F471 Feline sporotrichosis outcome and its impact in public health in Southern Brazil
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Sporotrichosis due to *Sporothrix brasiliensis* is an emerging and neglected disease in Brazil. Domestic cats are susceptible to a new presentation of this mycosis, carrying a high fungal load in their lesions. They frequently infect other animals and even humans by scratches and bites. Thus, the correct management and treatment of feline sporotrichosis are crucial aspects of the control of the disease in a population.

Objective: We aimed to evaluate the management and outcome of feline sporotrichosis cases in a hyperendemic city in southern Brazil (Rio Grande do Sul state).

Methods: Database from the Mycology Laboratory (LabMyc) of the Federal University of Rio Grande (FadEx-FURG) was consulted to gather data from all proven feline sporotrichosis cases (confirmed by mycological cultures), between January 2019 and December 2021. It was included in this study in all cases in which the phone number of the cat’s owner was available. All of them were contacted and invited for an interview by quick and short questions regarding the management and the outcome of their cats with sporotrichosis. Data collected from the owner’s interview, and phone number or/and contact were used as exclusion criteria.

Results: During the 3 year period studied a total of 62 owners, from 165 felines diagnosed with sporotrichosis in the LabMyc, had a phone number available. A total of 51 owners were included, totaling 57 participants in this study. More than half (51.9%, n = 14) reported treating only once to the veterinarian to clinical accomplishment, 48.1% (n = 15) of them do not use personal protective equipment to handle the infected animal. 44.4% (n = 12) highlighted the difficulty to daily administer drugs to the cat and only 16.5% (n = 5) affirmed to have isolated the infected animal during the treatment. Two animals (7.4%) with advanced signs of disseminated sporotrichosis died before starting treatment, and the others received iodine and/or potassium iodide as the drug of choice. Clinical cure was achieved in 40% of the cases treated (100/250, 28/702) resolved to death, 16% (62/393) are still in treatment due to new lesions (positive), and the other four animals were abandoned in the streets. In addition, asymptomatic transmission occurred in three (11.1%) owners, which developed lymphocutaneous sporotrichosis after a scratch or bite by the infected cat.

Conclusion: Sporotrichosis in Southern Brazil is a public health threat. In view of this, our study shows the urgent necessity of governmental strategies and interventions that promote health education and implement a service to attend, and provide treatment accomplishment to cats with sporotrichosis in view of control the current hyperendemic of this mycosis.

F473 Genomic epidemiology of antifungal-resistant Candida auris in Colombia
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Introduction: Candida auris is a public health threat. Five major clades of C. auris have been identified (Clades I-V). In Colombia, C. auris infections were first reported in 2016 with ongoing transmission reported from multiple cities. Here, we describe C. auris genomic epidemiology in Colombia detailing cases from 2016-2021.

Methods: A total of 99 C. auris cases were collected between June 2016 to January 2022 in Colombia, representing 15 geographic locations. Species confirmation, antifungal susceptibility testing, and whole-genome sequencing (WGS) were performed. In all, 37 genomic sequences generated previously from isolates from C. auris cases in Colombia, Venezuela, Panama, Israel, and United States were also analyzed. MycosNP workflows were used to assess sequence quality, map reads to the reference, and identify single-nucleotide polymorphisms (SNP). Patristic distances and a neighbor-joining tree were generated. 38CSE was used to generate a maximum-likelihood tree with bootstrap values.

Results: Phenotypic analysis identified 1,493 SNP positions. Isolates from Colombia clustered to Clade IV and predominantly grouped by country except for 19 fluconazole-resistant isolates from Bogota, Colombia that grouped with five isolates from Venezuela. In this cluster, 20% were resistant to fluconazole and 2% were resistant to fluconazole and the echinocandins micafungin. Remaining isolates from Bogota did not group in this cluster and were susceptible to fluconazole and micafungin.

A total of 98 isolated from Colombia clustered together. Within the Colombian cluster, there were two subgroups that had bootstrap support of 100% and were separated by 15 SNPs. The first subgroup was a cluster that contained 19 isolates from the north coast; 17 (94%)isolates were susceptible to amphotericin B and a second subgroup contained 24 isolates from Caraz and Norte de Santander, and 22 (91%) isolates were resistant to fluconazole.

Conclusions: Based on the phenotypic recombination, C. auris in Colombia continues to be of Clade IV. Antifungal-resistant isolates are predominantly from the north coast; fluconazole-resistant isolates were from a wider geographic area in Colombia, and echinocandin-resistant isolates were from Bogota. Within the Colombian cluster comparing two subgroups, we observed high genetic relatedness between isolates from different geographic locations suggesting transmission among cities.

F474 The value of PCR-based azole resistance detection in invasive aspergillosis: A prospective multicenter study
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Objective: Prospective detection of azole-resistant Aspergillus fumigatus will result in the timely start of active treatment against the emergence of invasive aspergillosis (IA). The use of a multiplex polymerase chain reaction (PCR) targeting Aspergillus species and fungi genes DNA as well as the most prevalent azole resistance-associated mutations (RAMs) in the cyp51A gene (TRG4, FHM and TRG4/V212I/RS299) could decrease the time to detect azole-resistant IA.

Methods: In a prospective study in 12 Dutch and Belgian centers, we evaluated the clinical value of the multiplex Aspergillus PCR in hematological patients with a pulmonary infiltrate undergoing bronchoalveolar lavage (BAL) sampling. The primary endpoint was antifungal treatment failure within 6 weeks after antifungal treatment initiation in the patients in which azole-resistant IA was detected. Treatment failure was defined as death or a switch to an antifungal agent from another class after at least 5 days of first-line therapy. Patients with a mixed azole-susceptible/ resistant infection were excluded from this analysis to ascertain that the infection was indeed caused by the resistant strain.

Results: Of 325 patients enrolled, sufficient BAL for PCR testing was obtained in 299. Probable fungal disease was diagnosed in 95 (31%). Aspergillus fumigatus in 24 (8.1%), Aspergillus fumigatus DNA as in 119 (39%), and A. flavus fumigatus DNA as in 89 (28%) patients. The resistance PCR was conclusive in 54/89 (41%) and RAMs were detected in 8 (15%). Table 1. All 8 had probable IA but 2 had a mixed infection and were excluded. In the 4 remaining patients, treatment failure was observed in one. Compared with the GM negative patients and despite antifungal therapy, a positive GM test was associated with a 13% higher 6-week overall mortality (P = .01). Table 2. Surprisingly, the 6-week mortality in the 65 patients who had a positive Aspergillus PCR but a negative GM and culture was not associated compared to those with a negative PCR (P = .14) or PCR 16% mortality, P = .68.

Conclusions: In patients with an underlying hematological disease and a pulmonary infiltrate, the detection of Aspergillus DNA by PCR on BAL was not associated with overall mortality. The exact place of the Aspergillus PCR in the DOTT-MIGREC invasive fungal infection criteria is therefore uncertain. In 13% of the patients in whom A. fumigatus DNA was present, azole RAMs were detected by PCR. In only 16% probable cases of IA with RAMs detected, antifungal treatment failure was observed. Being the choice of antifungal therapy on the result of a cyp51A resistance PCR may help to reduce the impact of azole resistance on mortality.