Medical Mycology, 2022, Vol. 60, No. S1

S8.3d Characterization of glycosylphosphatidylinositol-linked aspartyl proteases in Candida glabrata Role in pathogenicity

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S8.3j How the Fangal Call Wall Glycan Can Modulate the Immune Response?, September 23, 2022, 3:00 PM - 10:10 PM

Candida glabrata is the second most common yeast pathogen found in Candida bloodstream infections, depending upon the geographical location. C. glabrata, which belongs to the Nakasoneas-clade, possesses a distinct set of virulence attributes which distinguish it from other Candida species. In particular, polyphagy is a unique characteristic of the C. glabrata strains. In this study, we are delineating the cellular processes that are associated with polyphagy. These findings, in turn, will help in understanding the role of C. glabrata in the suppression of the host pro-inflammatory immune response, which is associated with the pathogenesis of the infections.

S8.4b Population biology of fumigating fungus Trichophyton erinacei

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S8.4 Causes of animal mycoses, September 23, 2022, 3:00 PM - 3:40 PM

Trichophyton erinacei is a main cause of dermatomycosis in hedgehogs and is increasingly reported from human infections worldwide. It is found in wild European hedgehogs (Erinaceus europaeus) but also in the African four-toed hedgehog (Atelerix albiventris) popular as a pet animal worldwide. Little is known about the reservoir and population genetics of this pathogen despite its increasing importance in clinical practice. Notably, there are different populations or even cryptic species associated with different hosts or geographic regions is not known. To answer these questions, we collected 161 isolates, per- formed DNA barcode analysis, determined genotypes, and characterized morphology and physiology. Multiple phylogenetic and multilocus analysis support T. erinacei as a monophyletic species, in contrast to highly incon- gruent values in biological population studies. One single genotype, one mainly to animals and the second to hedgehogs, were identified inside T. erinacei, and slight differences in the size of macroconidia and antifungal susceptibility were observed among them. Although the process of speciation into two-lineages is ongoing in T. erinacei, there is still a gene flow between those populations. Several morphological traits were observed in T. erinacei, and phylogenetic and physiologic differences were observed in the hedgehogs. The data from wild hedgehogs indicated that sexual reproduction in T. erinacei and the dose-infection of hedgehogs from seeds are probably rare cases and that clonal horizontal spread is strong. The molecular typing approach used in this study allows for the first time to identify the T. erinacei genotypes and to studing differences in both animals and humans. The results of this study also highlighted the need to use a multiple phylogeny ideally in combination with other datasets including molecular markers to understand the species boundaries of dermatomycosis.

S8.5c MLST genotyping and phylogenetics of AD-hybrids

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S8.5j Genotyping of Cryptococcus neoformans and C. gattii, September 23, 2022, 3:00 PM - 4:30 PM

Objective: In a previous study a set of new mycosis-type specific primers were designed to apply the standard DHSAM consumes multi-locus sequence typing (MLST) scheme to Cryptococcus neoformans AD-hybrids. In the present study, we report the preliminary results of the investigations by MLST of a large number of AD hybrids with the aim to identify the circulating genotypes, their population genetics.

Methods: A total of 50 AD hybrid isolates from different parts of the world and from different regions were genotyped. The MLST scheme. Minimal spanning trees and Cochard algorithm were generated by comparing hybrid genotypes and by computing separately either allele- A and allele- D parts of the hybrid genotypes to the hyperfile recorded in the MLST global database. Results: Analysis identified 32 hybrid genotypes grouped in these distinct main clusters (CC2, CC21, and CC11) includ- ing 12 isolates each. Both CC2 and CC21 clusters included isolates from different countries and continents but the former grouped only isolates with mating type a and Diplospora whereas the latter those with mating type a Diplospora. Cluster CC11 consisted only isolates from Egypt. Heterosis alleles combinations in some of these MLST hybrids presented two or three com- binations more frequent than the others. In some isolates, one or two alleles were not amplified after multiple attempts, and therefore, the genotype was not assigned. In total, 60 MLST profiles were identified by analyzing separately the allele-A and allele-D combinations of the hybrids. Comparison with all MLST profiles of Yln, Ynl, and Ynh included in the MLST global database showed that the allele-A portion of the hybrid genotypes was grouped in few Ynl or Ynh clusters. In none of the investigated hybrids, the combination of alleles originated from Ynp genomes. Similarly, when the MLST profile of allele-A portion of hybrids was compared to all Ynp genomes present in the global MLST database, few clusters were identified but, in this case, mostly originated from human isolates. Conclusions: These preliminary results suggest that the AD hybrids have invaded progressively from the mating of A haploids very common in both clinical and environmental isolates and D haploids that are not circulating at present or very rare. Therefore, it is likely that clusters originated in the environment where Ynp genomes diversity is high and suitable AD combinations can occur. Sequencing of further AD hybrids is in progress to confirm these results.

S8.6d Cryptococcus neoformans and Cryptococcus gattii clinical isolates from Colombia develop heteroresistance to fluconazole at high concentrations

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S8.6j Genotyping of Cryptococcus neoformans and C. gattii, September 23, 2022, 3:00 PM - 4:30 PM

Introduction: Cryptococcus is a worldwide mycoses caused by Cryptococcus neoformans and Cryptococcus gattii. Although resistance to antifungals is infrequent, isolates with decreased susceptibility to fluconazole have been reported globally, including Colombia, which may be due to 1) heteroresistance, defined as the ability to adapt to increasing concentrations of this antifungal agent, and 2) point mutations in the ERG11 gene encoding the fluconazole target enzyme, lanosterol 14-alpha-demethylase. Objective: To determine the development of heteroresistance to fluconazole in C. neoformans and C. gattii clinical isolates from Colombia and to evaluate and quantify the ERG11 gene of the isolates to seek mutations that might characterize resistance or heteroresistance phenotypes. Methods: The minimum inhibitory concentration (MIC) to fluconazole was determined in 28 and 24 isolates of C. neoformans and C. gattii, respectively, using broth microdilution. Heteroresistance was evidenced by plating each isolate on YPD agar that contained fluconazole at concentrations equal to the MIC of each isolate. Heteroresistant colonies were then regrown in isolating concentrations of fluconazole. Results: All isolates were susceptible to fluconazole with MICs of 1 µg/mL (n = 2), 2 µg/mL (n = 4), 4 µg/mL (n = 17), 8 µg/mL (n = 23), 16 µg/mL (n = 4), and 32 µg/mL (n = 1). However, all isolates developed heteroresistance colonies, with increased MIC of fluconazole. At MIC of 20 µg/mL, 32% (5/16) of C. neoformans and 83.3% (5/3) of C. gattii grew up to 64 µg/mL of fluconazole, which is in the MIC that define resistance to this antifungal, and 12.5% (2) isolates of C. neoformans and 4 (16%) isolates of C. gattii were up to 32 µg/mL of fluconazole Figure. A single isolate from each strain displayed the pattern of susceptible- resistant- susceptible. conclusion: Clinical isolates of C. neoformans and C. gattii that develop heteroresistance to fluconazole in high concentrations of Colorado, is important since this characteristic contributes to the failure of association therapy with this triazole.