Oral Presentations

S1.1d Risk factors associated with oropharyngeal carriage in COVID-19 patients: a case-control study

Mohammadreza Saeidi1, Reyhaneh Sadat Kiyaie1, Sadegh Khodavansary2, Nasim Khajehrad3, Seyed Ali Dehghan Darb1, Arash Sath1
1 Tehran University of Medical Sciences, Tehran, Iran
2 Tehran University of Medical Sciences, Tehran, Iran
3 Shahid Beheshti University of Medical Sciences, Tehran, Iran
4 Tehran University of Medical Sciences, Tehran, Iran
5 University of Missouri, Columbia, USA

S1.1d Controversies in the clinical management of sepsis patients in critically ill patients, September 21, 2012, 11:00 AM - 12:10 PM

Objectives: To evaluate the spread and prevalence 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 carriage (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 with no evidence of OPC). The questionnaires used in the study consists of demographics data, pre-existing diseases, underlying disease, and underlying diseases to collect information at the onset of clinical symptoms and follow them until the date of hospitalization.

Results: Pseudomonas aeruginosa (77.5%), S. aureus (73.5%) was the most prevalent form of OPC in case patients. The majority of cases (69/105) were male and 95 (90.5%) were married. The mean age of cases (P = 0.04) was significantly associated with OPC. Diabetes (P = 0.019), hypertension (P = 0.001) were the most common underlying conditions. Use of diabetes (P = 0.007) and poor oral hygiene (P = 0.003) were related to OPC in case patients. Therapy with diuretics (P = 0.011), vitamin-C (P = 0.013), diuretics (P = 0.001), and corticosteroid pulse therapy (P = 0.003) were significantly associated with the development of OPC in case patients.

Conclusions: It is minimally affected that old age, length of hospital stay, corticosteroid usage, 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

Andina Paez

University of Turin, Gruppo, Italy

S1.2 Emerging and Emerging Endemic Mycoses, September 21, 2012, 11:00 AM - 12:00 PM

There is a broad spectrum of fungal infections involving companion, agricultural and wild animals. Some fungi are described as emerging infectious pathogens. Others, such as the dimorphic fungus Blastomyces dermatitidis and Sporothrix schenckii, are primary pathogens with a more defined geographical distribution. Dermatomycoses cause severe diseases limited to the skin. However, they are more often seen as rare diseases. 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, Candidiasis, 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). Hence, Bednarek and Wickersham 2014. Cold Spring Harb Perspect Med. 4, a014299). Moreover, the spectrum of fungal causes of infections is expanding, which includes an identification challenge for even the most experienced mycologists and access to appropriate methods for the detection of fungal elements in tissue samples (e.g., PCR-based techniques, molecular methods and fungal identification (e.g., matrix-assisted laser desorption/ionization time-of-flight analysis) technology are now available in addition to traditional methods (microscopic examination of clinical samples). Culture and culture are often used in parallel. New methods are currently developed in the field of fungal identification, which leads to an increased number of cases among veterinarians. However, there is an increasing awareness of these infections in veterinary medicine. Therefore, new diagnostic procedures are being applied more and more to animal infections (Eld and Segal, 2018. Front Microbiol, 9:1303).

Direct microscopy remains of importance as a quick and inexpensive tool to “screen” a fungal infection. It also allows observing the characteristic morphology of the infection in the immune response and finding other pathogens. It is helpful to interpret the results of more advanced tests (culture, PCR). The sensitivity of microscopic exams varies with the individual agent, source and quality of the specimen, and the skills and experience of the laboratorian. Diagnosis of fungal infections by direct microscopy and histopathology may help resolve the issue of biopsy of deep tissues, which may pose a risk for the patient. Often it does not allow fungal identification.

Fungal culture can yield the specific ecological agent if possible, which allows antifungal susceptibility testing (AST). It may take many days to achieve a result. Identification of most common fungi requires a high level of expertise and equipment. A widely employed identification method in PCRs is 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 databases. Database searches must be performed with caution owing to the public nature of the database and the high frequency of erroneous deposition. The suggestion is to employ verified, published, recent sequences.

