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Abstract (publication only)

Outbreak of neonatal invasive candidiasis due to *Candida albicans* investigated by molecular typing

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Objective: Invasive candidiasis (IC) has emerged as a major problem in neonatal intensive care units (NICUs). We investigated herein the temporal clustering of six cases of neonatal IC due to *Candida albicans* in the NICU of Farhat Hached teaching Hospital at Sousse City, Tunisia. **Methods:** Eighteen isolates obtained from six infected neonates (eleven isolates were collected from blood and deep-site samples, six isolates from implanted medical devices and one isolate from a urine sample) and two isolates from two nurses working at the same unit and suffering from fingers' onychomycosis were genotyped by electrophoretic karyotyping (EK) and restriction endonuclease analysis of genomic DNA by using Sfi I (PFGE-Sfi I). **Results:** The 20 tested isolates generated 9 different PFGE-Sfi I patterns but only 4 different karyotypes. PFGE-Sfi I was more effective in discriminating between the temporally related isolates. It showed that: (i) Both HCWs had specific strains excluding them as source of infections in neonates. (ii) Isolates collected from three neonates were identical providing evidence of their clonal origin and the occurrence of a horizontal transmission of *C. albicans* in the unit. (iii) The three remaining neonates had specific strains confirming that the IC cases were coincidental. (iv) Microevolution occurred in one catheter-related candidemia case. **Conclusion:** Our results illustrate the relevance of the molecular approach to investigate suspected outbreaks in hospital surveys and the effectiveness of PFGE-Sfi I for the typing of epidemiologically related *C. albicans* isolates.