The underlying condition of the patient at admission was accidental trauma in 4/14 (28.7%) chronic kidney disease in 2/14 (14.2%), hematological malignancy in 2/14 (14.2%), pneumonia in 1/14 (7.1%), retroviral disease in 1/14 (7.1%), acute febrile illness in 1/14 (7.1%). The risk factors for acquisition of infections with *Trichosporon* species in the 14 patients were administration of broad-spectrum antibiotics in 13 (92.8%), urinary catheterization in 11 (78.5%), central venous catheterization, and prolonged ICU stay in 8 (57.1%) each, previous antifungal therapy in 6 (42.8%). The other risk factors were chemotherapy, steroid usage, and neutropenia.

The clinical presentations were urinary tract infections in 10/14 (71.4%) patients (9 were catheter-associated UTIs), fungemia in 2/14 (14.2%), and wound infections in 2/14 (14.2%) patients.

Trichosporon asahii is the predominant species isolated in 12/14 (85.7%) patients. Other *Trichosporon* spp. isolated include *T. inkin* and *T. dohaense*. All the isolates were correctly identified by VITEK 2 except one which was identified as *T. inkin* in VITEK 2 and *T. dohaense* by MALDI-TOF.

All the isolates were susceptible to voriconazole and amphotericin B. 9/14 (64.2%) of the isolates were susceptible to fluconazole. *Trichosporon* spp. is inherently resistant to echinocandins.

A total of 7 patients (50%) were successfully treated with voriconazole for a period of 14 days with advice to follow up and discharged. In all, 5 patients (35.7%) died due to underlying diseases before treatment could be started.

Conclusion: Urinary tract infection, mostly CA-UTI was the commonest clinical presentation of Trichosporonosis in our study followed by bloodstream infection and wound infection. The commonest risk factor was prolonged broad-spectrum antibiotic therapy followed by urinary catheterization. The growth of *Trichosporon* spp. from various samples has to be interpreted with caution as the organism can also exist as a colonizer in different body sites. Voriconazole was effective in the treatment of trichosporonosis.

P255

Facial Tinea incognito: a clinical, dermoscopic, and mycological study

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Poster session 2, September 22, 2022, 12:30 PM - 1:30 PM

Objectives: Tinea incognito (TI) occurring on the face is the most frequently misdiagnosed cutaneous fungal infection; however, very limited information is available on facial TI. This study aimed to characterize the clinical, dermoscopic, and mycological features of facial TI.

Methods: We retrospectively evaluated 38 patients with mycologically proven facial TI at a single institution in Korea between July 2014 and July 2021.

Results: The patients had a mean age of 59.6 ± 20.4 years and showed a slight female predominance (male-to-female ratio, 1:1.5). The most common clinical presentation was an eczema-like pattern (47.3%), followed by rosacea-like (15.7%), psoriasis-like (10.5%), lupus erythematosus-like (10.5%), cellulitis-like (7.8%), and folliculitis-like (7.8%) patterns. The mean duration from disease onset to diagnostic confirmation was 3.4 months. Overall, 78.9% of the patients had accompanying chronic systemic diseases and 57.9% had concurrent tinea infections on other skin sites, mainly on the feet and toenails. Among the 23 (60.5%) cultured specimens, *Trichophyton* (*T.*) *rubrum* was the most frequently detected causative species, followed by *Microsporum* (*M.*) *canis*. *T. mentagrophytes* and *T. verrucosum* were also isolated from one case each. On dermoscopy, scales (92.1%) and dilated vascular patterns (arborizing vessels and telangiectasia, 76.3% and 63.2%) were commonly observed in glabrous skin, with follicular patterns such as black dots, broken hairs, and empty follicles. The characteristic trichoscopic features were comma hairs, corkscrew hairs, Morse code-like hairs, and translucent hairs.

Conclusion: The clinical characteristics and distinct dermoscopic features described in this article can aid in the differential diagnosis of facial TI while reducing diagnostic delays and unnecessary treatments.

P256

A rare case of co-infection with *Nigrospora oryzae* with mucormycosis in an immunocompromised post-COVID patient

