decrease mortality and morbidity rates.

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