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Genetic diversity of the emerging human fungal pathogen Phialosnorvegensis
Sander Boelen1,2, Piet-Jan Haas1,2, Karin van der Krogt1, Erik Baarsma1, Perry Hagen1,2
1Westerdijk Fungal Biodiversity Institute, Utrecht, Netherlands
2University Medical Center Utrecht, Utrecht, Netherlands
Poster session 2, Saturday, 22 April, 12:00 PM - 1:30 PM
Objective: Phialosnorvegensis (commissioned phialophora) is increasingly isolated from hospital settings, especially from immunocompromised patients. Under proper treatment, its emergence and distribution is crucial for accurate diagnosis and infection prevention. We studied the genetic diversity of a large collection of clinical P. norvegensis isolates obtained from Dutch hospitals along with a set of non-Dutch clinical and environmental isolates.
Methods: Clinical (n = 236, 93.6%) and environmental (n = 24, 9.2%) P. norvegensis isolates were subjected to Amplified Fragment Length Polymorphism (AFLP) fingerprinting and a novel six locus microsatellite typing panel. Data were analysed with BioNumerics and Structure. We applied a novel matching assay to determine the MALTE fungal species classification.
Results: AFLP fingerprinting separated the P. norvegensis isolates into three main clusters. Two clusters fully consist of clinical isolates, the third represented a mix of clinical and environmental isolates. By microsatellite typing, the overall genetic diversity was low (SimuPop-b = 0.915), due to a large number of Dutch clinical isolates with similar genotypes. Minimum spanning tree analysis showed that Dutch clinical isolates fell into two clusters. Environmental and non-Dutch isolates were more distinctly related. Structure analysis showed the presence of four genotypes, with signs of genetic admixture between geographic locations and environmental/clinical isolates. Nearly all isolates harbor the MATa mating-type allele.
Conclusions: The P. norvegensis isolates obtained from Dutch hospitals appeared to be largely closed, independent of geographic origin and isolation date. The observed clonality is supported by the common number of MALTE isolates. Microsatellite typing indicated potential admixture between clinical and environmental isolates.

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First report of Mycetoma due to Madurella fahalii from India
Vinaykumar Mallur, Pritika Gahlot, Chandra Sekar Srikar, Supriya Sahu, Malati Tudu
All India Institute of Medical Sciences, Bhubaneswar, Bhubaneswar, India
Poster session 1, Saturday, 22 April, 12:00 PM - 1:30 PM
Objective: To describe the first case report of Madurella fahalii from India.
Methods: A 70-year-old non-diabetic man from Bhadrak district who worked as a soldier in past came to us with a history of pus discharge containing black grains of more than two months duration in the posterior aspect of the thigh. He had been operated 2 years back for the same complaint, however, finding no relief he trusted us. On examination, a deformed lesion measuring 10 × 10 cm, containing 6-8 lesions which discharged pusky yellow colored pus containing black grains measuring 0.5 ± 1 cm was found on the posterior aspect of the thigh. The lesion was painless, doughy in consistency, and associated with enlarged and non-tender and non-tender inguinal lymph nodes measuring 2 ± 2 cm. General physical examination and routine haematological laboratory examination revealed no abnormalities. Serological tests did not reveal the presence of H1N1, Hepatitis B, or Hepatitis C. A clinical diagnosis of black grain mycetoma was made and the patient was sent to microbiology laboratory for fungal culture. Black hair grains were found on KOH mount and culture on subculture mold agar grow a brown colony which differed a brown pigment into the medium after 15 days of incubation. LPCR examination showed brown non-spore forming mold. DNA was extracted using phenol-chloroform-isooctyl alcohol after grading the resultant in liquid nitrogen and subjected to PCR using ITS1 and ITS4 primers as described previously. The product was subjected to sequencer sequencing and subjected to blast and it showed 99.41% similarity to M. fahalii (M696363). The patient was started on Voriconazole in lieu of voriconazole as the patient could not afford the drug. While there is no reduction in the size of the lesion the patient reported symptomatic relief and is still on follow-up.
Conclusions: To the best of our knowledge this is the first case of Mycetoma due to M. fahalii from India.