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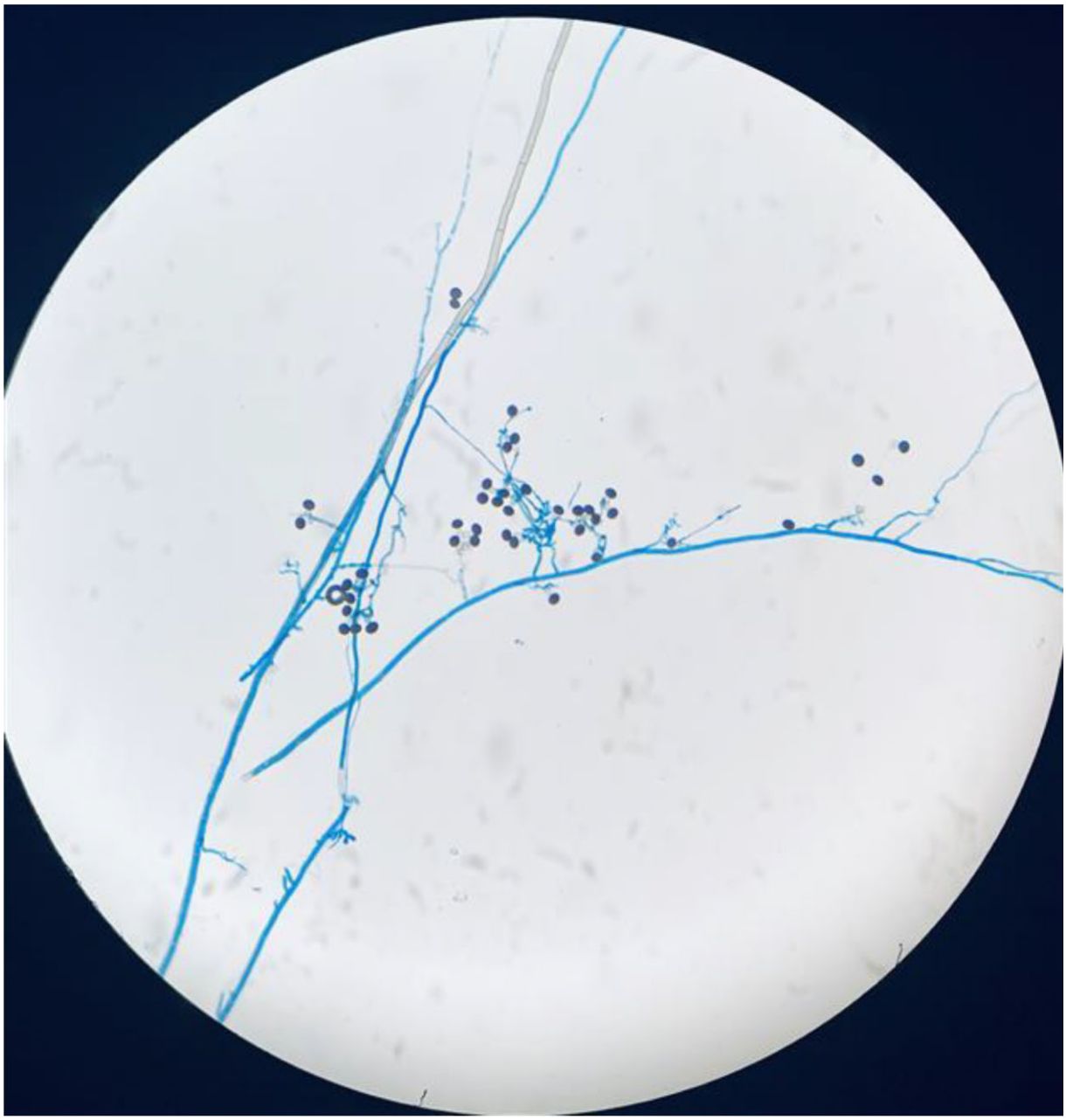
Objective: A rare case of co-infection of *Nigrospora oryzae* with mucormycosis in an immunocompromised post-COVID patient.

Methods: A 41-year-old male diabetic patient, with sub-optimal glycemic control, contracted COVID-19 infection and was managed with high-dose steroids. A month after recovery from COVID-19 infection, he developed severe headache with sudden onset right-sided facial swelling. A contrast-enhanced magnetic resonance imaging was done which was suggestive of infective/inflammatory rhinosinusitis with intracranial extension with a possibility of fungal etiology. Functional endoscopic sinus surgery was performed and tissue was sent for microbiological processing. On KOH mount, broad pauciseptate fungal hyphae were seen. Fungal growth was obtained on SDA at 25°C and 37°C within 4 days of inoculation. It was confirmed as *Rhizopus arrhizus* both phenotypically as well as by MALDI-TOF. Patient was put on antifungal therapy in form of Inj liposomal Amphotericin B 500 mg/d. However, patient had persistent headache, vomiting, and low-grade fever post-procedure. A repeat CE-MRI was performed which was suggestive of necrotic brain tumor/abscess and was planned for frontal lobe abscess drainage. Pus was inoculated on routine mycological media. On KOH mount, broad pauciseptate hyphae along with narrow septate hyphae were seen. Fungal growth was obtained on SDA at 25°C within 5 days of inoculation, which on LPCB were identified as *Nigrospora* spp. The identity of the isolate was confirmed by Next generation sequencing as *Nigrospora oryzae*. Post-2 weeks of treatment and strict glycemic control, patient started improving. The headache and swelling subsided. He was further started on oral hypoglycemic agents and discharged and was asked to follow up after a month.

