Antifungal agents susceptibility: profile of a tropical black yeast strain

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Objective

The aim of this research was to evaluate susceptibility to antifungal agents of a environmental isolate of black yeast, obtained from samples of water.

Methods

The yeast was obtained from a subtropical coastal lagoon in South America (fig 1). Identified from the D1/D2 domain of the 26S and ITS gene of the LSU rRNA, using the NL1/NL4 and ITS1/ITS4 universal primers, through the BLAST tool provided by the National Center for Biotechnology Information. The *in vitro* assay was performed using the microdilution technique according to protocol M27-A3 of the Clinical and Laboratory Standards Institute. The isolates were cultured on Sabouraud agar for 6 days at 30 ° C.

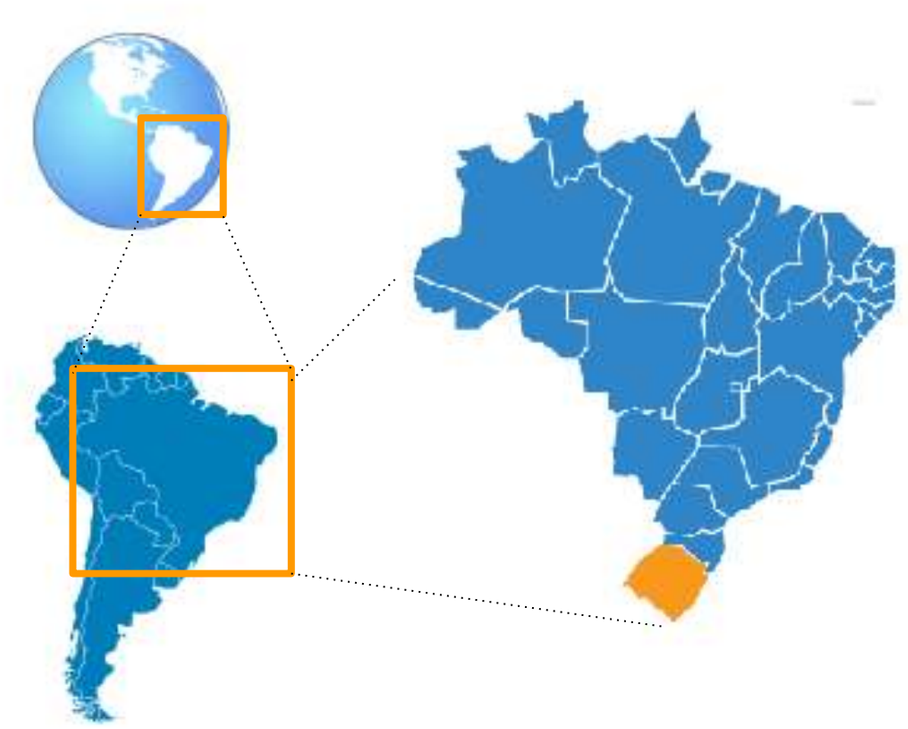

Figure 1. Study area filled in orange.

The inoculum was prepared in a 85% saline solution. The antifungals itraconazole, voriconazole, tioconazole, terbinafine and amphotericin B were tested at a concentration ranging from 16-0.0625 µg/mL. Fluconazole was tested at a concentration ranging from 64 to 0.125 µg/mL and caspofungin at 8 to 0.015 µg/mL. The whole test was done in triplicate. Incubation was performed for 7 days at 30 ° C. MICs were visually established as wells that showed total inhibition of growth.

Results

The black yeast was identified as *Hortaea werneckii*. The sequences obtained were compared to the sequences of the CBS 167.67 T strain available in the database GenBank. The isolate was resistant only to caspofungin (MIC ≥ 8 µg/mL) and susceptible to all the others antifungal agents tested, with the highest MICs for fluconazole (MIC ≥ 16 µg/mL), followed by amphotericin B (MIC ≥ 1 µg/mL), itraconazole, terbinafine, voriconazole and thioconazole.

Conclusion

Hortaea werneckii is frequently associated with *Tinea nigra* disease in tropical and subtropical coastal areas which commonly affects palms of the upper and lower limbs. It is a harmless disease except when it affects immunocompromised patients. *In vitro* studies contribute with information to medical community referring to the ideal treatment design from the resistance profiles already published.