The most popular PCR test uses a real-time PCR assay that is specific for fungi, and the main types of fungi are given in the table below.

| NAME OF THE ORGANISM | TYPE OF SAMPLE | MULTIPLE | SENSITIVITY | SPECIFICITY | RELEVANCE |
|----------------------|---------------|-----------|-------------|------------|-----------|
| A. fumigatus | Bronchial wash | Yes | 90% | 95% | Allergic fungal sinusitis, asthma, Aspergillosis, and allergic bronchopulmonary fungal disease |
| C. albicans | Blood | Yes | 90% | 95% | Candidaemia, disseminated candidiasis |
| S. cerevisiae | Urine | Yes | 90% | 95% | Yeast infections |
| B. dermatitidis | Skin biopsy | Yes | 90% | 95% | Blastomycosis |
| D. pulcherrimum | Sputum | Yes | 90% | 95% | Histoplasmosis |

To ensure the accuracy of the diagnosis, it is important to identify the species of fungi responsible for the infection. This can be done by means of fungal cultures or direct microscopy. In addition, it is important to determine the virulence factors of the fungus, which can help in selecting the appropriate antifungal treatment.

S1.2d The human pathobiology (Malassezia furfur secreted protease MIPA1) regulates cell dispersal and exacerbates skin inflammation

Jochen Gehr1, Paolina Rubido2, Si-Eun Peh3, Winston L.C. Koh4, Kiat Y. Tan5, Yan Ting Lim4, Steven G. Ting3, Radoslaw S. Sobota6, Shawn S. Hofer2, Chin-Lu Lo6, Anthony J. D’Orazio3, Sebatin Leimbach-Buitendam7, Haesh 8, Hsu 9, Ho10, Thomas L. Dawson11

1AI*STAR Skin Research Labs, Agency for Science, Technology and Research, Singapore, Singapore
2School of Veterinary Medicine, University of Sydney, Sydney, Australia
3Molecular Engineering Lab, Institute of Molecular and Cell Biology, Agency for Science, Technology and Research, Singapore, Singapore
4Functional Proteomics Laboratory, Institute of Cell and Molecular Biology, Agency for Science, Technology and Research, Singapore, Singapore
5National Skin Centre, National Health Group, Singapore, Singapore
6School of Pharmacy and Pharmaceutical Sciences, University of California—San Diego, La Jolla, USA
7Department of Chemistry, National University of Singapore, Singapore, Singapore
8Department of Drug Discovery, School of Pharmacy, Medical University of South Carolina, Charleston, USA

S1.2d Malassezia: genomics, genetics, and biology, September 21, 2012, 11:00 AM - 12:10 PM

Objectives: Malassezia is the dominant eukaryotic microbial community on the skin. The Malassezia genus poses a repertoire of secretory hydrolytic enzymes involved in protein and lipid metabolism which alter the external cutaneous environment. The exact role of most Malassezia secreted enzymes, including those in interaction with the epithelial surface, is not well characterized.

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 atopic dermatitis patients. We observed upregulated gene expression of the previously characterized secretory amphoteric protease MIPA1 in both the keratotic and non-keratotic skin of AD. MIPA1 is compared to be a key molecule in skin pathogenesis. To explore the functional role of MIPA1 in skin disease, we generated a lesion mouse of the homologous protease MIPA1 in the genetically tractable M. furfur. We observed the loss of MIPA1 resulted in dramatic changes in the cell adhesion and dispersed in both culture and a human 3D reconstructed epidermis model. In a murine model of Malassezia colonization, we further demonstrated MIPA1 contributes to inflammation as observed by reduced edema and myeloid populations formation with the knockout mouse versus wildtype.

Conclusions: Together, we show that the dominant secretary M. auris proteases have an important role in enabling a pleiotropic cellular state that may potentially aid in coloration and additionally as a virulence factor in barrier-compromised skin.