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Genotypic variability and antifungal susceptibility of *Candida* spp. isolated from hospital surfaces and hands of healthcare professionals

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Objectives *Candida* spp. are responsible for 90–95% of hematogenous fungal infections. In Brazil and Latin America, *C. albicans* is the most common specie, followed by *C. parapsilosis* and *C. tropicalis*. Infections caused by *Candida* spp. may have their origin in exogenous sources, transmitted to patients via contaminated infusions, biomedical devices or even by the hands of the hospital staff members. Molecular biology techniques such as Randomly Amplified Polymorphic DNA (RAPD) can show that the strains found in anatomical sites or abiotic surfaces have the same pattern genome. Moreover, in the last decades it has been observed increasing the number of yeasts isolated from hospital environment resistant to antifungals. Thus, the aim of this study was to determine the susceptibility to antifungals and intraspecies similarity among isolates of different hospital surfaces and hands of healthcare professionals.

Methods The study was conducted with 25 isolates of *Candida* spp.: 5 strains of *C. albicans* and 5 strains of *C. parapsilosis* isolated from hospital surfaces. 5 strains of *C. albicans*, 5 strains of *C. parapsilosis* and 5 strains of *C. tropicalis* isolated from hands of healthcare professionals. Professionals and surfaces belonged to intensive care units. The minimal inhibitory concentration (MIC) was determined to voriconazole (VOR), fluconazole (FLZ), amphotericin B (AMB) and micafungin (MFG) according to M27-A3 of the Clinical and Laboratory Standards Institute (CLSI). To determine the intra-species similarity, 3 primers were used: P4 (5'-AAGAGCCCGT-3'), OPA-18

Table 1. Antifungal susceptibility of *Candida* spp. isolated from hospital surface and hands of healthcare professionals by the CLSI method

Species		Antifungals									
		Voriconazole			Fluconazole			Micafungin		Amphotericin B	
		S (%)	DDS (%)	R (%)	S (%)	DDS (%)	R (%)	S (%)	R (%)	S (%)	R (%)
<i>C. albicans</i>	Hospital surface	100	-	-	100	-	-	100	-	80	20
	Hands	60	20	20	80	20	-	80	20	80	20
<i>C. parapsilosis</i>	Hospital surface	100	-	-	100	-	-	20	80	100	-
	Hands	100	-	-	100	-	-	20	80	100	-
<i>C. tropicalis</i>	Hands	-	40	60	100	-	0	80	20	100	-

S: susceptible; DDS: dose-dependent susceptible; R: resistant

(5'AGCTGACCGT3') and OPE-18 (5'GGACTGCAGA 3'). RAPD profiles were analyzed using BioNumerics software version 4.6. The study was approved by the Ethics in research involving human subjects, CAAE 0448.0.093.000-11 protocol.

Results In relation to susceptibility testing (Table 1), it is important to highlight that *C. parapsilosis* showed 80% of MFG resistance. *C. albicans* and *C. tropicalis* showed reduced susceptibility to VOR, and resistance of the AMB was observed for *C. albicans* (20%). All amplifications revealed distinct polymorphic bands. Genetic distances between each of the isolates were calculated and cluster analysis was used to generate a dendrogram showing relationships between them. The analysis of all primers showed similarity greater than 80% between strains of hands and hospital surfaces for intraspecies.

Conclusion Our work shows that, healthy people and hospital surfaces may be colonized by different species yeast. Furthermore, the strains studied had relative resistance to antifungal drugs most frequently used in clinical practice. Finally, there was a high similarity between samples from hands (hospital staff members) and surfaces, providing an infection risk to susceptible individuals. Healthy people working in hospitals can carry yeasts on their hands with the same potential virulence, and which therefore offer the same risk of infection. This information should be considered when preventive measures are established. Attention to the colonization of hands and surfaces should not be restricted to high-risk units such as NICUs, but should also include other sections of hospitals.