Oral Presentations

S1.1d Risk factors associated with oropharyngeal candidiasis in COVID-19 patients: a case-control study
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S1.1 Controversies in the clinical management of orofacial infections in critically ill patients, September 21, 2022, 11:00 AM - 12:10 PM
Objectives: To understand the emergence and spread of the coronavirus disease-19 (COVID-19) in the world, humans have been faced with the biggest challenge in health care systems in recent decades. The aim of the present study is to identify risk factors associated with oropharyngeal candidiasis (OPC) in COVID-19 patients.
Methods: The total number of confirmed COVID-19 patients was 218 (105 participants as cases who experienced OPC and 113 participants as controls without any evidence of OPC). The questionnaires used in this study consists of demography data, medical history, current and other diseases, and underlying diseases to collect information at the time of clinical diagnosis and follow them until the day of hospitalization.
Results: Pseudomembranous candidiasis (77.0%) was the most prevalent form of OPC in case patients. The majority of cases (91.5%) experienced OPC in organ transplants. Increasing age (4.64) and control (4.64) were found to significantly increase the OPC risk (OR = 0.02) were significantly associated with OPC cases. Diabetes (P = 0.02), solid tumor (P = 0.19), and hypertension (P = 0.00) were the most common underlying conditions. Use of diuretics (P = 0.02) and poor oral hygiene (P = 0.00) were related to OPC in case groups. Therapy with digoxine (P = 0.02), IVG (P = 0.02), dexameth (P = 0.00), and coticorron pulsh therapy (P = 0.02) were significantly associated with the development of OPC in case patients.
Conclusions: This investigation showed that patients with OPC were old, long hospitalization, corticosom, nausea, diabetes, solid tumor, and hypertension may predispose to the development of OPC in COVID-19 patients.

S1.2c Diagnosis of fungal infections in animals: Combining the old and the new to maximize results
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S1.2 Emerging and Exploding Fungal Mycoses, September 21, 2022, 11:00 AM - 12:50 PM
There is a broad spectrum of fungal infections involving companion, nonclinical and wild animals. Some fungi are distributed in specific taxonomic infections. Others, such as the dermatophyte Malassezia dermatitidis and Aspergillus fumigatus, are primary pathogens with a more defined geographical distribution. Dermatomycosis causes less severe disease limited to the skin. However, they are relevant cases that are widely diffused. Moreover, some dermatophytes are transmitted from animals to humans; therefore, these infections represent a public health problem.
In recent years, opportunistic fungal infections (e.g., Aspergillus, Candida, Cryptococcus) in human medicine have increased. The main reason is the rise of people with immunosuppression of various origins (ADHD, chemotherapy, immunosuppressive therapies in organ transplant); Ward and Wicker 2014). The spectrum of fungal causing infections is expanding, which constitutes an identification challenge for even the most experienced mycologist. There are several new and more precise diagnostic methods for the detection of fungal elements in tissue samples (e.g., PCR-based techniques, serological test, and fungal identification (e.g., matrix assisted laser desorption/vacuum ionization time of flight analyzer technology) that are now available in addition to traditional methods (microscopy examination of a sample, histopathology, culture, and culture). The most commonly used tests, deep mycoses are more rarely reported in animals because the situations leading to immunosuppression in human patients are not paralleled in veterinary medicine. However, there is an increasing interest in these cases involving animals. Thus, new diagnostic procedures are being applied more and more to animal infections (Eid and Segal 2018). For now, Microzid, 91030.
Direct microscopy remains its importance as a quick and inexpensive tool to ‘‘suspect’’ a fungal infection. It also allows observing the mycelium and sporulation in the immune response and finding other pathogens. It is helpful to interpret the results of more advanced tests (culture, PCR). The sensitivity of matrix-assisted techniques varies with the individual species, and the skill and experience of the laboratory staff. Diagnosis of invasive fungal infection by direct microscopy and histopathology may require the use of biopsies of deep tissues, which may pose a risk for the patient. Often it does not allow fungal identification.
Fungal culture can yield the specific etiologic agent or, if positive, allows antifungal susceptibility testing (AST). It may take many days to achieve a result. Identification of the common fungi requires a high level of expertise and equipment.
A widely employed identification method in PCR = sequencing of the ITS region (other DNA regions used are LSU, SSU, β-tubulin, and Calmodulin). Data generated from unknown fungi can be used to search public databases, such as GenBank, using the web-based BLASTa algorithm. Database searches must be performed with caution owing to the nature of the database and the high frequency of erroneous depots. The suggestion is to employ reliable, published, recent sequences.
The most popular non-nucleic acid-based molecular diagnostics assay for fungi is Matrix Assisted Laser Desorption Ionization Time of Flight (MALDI-TOF). The technique generates spectra that are sequential by a list of reference spots, which correspond to individual species. The strength of MALDI-TOF technology is in the rapid sample analysis (minute) and the absence of any downtime data manipulation. Weakness of this system include the need for an existing library to compare general data species to potential variability in results of unknown fungi if they are not grown under conditions similar to reference spectra.
Thanks to the improvement of the identification methods in veterinary medicine, it has been possible to describe new cryptic species in animals. In the case of animals, the species included in the Aspergillus fumigatus complex, apart from Aspergillus fumigatus, and Aspergillus terreus, are frequently reported in animals. The identification of a pseudolab mating system and the analysis of the mating type locus provide evidence that sexual lines of mating compatible to the potential lines have diploid genotype in the hybrid lineage. Sequence similarity percentage studies of the same species complex are evaluated in relationship to host background and phenotype.

S1.2d The human pathobiont Malassezia furfur secreted protease MSGAP1 regulates cell dispersal and exacerbates skin inflammation
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9Malassezia: genomics, genomics, and biology, September 21, 2022, 11:00 AM - 12:10 PM
Objectives: Malassezia furfur secretes a protease MSGAP1 that regulates cell dispersal and exacerbates skin inflammation
Methods and Results: In this study, we compared the expression level of secreted proteases, lipases, phospholipases, and sphingomyelinases of M. globosa in healthy subjects and atopic dermatitis or atopix dermatitis patients. We observed upregulation gene expression of the previously characterized secretory arena protease MSGAP1 in both the keratin and non-keratin skin of atopic dermatitis patients compared to healthy controls. To explore the functional role of MSGAP1 in skin disease, we generated a knockout mutant of the homologous protease MSGAP1 in the genetically tractable M. furfur. We observed the loss of MSGAP1 resulted in dramatic changes in the cell adhesion and dispersal in both culture and a human 3D reconstructed epidermal model. In a murine model of Malassezia colonization, we further demonstrated MSGAP1 contributes to inflammation as observed by reduced edema and myeloid parasitemia formation with the knockout mutant versus wildtype.

Conclusion: Together, we show that the dominant secretory M. apertus protein has a important role in enabling a plakocyte cellular state that can potentially aid in colorization and additionally as a virulence factor in barrier-compromised

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