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Abstract (publication only)

Genotypic analysis of Candida parapsilosis isolates causing fungaemia: evidence of endemic genotypes in the hospital

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Objectives: Nosocomial outbreaks of Candida parapsilosis candidemia have been reported in adult and neonatal intensive care units (ICUs). However, the proportion of genotypes clustered and the hospital location of patients within each cluster remain unknown. The aim of this study was to assess the frequency of nosocomial clusters of C. parapsilosis isolates causing candidemia in a large hospital. Methods: We analyzed 134 C. parapsilosis sensu stricto isolates from the blood cultures of 118 patients (January 2007 to July 2012) located on the following wards at the time of sample collection: oncology (n=27), neonatology (n=25), surgery (n=18), adult and paediatric ICU (n=13), and other (n=35). Each isolate represented 1 episode of candidemia. Subsequent episodes were defined as isolation of C. parapsilosis in further blood cultures taken >=7 days after the last isolation in blood culture. Patients had 1 episode (n=103), 2 episodes (n=14), or 3 (n=1) episodes. A panel of 4 short tandem repeat markers was used for genotyping. Clusters included isolates with identical alleles for the 4 markers. Results: We found 78 different genotypes in the 134 isolates. The genotypes causing the first and subsequent episodes were different in 2/15 patients with multiple episodes. Of the 78 genotypes, 64 infected 1 patient each; the other 14 genotypes clustered and infected 56 patients. Each cluster involved 2-13 patients each. In 11/14 clusters, the patients involved were located on different wards, mostly in oncology (6/11). The remaining 3/14 clusters involved patients located in paediatric (n=1) or neonatal (n=2) units; patients included in each cluster were not necessarily admitted to the unit at the same time. One of the clusters included 13 patients who were admitted to the neonatology ward from 2007 to 2011. Conclusions: Half of all patients with candidemia caused by C. parapsilosis were infected by a genotype found in at least one other patient. Clusters mainly involved patients admitted to the oncology and neonatology units, and some of the endemic genotypes persisted for years. Our findings suggest the presence of nosocomial transmission of C. parapsilosis in our hospital. Prospective studies are needed to identify the source of the infections.