Geographic variation in the prevalence of cryptic species of the *C. parapsilosis* complex in 6 Latin American countries.

Ana Carolina Remondi Souza[1], Ricardo Andreotti Siqueira[1], Marcio Nucci[2], Flávio de Queiroz-Telles[3], Tito Alvarado Matute[4], Iris Nora Tiraboschi[5], Jorge Alberto Cortes[6], Luis Thompson-Moya[7], María E. Santolaya[8], Manuel Guzman-Blanco[9], Jeannete Zurita[10], Arrnaldo Lopes Colombo[1] on behalf of Latin American Invasive Mycosis Network.

[1] UNIFESP – Universidade Federal de São Paulo (São Paulo, Brazil). [2] Hospital das Clínicas Universidade Federal do Paraná (Paraná, Brazil). [3] UFRJ – Universidade Federal do Rio de Janeiro (Rio de Janeiro, Brazil). [4] Hospital Escuela, (Tegucigalpa, Honduras). [5] Hospital de Clínicas José de San Martín, University of Buenos Aires (Buenos Aires, Argentina). [6] Universidad Nacional de Colombia (Bogotá, Colombia). [7] Clínica Alemana, Universidad del Desarrollo (Santiago, Chile). [8] Hospital Luis Calvo Mackenna, Universidad de Chile (Santiago, Chile). [9] Hospital Privado Centro Médico de Caracas (Caracas, Venezuela). [10] Hospital Vozandes Facultad de Medicina, Pontificia Universidad Católica del Ecuador (Quito, Ecuador)

C. parapsilosis is a common human pathogen able to cause superficial and invasive diseases worldwide. Recently, *C. parapsilosis* was characterized as a complex of species involving *C. parapsilosis* (*sensu stricto*), *C. orthopsilosis* and *C. metapsilosis*. There is little data about the real prevalence of cryptic species of *C. parapsilosis* complex in invasive human infections documented in different geographic areas. The aim of this study was to describe the prevalence and antifungal susceptibility profile of bloodstream isolates of *C. parapsilosis* species complex in Latin American hospitals. During a 24-month period we performed a laboratory-based survey of candidemia in 20 medical centers from Argentina, Brazil, Chile, Colombia, Ecuador, Venezuela and Honduras. A total of 218 bloodstream isolates of *C. parapsilosis* (*sensu lato*) were collected and tested. Speciation of the isolates was confirmed through molecular identification using a real time PCR. Antifungal susceptibility testing was performed using the CLSI broth microdilution method. Among the 218 isolates, 199 (91%) were identified as *C. parapsilosis* (*sensu stricto*), 15 (7%) as *C. orthopsilosis* and 4 (2%) as *C. metapsilosis*. Prevalence of *C. orthopsilosis* and *C. metapsilosis* ranged between 0 and 17.5% and 0 and 7%, respectively, among different countries. Chile had no single isolate of *C. orthopsilosis* and *C. metapsilosis.* All isolates were susceptible to amphotericin B (MIC ≤ 1 µg/mL), and anidulafungin (MIC ≤ 2 µg/mL). Regarding the azoles, 3 and 2 *C. parapsilosis* (*sensu stricto*) isolates were susceptible-dose dependent to fluconazole (MIC = 4µg/mL) and voriconazole (MIC = 0.5 µg/mL), respectively. Our data suggest that *C. orthopsilosis* is quite rare in Latin America being the vast majority of cases caused by *C parapsilosis* (*sensu strict*o). The currently used antifungal agents generally exhibited good in vitro activities against all *C. parapsilosis* (*sensu lato*) species.

Key words: *C. parapsilosis* species complex, Latin America, antifungal susceptibility
Grants: FAPESP and CNPQ