

P2178 Genotyping proved that *Candida* colonising isolates can be further found causing candidaemia

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Background: *Candida* colonization on non-sterile sites has been proven to be a risk factor for further acquisition of candidemia. Although the presence of identical species in both blood and colonising samples is frequently considered as identical strains, in the absence of genotyping that cannot be proved. We genotyped *C. albicans*, *C. parapsilosis*, and *C. tropicalis* strains from patients with candidemia who were previously colonized by the same species in order to get more insight of the dynamics of genotypes found in the patients.

Materials/methods: We studied patients admitted to Hospital General Universitario Gregorio Marañón in Madrid (Spain) from January 2016 to July 2018 with candidemia who had been previously colonized. All available isolates from the patients (one colony per sample) were genotyped by species-specific microsatellite markers. Isolates were considered identical when they showed identical alleles for all loci. Antifungal susceptibility to amphotericin B, fluconazole, voriconazole, posaconazole, micafungin, and anidulafungin was tested according to EUCAST 7.3.1 method.

Results: A total of 86 patients (*C. albicans*, n=47; *C. parapsilosis*, n=24; *C. tropicalis*, n=5) developed candidemia during the study period, and 9.2% of them (*C. albicans*, n=5; *C. parapsilosis*, n=1; *C. tropicalis*, n=2) were previously colonized. The 8 patients yielded a total of 13 colonizing isolates sourcing the lower respiratory tract (n=11) and urine (n=2). In all cases, we found matches between genotypes found in non-sterile samples and bloodstream isolates; none of genotypes was found in more than one patient (Figure). Colonizing isolates preceded the ones from blood a mean of 30.4 days (range 1-120 days). Patient no. 5 had respiratory samples and intra-abdominal abscesses with the same genotype found 3 months before the outset of candidemia. In each patient, no differences in terms of antifungal susceptibility was found among isolates.

Conclusions: We proved that genotypes found in non-sterile samples may be found further causing candidemia. Future studies to explore the potential of some genotypes to first colonise the patient and then cause candidemia later on are warranted.

Specie	Patient	Sample	Days	Genotype
<i>C. albicans</i>	1	Urine	0	CA-844
		Traqueal aspirate	+ 2	
		Blood	+ 4	
	2	Bronchial aspirate	0	CA-434
		Bronchial aspirate	+ 4	
		Blood	+ 11	
	3	Bronchial aspirate	0	CA-946
		Bronchial aspirate	+ 40	
		Blood	+ 60	
	4	Bronchial aspirate	0	CA-618
		Bronchial aspirate	+ 4	
		Blood	+ 5	
	5	Bronchoalveolar lavage	0	CA-947
		Intra-abdominal abscess	+ 12	
		Traqueal aspirate	+ 21	
Intra-abdominal abscess		+ 46		
Blood		+ 120		
<i>C. parapsilosis</i>	6	Bronchoalveolar lavage	0	CP-065
		Blood	+ 1	
<i>C. tropicalis</i>	7	Bronchial aspirate	0	CT-164
		Blood	+ 4	
	8	Urine probe	0	CT-031
		Blood	+ 30	

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