A)

Age Groups (n)	Occurrence of infusion-related side effects Yes	No	%(Yes)	Turning point	Occurence, by Group Yes	No	Fisher's exact test
< 37 weeks PMA (45)	0	45	0.0%	Group A (up to 12 months)	0	97	p-value: **0.0027***
birth - 27 days (27)	0	27	0.0%				
28 days - 12 months (25)	0	25	0.0%				
13 months - 2 years (9)	1	8	11.1%	Group B (13 months or more)	4	26	IC 95%, to p-value: [0 ; 0.4395]
3 a 5 years (7)	1	6	14.3%				
6 a 11 years (8)	1	7	12.5%				
12 a 18 years (6)	1	5	16.7%				

B)

Age Groups (n)	Laboratory parameters adequacy Inadequate	Adequate	%(Inadequate)	Turning point	Inadequacy, by Group %Inadquacy	Chi-squared test
< 37 weeks PMA (409)	160	249	39.1%	Group A (up to 12 months)	37.8%	p-value: **0.0467***
birth - 27 days (251)	93	158	37.1%			
28 days - 12 months (228)	83	145	36.4%			
13 months - 2 years (91)	39	52	42.9%	Group B (13 months or more)	44.3%	Diference: 6.5% IC 95%, to difference: [0.1% ; 13.0%]
3 a 5 years (70)	27	43	38.6%			
6 a 11 years (82)	36	46	43.9%			
12 a 18 years (57)	31	26	54.4%			

P044

Demonstration of the yeasticidal efficacy of povidone-iodine-based commercial antiseptic solutions against *Candida auris*

Adélaïde Chesnay[1], Eric Bailly[1], Victor Evplanov[2], Filippo Favalli[3], Guillaume Desoubeaux[1]
[1]CHRU Tours, Tours, France
[2]Mylan SAS, a Viatris company, Paris, France
[3]Meda Pharma S.p.A. A Viatris Company, Monza, Italy

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Objectives: *Candida auris* is an emerging yeast pathogen with worldwide distribution and a great propensity for nosocomial spread. Recent reports have warned of the significant emergence of *C. auris* in several healthcare facilities. In order to stop its nosocomial transmission, use of antiseptics constitutes the first-line lever of action in fighting against *C. auris* skin colonization. However, little is known about the efficacy of these products, and moreover, no antiseptics are currently registered for use against *C. auris*.

Material and Methods: This study investigated the *in vitro* yeasticidal activity of povidone-iodine (Betadine®) against *C. auris*, and compared the findings to *C. albicans* and *C. glabrata*.

Results: In all the samples, the fungal load was substantially reduced by ≥4.2 Log10 colony-forming units, according to the EN standard 1275:2005. Moreover, even when largely diluted, povidone-iodine products still allowed a sustainable decrease of the yeast viability below 0.1%.

Conclusion: Overall, these results support the use of such commercial antiseptics in the context of colonization with this yeast.

P045

The association of performance of air pollutants on *Candida* drug resistance

Sahar Ghazanfari[1], Shahla Roudbar mohammadi[1], Sasan Rezaei[2]
[1]Department of Medical Mycology, Faculty of Sciences, Tarbiyat Modares University, Tehran, Iran, Tehran, Iran
[2]Department of Medical Parasitology and Mycology, School of Public Health, Tehran University of Medical Science, Tehran, Iran, Tehran, Iran

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Objective: Therapeutic methods are very important in the prevalence of opportunistic fungal infections, which are among the main causes of human diseases. In this study, air pollution agents that are in direct contact with microorganisms and as a carbon source using CO2 and MTBE and their effects on aspects such as growth and particularly the evaluation of changes in the expression of interfering genes in susceptibility and drug resistance in these fungi were investigated.

Materials and Methods: Collecting samples and isolating *Candida glabrata* (*C. glabrata*) and *Candida albicans* (*C. albicans*) with phenotypic methods were accomplished. In this way, evaluating the minimum inhibitory concentration (MIC) with M27A4 protocol of CLSI was done. Adjusting to sensitive strains from the MIC test, which included 20 *C. albicans* and 10 *C. glabrata* which were sensitive to fluconazole and itraconazole drugs with 5% CO2 and 5 mg/ml MTBE interfering agents that are considered as air pollutants and also re-evaluating MIC testing to separate strains resistant to azole drug were accomplished.