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Fungal isolates of the respiratory tract in symptomatic patients hospitalized in pulmonary units: A mycological and molecular epidemiologic study
Seyed Jamal Hashemi
Tehran University of Medical Sciences, Tehran, Iran
Poster session 2, Saturday, 22 April, 12:00 PM - 1:30 PM
Objective: Fungal respiratory infections are being recognized with increasing frequency in parallel with an expanding population of immunocompromised patients. In most cases, colonization is the first step in the progression to pulmonary fungal infection. This study was designed to evaluate the distribution of fungal elements in the respiratory tract of symptomatic patients hospitalized in pulmonary units.
Methods: This descriptive cross-sectional study was carried out over a period of 2 years, from October 2017 to October 2019 in Golestan province, located in Iran’s northern region. In the current study, bronchial/alveolar lavage or sputum specimens were collected. All samples were analyzed by direct microscopy using KOH 10% and culture. Fungal identification was accomplished by internal transcribed spacer (ITS) and beta-tubulin sequencing. Also, in patients suspected of invasive pulmonary aspergillosis, BAL specimens were tested for galactomannan (GM) antigen.
Results: A total of 184 lung specimens (192 bronchial/alveolar lavage (BAL) and 192 sputum samples) were obtained from symptomatic patients hospitalized in pulmonary units. Of these, 137 (75.67%) were positive in direct examination and cultures. Among the 157 positive cases, most isolates were from male patients (86.27%) and most of them were between 66 and 72 years. Candida albicans (57.22%) and C. tropicalis (21.88%) represent the two most commonly isolated species in the current study. C. glabrata (9.46%), dipospora (9.02%), paraklonea (62.04%), and weak local (56.2%) were the predominant opportunistic and relavations (24.84%), chromohyphomycosis (21.86%) and diabetes mellitus (19.70%) were the predominant underlying conditions. Also, 5 cases of invasive pulmonary aspergillosis and 2 cases of mucormycosis were diagnosed.
Conclusions: Candida albicans was the most common fungal species isolated from symptomatic patients hospitalized in pulmonary units. Tuberculosis, chromohyphomycosis and diabetes mellitus were important underlying conditions for pulmonary fungal colonization and/or infection.

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Fungal and bacterial co-infections of the respiratory tract among patients with COVID-19 hospitalized in intensive care units
Hasiti Karaul Sarvestani1, Mehrdad Khamseh2, Zehra Rezaei3, Alireza AbdiShahi4
1Tehran University of Medical Sciences, Tehran, Iran
2Department of Surgery, Sina Hospital, Tehran University of Medical Sciences, Tehran, Iran
3Tehran, Iran
4Department of Pathology, Imam Hospital Complex, Tehran University of Medical Sciences, Tehran, Iran
Poster session 2, Saturday, 22 April, 12:00 PM - 1:30 PM
Backgrounds: The pandemic of COVID-19 has created a global public health crisis. ICU patients with COVID-19 are prone to infections of bacterial and fungal origin due to several risk factors. Consequently, the current study was conducted to evaluate the frequency, demographic characteristics, underlying conditions, and etiologic agents of fungal and bacterial co-infections of the respiratory tract among ICU patients with COVID-19 in Iran.
Methods and Materials: From May to October 2020, sputum and bronchoalveolar aspirates were collected from ICU patients hospitalized with COVID-19 who also were suspected of bacterial and/or fungal co-infections according to inclusion criteria. The etiologic agents of bacterial co-infections were identified using the VITEK 2 identification method. For fungal identification, all samples were analyzed by direct microscopy using KOH 10% and culture. Furthermore, all isolates were subjected to sequencing method.
Results: A total of 75 lung specimens were obtained from patients who met the inclusion criteria. Of these, in 35 cases (20.54%) fungal and/or bacterial co-infections were confirmed. Males were more infected (75.53%) and all of them were between 49 and 72 years. Candida albicans (n = 8, 41.18%) and Klebsiella pneumoniae (n = 5, 28.64%) were the most frequent etiologic agents related to fungal and bacterial co-infections, respectively. Penicillia (n = 15, 100%) and diabetes mellitus (n = 8, 53.33%) were documented as the most prevalent underlying conditions. In the current study, 5 out of 15 patients (20%) died.
Conclusions: The frequency of bacterial co-infections of the respiratory tract in ICU patients hospitalized with COVID-19 was relatively high. According to the results, one of the causes of death in these patients could be a secondary infection.