

P745

Abstract (poster session)

**Clonal diversity of *Candida albicans* isolates causing candidaemia over a 4-year period: patients located in different departments can be infected by identical genotypes**

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**Objectives:** Most episodes of fungaemia are caused by *Candida albicans*. Genotyping of *C. albicans* strains isolated from blood may clarify the genotypic diversity of this species, although the technique is rarely performed. We studied the clonal diversity of *C. albicans* isolates using a highly reproducible and discriminatory microsatellite marker panel. **Methods:** We studied 186 *C. albicans* strains isolated from the blood cultures of 174 patients with candidaemia (Jan 2007 to Dec 2010). Each isolate represented 1 episode of candidaemia. Multiple episodes were defined as isolation of *C. albicans* in further blood cultures taken  $\geq 7$  days after the last isolation in blood culture. The isolates were identified after amplification and sequencing of the ITS1-5.8S-ITS2 region and further genotyped using a panel of 6 microsatellite markers (Botterel JCM 2001, Sampaio JCM 2003, Sampaio JCM 2005). Patients had 1 episode (n=160), 2 episodes (n=9), or 3 (n=1) episodes. Patients with mixed genotypes in the same culture were excluded (n=4). Identical genotypes showed the same alleles for all 6 markers. A similarity dendrogram was constructed using the remaining 181 strains from the 170 patients included. **Results:** An inpatient analysis revealed that the genotypes causing both episodes were identical in most patients with 2 episodes (7/9). In contrast, 2 different genotypes were found in the patient with 3 episodes, one causing the first and second episodes and the other causing the third episode (isolated 6 months later). An interpatient analysis revealed that 124 of the 143 different genotypes found were involved only in 1 episode (n=121 patients); the remaining genotypes grouped in 19 clusters (n=49 patients) including 2-5 patients each. In 13 of the 19 clusters, the patients were infected by the same genotype but had been admitted to different departments. In contrast, each of the remaining 6 clusters grouped isolates from patients infected by the same genotype in the same department; interestingly, 4 of the clusters had a different genotype and involved patients admitted to the same unit (neonatology). **Conclusion:** We showed that patients admitted to hospital could develop candidaemia caused by an identical genotype of *C. albicans*. In up to 70% of cases, patients were not located in the same department at diagnosis. In contrast, in patients with multiple episodes of *C. albicans* candidaemia, the genotype causing the first episode was found in the subsequent episodes.