Results: Up-regulation of some genes on two mentioned yeast had led to drug resistance in them, which were previously sensitive to both drugs. Correspondingly, 41% of *C. glabrata* samples in sputum showed sensitivity to these drugs. Up-regulation of ERG11(71%) and EPA1 (90%) were observed in resistant strains. Up regulation of genes associated with aspartate proteins and down regulation of SAP3 genes were recognized in *C. glabrata* in sputum and a 15% down-regulation of BAL isolate and 50% up-regulation of SAP1 gene in *C. albicans* sensitive samples were observed and compared with fluconazole and itraconazole with oral and joint source. Remarkably, decreased SAP2 expression in oral sources and 60% increase in resistant strains in *C. albicans* was observed. The down-regulation of SAP3 expression showed in the joint samples. An increase in HWP1expression (30%) was noted in isolated and drug-sensitive samples at the sputum and BAL source. CDR1 expression was increased in MTBE-affected species however, it decreased in the vicinity of CT.

Conclusion: Air pollutants such as CO2 and MTBE eventually caused drug resistance in *Candida*, which can be one of the causes of drug resistance in candidiasis infections.

P046

Local adaptation to antifungal compounds in the model organism *Neurospora crassa*

A. Pedro Gonçalves
National Cheng Kung University, Tainan, Taiwan

Poster session 1, September 21, 2022, 12:30 PM - 1:30 PM

The domestication of *Neurospora crassa* has been a major driver of the fields in fungal molecular and cell biology. Not only this filamentous species enjoys modest nutritional requirements and grows swiftly in the laboratory, but also its genome is considerably well annotated, and a near-complete deletion strain collection is available for functional analyses. Furthermore, decades of research with *N. crassa* have been accompanied by the accrual of wild isolates from different points of the globe, which are an invaluable tool to study local adaptation. Using a panel of antifungal compounds, we found that drug resistance is naturally heterogeneous in wild populations of *N. crassa*, and chromosomal mapping of the causal loci is underway to unveil the genetic basis of the observed natural diversity. Furthermore, we are interested in the regulatory role played by two Zn2Cys6 transcription factors, CZT-1, and TAH-3, during fungal responses to various drugs. In summary, despite it being non-pathogenic, *N. crassa* presents many advantages as a model to study antifungal drug resistance. Since the paucity of valid molecular targets in the fungal cell has been hindering the discovery of new antifungal drugs, we consider that the identification and functional characterization of new genes and pathways involved in drug resistance may inform the adoption of new therapeutic schemes.

P047

Comparative evaluation of disc diffusion and E-test with broth micro-dilution in susceptibility testing of amphotericin B, posaconazole, isuvuconazole, itraconazole against *Rhizopus* isolates of post COVID mucormycosis

Prashant Gupta, Mohd Saqib Hasan
Department of Microbiology, King George's Medical University, Lucknow, India

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Objectives: To investigate and compare susceptibility pattern of *Rhizopus* isolates in post-COVID mucormycosis by disc diffusion (DD), E-test, and broth micro-dilution for amphotericin B, posaconazole. DD and BMD for isavuconazole and itraconazole.

Methods: All the isolates were identified by MALDI-ToF (Vitek MS). A total of 72 isolates of *R. oryzae* complex and 48 isolates of *R. microsporus* complex were selected. AFS by DD and E-test was done on non-supplemented Mueller Hinton Agar (MHA) and was compared with the Clinical Laboratory Standard Institute (CLSI M 38 A2) broth micro-dilution (BMD) method of AFS.

Results: The disk diffusion method for amphotericin B showed 91.6% agreement while E-test showed 97.2% agreement with broth micro-dilution. Disk diffusion method for posaconazole showed 93% agreement while E-test showed 97.2% agreement with broth micro-dilution. Disk diffusion method for ITZ and ISC showed 94.4% and 100% agreement respectively with broth micro-dilution.

Conclusion: CLSI method of DD promises to be an easier, reproducible, and cost-effective method of susceptibility testing, but this method must be interpreted with caution in the case of amphotericin B susceptibility testing. E-test correlates better than DD with BMD.