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Elucidating the Origins of *Candida albicans* in an ICU

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Marco and colleagues from the University of Iowa and the CDC's Hospital Infections Program have reported on a study that used computer-assisted DNA fingerprinting with the complex probe Ca3 to analyze the relatedness of isolates collected from individuals with nosocomial bloodstream infections (BSIs) and hospital care workers (HCWs) in the surgical and neonatal intensive care units (ICUs) of four hospitals. The results demonstrate that, for the majority of patients (90%), isolates collected from commensal sites before and after collection of a BSI isolate were highly similar or identical to the BSI isolate. In addition, the average similarity coefficient for BSI isolates was similar to that for unrelated control isolates. However, the cluster characteristics of BSI isolates in dendrograms generated for each hospital compared to those of unrelated control isolates in a dendrogram demonstrated a higher degree of clustering of the former. In addition, a higher degree of clustering was observed in mixed dendrograms for HCW isolates and BSI isolates for each of the four test hospitals. In most cases, HCW isolates from an ICU were collected after the related BSI isolate, but in a few cases, the reverse was true.

Although the results demonstrate that single dominant endemic strains are not responsible for nosocomial BSIs in neonatal ICUs and surgical ICUs, they suggest that multiple endemic strains may be responsible for a significant number of cases. The results also suggest that cross-contamination occurs between patients and HCWs and between HCWs in the same ICU and in different ICUs. The temporal sequence of isolation also suggests that, in the majority of cases, HCWs are contaminated by isolates from colonized patients; in a significant minority, the reverse is true. The results of this study provide the framework for a strategy for more definitive testing of the origins of *Candida albicans* strains responsible for nosocomial infections.

FROM: Marco F, Lockhart SR, Pfaller MA, Pujol C, Rangel-Frausto MS, Wiblin T, et al. Elucidating the origins of nosocomial infections with *Candida albicans* by DNA fingerprinting with the complex probe Ca3. *J Clin Microbiol* 1999;37:2817-2828.

Longitudinal Analysis of MRSA at a Teaching Hospital in Taiwan

In Taiwan, the frequency of nosocomial infections caused by methicillin-resistant *Staphylococcus aureus* (MRSA) has increased rapidly during the past 10 years. Chen and colleagues from the Department of Laboratory Medicine, National Taiwan University Hospital, Taipei, Taiwan, performed a study to investigate the epidemiology of MRSA infections. A total of 140 MRSA isolates collected at National Taiwan University Hospital from 1992 to 1996 were characterized by pulsed-field gel electrophoresis (PFGE) profiles and antibiotypes, as determined with the disk-diffusion method. Among these isolates, six PFGE types (with 20 subtypes) and six antibiotypes were identified. Antibiotyping proved to be a poor method for epidemiological analysis, because almost all of the MRSA isolates analyzed shared a very similar multidrug-resistant antibiotype.

Most MRSA infections and colonizations in this hospital were due to the spread of strains belonging to three major PFGE types (A, B, and C). However, the major type changed in different years with types A, B, and C being predominant in 1992 through 1993, 1994 through 1995, and 1996, respectively. The three major PFGE types spread easily throughout the hospital wards, presumably carried by healthcare workers and environmental contamination. The results demonstrate that there was a dominant strain spreading in their hospital each year and the dominant strain may shift in different years.

FROM: Chen ML, Chang SC, Pan HJ, Hsueh PR, Yang LS, Ho SW, et al. Longitudinal analysis of methicillin-resistant *Staphylococcus aureus* isolates at a teaching hospital in Taiwan. *J Formos Med Assoc* 1999; 98:426-432.