Genotyping of Candida albicans and Candida parapsilosis isolates causing fungemia in neonates: persistent or sporadic clusters?

P. Escribano1,2,3, L.J. Marcos-Zambrano1,2, C. Sánchez-Carrillo1,2,3, B. Padilla1,2,3, E. Zamora2,4, M. Sánchez-Luna2,4, E. Bouza1,2,3,4, J. Guinea1,2,3,4

1 Clinical Microbiology and Infectious Diseases, Hospital General Universitario Gregorio Marañón, Madrid, Spain. 2 Instituto de Investigación Sanitaria Gregorio Marañón, Madrid, Spain. 3 CIBER Enfermedades Respiratorias-CIBERES (CB06/06/0058), Madrid, Spain. 4 Medicine Department, Faculty of Medicine, Universidad Complutense de Madrid. 5 Neonatology, Hospital General Universitario Gregorio Marañón

INTRODUCTION AND PURPOSE

Candidemia is generally a nosocomial infection. The incidence of candidemia in neonatal intensive care units (NICUs) has increased considerably in the last decade due to the increased survival of low birth weight neonates and the improvements in diagnostic and therapeutic procedures.

Candida albicans and C. parapsilosis are common causes of candidemia in NICUs. C. albicans and C. parapsilosis are part of the microbiota of patients, but candidemia caused by exogenous strains can be acquired during the hospital stay and can even cause nosocomial outbreaks.

Genotyping can detect clusters of C. albicans and C. parapsilosis causing candidemia, which may suggest hospital transmission, and enable us to implement prevention measures. We assessed the frequency of C. albicans and C. parapsilosis clusters causing candidemia in the NICU and their chronological distribution during a long period of time.

Overall, we found 54 genotypes and 18.5% of them were clusters (Figure 2). We did not find statistically significant differences between C. albicans and C. parapsilosis.

MATERIAL & METHODS

We retrospectively studied 78 patients admitted to the NICU of Gregorio Marañón Hospital (Madrid, Spain) with candidemia caused by C. albicans (n=47) or C. parapsilosis (n=31) between January 2007 and December 2014.

The incident isolates were identified after amplification and sequencing of the ITS1 and ITS2 regions and further genotyped using species-specific highly polymorphic microsatellite markers.

Isolates were considered to be identical genotypes when they showed the same alleles for all loci. A cluster was defined as a group of 2 or more patients infected by an identical genotype.

RESULTS

The distribution of the 78 patients with candidemia caused by C. albicans and C. parapsilosis is shown in Figure 1.

The number of patients infected per year ranged from 0 to 17 for C. albicans and from 1 to 7 for C. parapsilosis. The highest number of episodes were found 2010 (Figure 4).

CONCLUSIONS

✓ A high proportion of C. albicans and C. parapsilosis clusters causing candidemia in neonates were detected and involved a high number of patients.

✓ The chronological distribution of clusters differed between species: C. albicans clusters were sporadic, whereas one C. parapsilosis cluster persisted in the unit for a long period and affected a high number of neonates.