Results: COVID-19 epidemic that emerged by the end of 2019 has been associated with a huge number of deaths globally. Acute invasive fungal rhino-sinusitis is a potentially fatal infection in immune-compromised patients post COVID-19. Various studies reveal that invasive fungal infections have been the leading cause of death in 25%-73.7% of patients. Among these invasive fungal infections, *Mucor* spp. were detected in 77.8% patient, *Aspergillus fumigatus* in 30.6% while 8.3% showed mixed infection with both the fungi. Along with the established pathogenicity of Mucorales in causing invasive fungal infection, other fungal co-infections are also being observed. These invasive fungal infections in an immune-compromised host carry a high mortality and morbidity rate (18%-80%). Therefore, early diagnosis, followed by aggressive medical care, surgical debridement, and control of underlying diseases is of utmost importance.

Conclusion: Acute invasive fungal rhinosinusitis saw a spurt in incidence during the widespread COVID-19 pandemic.

Diagnosis of invasive fungal infection is based on the clinical setting and characteristic presentation, supported by radiological and microbiological evidence. Prompt diagnosis and treatment are the need of the hour.



P257

Amplified fragment length polymorphism fingerprinting supports the absence of correlation of genotype with clinical phenotype or source of the isolate in *Aspergillus flavus* infections

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Objectives: *Aspergillus flavus* accounts for ~ 10% of bronchopulmonary aspergillosis and is the second leading etiological agent of invasive aspergillosis worldwide. It is the commonest cause of fungal rhinosinusitis and ocular mycoses in tropical countries including India. We report amplified fragment length polymorphism genotyping of a set of clinical and environmental isolates to unravel the genetic diversity of *A. flavus* in India and to further determine correlation between isolate genotype and the source/clinical phenotype of the *Aspergillus* infection.

Methods: Two sets of morphologically identified isolates of *A. flavus* from clinical ($n = 71$) and environmental sources ($n = 22$) were included in the study using a stratified random sampling method. Clinical strains were isolated from lower respiratory tract specimens ($n = 22$), sinus and sino-nasal biopsies ($n = 25$), corneal samples ($n = 12$), and others ($n = 12$). Environmental strains were isolated from different niches like air, soil, and infected crop samples. *Aspergillus fumigatus* F145 was used as an out-group. DNA was extracted from the fungal broth culture following the method of Lee et al. AFLP was done as per an earlier described method using HpyCH41V and Mse1 (New England BioLabs) for restriction digestion followed by selective amplification of restriction-digested products with 1 mM HpyCH4 IV primer with one selective residue (5-Flu-GTA-GACTGCGTACCCGTC-3'), 1 mM MseI primer with four selective residues (5-GATGAGTCCTGACTAATGAA). Fingerprint data was analyzed in BioNumerics software version 7.6 (Applied Maths, Belgium). The phylogenetic tree was constructed using Pearson's Correlation coefficient. An AFLP genotype was assigned to a cluster using an arbitrary cut-off value of ≥90% fingerprint similarity. The distribution of genotypes among different categories was analyzed by Fisher's exact test or Pearson's χ 2 goodness of fit test with Yates correction factor as appropriate and two-tailed *P*-values of <.05 were considered statistically significant.

Results: The analyses revealed a total of 16 AFLP genotypes with 5 major clusters (≥ 5 isolates) reflecting the extent of genetic diversity in *A. flavus*. Genotype VIII encompassed predominantly clinical isolates (P <.01) and genotype XI with majority of isolates from environmental sources (P <.0001). The strains which were isolated from invasive and non-invasive forms or from different sites (pulmonary, sinus, and ocular) did not diverge into separate or unique clusters. Although the genotypes had an asymmetric distribution in different clinical presentations as revealed by the χ2 goodness of fit test, none of the genotypes was exclusively responsible for causing a particular infection. Isolates from the north zone of India shared genotypes with those from the southern region of the country. Three isolates formed a separate genotype XVI and diverged from the *A. flavus* cluster by 42% fingerprint similarity. Partial β-tubulin and calmodulin gene sequencing-based phylogeny reconstruction placed those three isolates in *A. tamarii* clade of the *A. flavus* species complex.

Conclusions: This study suggests that every genotype of *A. flavus* has the potential of causing an allergic, non-invasive or invasive infection. Further, *A. flavus sensu stricto* was predominantly (97%) isolated from clinical specimens revealing the majority of infections/colonization are caused by this species compared to other members in the Flavi complex.

P258

Incidence of Histoplasmosis, Cryptococcosis, and TB Among People Living with HIV in Paraguay-Preliminary Report

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Objectives: Endemic fungal infections such as Histoplasmosis and Cryptococcosis as well as tuberculosis (TB) are important causes of mortality among people living with HIV (PLHIV) in Latin America. Rapid diagnostic assays (RDAs) could