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Genotypic analysis of C. albicans, C. parapsilosis and C. tropicalis isolates causing candidaemia in Copenhagen over a 2-year period

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Background: Candidaemia is generally nosocomially acquired and genotyping of *Candida* spp. isolates can unravel the presence of clusters (identical genotypes infecting different patients) in order to study the patient-to-patient transmission or a common source for infection. We genotyped a collection of candidaemia isolates from patients admitted to tertiary hospitals located in greater Copenhagen, Denmark to gain more insight into the genotypic relationship between isolates.

Material/methods: : We studied 169 isolates [*C. albicans* (n= 139), *C. parapsilosis* (n=14) and *C. tropicalis* (n=17)] from blood cultures of 161 patients with candidaemia (Jan 2014 to Dec 2015) admitted to tertiary hospitals in greater Copenhagen (HI, GE, BBH, HE, RH FRH, GL, HV). We used a panel of 6 microsatellite markers for genotyping *C. albicans* (CDC3, EF3, HIS3, CAI, CAIII, and CAVI), 6 markers for *C. tropicalis* (Ctm1, Ctm10, Ctm12, Ctm21, Ctm24, and Ctm28); and 4 for *C. parapsilosis* (CP1, CP4a, CP6, and B). Identical genotypes showed the same alleles for all markers and a cluster was defined as group of ≥2 patients sharing an identical genotype.

Results: A total of 147 unique genotypes [*C. albicans* (n= 120), *C. parapsilosis* (n=13) and *C. tropicalis* (n=14)] were found. Overall, 13% and 23.5% of *C. albicans* and *C. tropicalis* isolates, respectively, were in clusters. From 7 patients sequential isolates were included (5 with *C. albicans*, 1 with *C. parapsilosis,* and 1 with *C. tropicalis*) and in all cases sequential isolates were isogenic.

Additionally, we found 9 clusters [*C. albicans* (CA, n= 7), and *C. tropicalis* (CT, n=2)]. CA clusters involved 18 patients (2-5 patients each) whereas CT clusters involved 2 each. 8/9 clusters involved patients admitted to different hospitals. The remaining cluster (CA-1) involved two patients admitted to the same hospital but at to different wards (thorax-surgical vs. gastro-surgical departments) and more than a year apart:

Cluster code	**No. of patients involved**	**Sampling interval (days)**	**Hospital (Department)**
CA-1	2	+508	RH (Thorax-Surgery) RH (Gastroenterology-Surgery)
CA-2	2	+64	HV (Gastroenterology-Medicine) GL (General Medicine)
CA-3	5	+450	RH (Hepatology) RH (Gastroenterology-Surgery) RH (Gastroenterology-Medicine) RH (ICU-a) FRH (Urology)
CA-4	2	+458	RH (ICU-b) HI (ICU)
CA-5	3	+332	RH (Traumatology) RH (ICU-b) GE (General Medicine)
CA-6	2	+241	HV (Gastroenterology-Medicine) FRH (Medical Admission Unit)
CA-7	2	+547	BBH (Orthopedic-Surgery) RH (Gastroenterology-Medicine)
CT-1	2	+186	GL (General Medicine) RH (ICU-b)
CT-2	2	+178	HE (ICU) HI (Cardio/nephro/endocrine-Medicine)

Conclusions: Microsatellite genotyping is a well-established genotyping method and indeed all sequential isolates from individual patients were isogenic. However, we found no obvious geographic/temporal links between different patients sharing identical genotypes. This suggests that clusters are probably explained by ubiquitous genotypes or that the insufficient discriminatory potential of the adopted genotyping method rather than by horizontal transmission among our hospitalized patients.