

P2179 Genotyping of *Candida* species isolates from non-blood samples: is clonal diversity similar to that found in blood?Judith Diaz-Garcia¹, Aina Mesquida¹, Ana Gómez¹, Patricia Muñoz¹, Emilio Bouza Santiago¹, Jesus Guinea Ortega¹, Pilar Escribano¹¹ Gregorio Marañón Hospital, Madrid, Spain

Background: Genotyping has been useful to get insight about the presence of *Candida* clusters infecting different patients, thus suggesting patient-to-patient transmission, and therefore offering scenarios for prevention campaigns of candidemia. However, clonality of isolates sourcing for anatomical sites other than blood has been poorly studied. We here present data on genotyping of a large collection of three relevant *Candida* species isolates from blood and non-blood compartments.

Materials/methods: We studied 361 *Candida* spp isolates from 312 patients admitted to Hospital General Universitario Gregorio Marañón, Madrid, Spain (January 2016 to July 2018) (Table). Isolates sourced from blood (n=83), and other anatomical sites (n=278; non-blood sterile samples [n=60], and non-sterile samples [n=215]). All isolates were genotyped by means of species-specific microsatellite markers. Cluster was defined as a group of ≥ 2 patients infected by an identical genotype.

Results: Overall, we found 297 genotypes, 276 of them were singleton and 21 (7%) were clusters. The percentage of isolates involved in cluster trended to be higher in *C. albicans* and *C. tropicalis* (15%) compared to *C. parapsilosis* (12%). No isolates coming exclusively from blood were found to be clustering patients. In contrast, most of clusters were *C. albicans* (n=10) and *C. tropicalis* (n=3) isolates sourcing from non-blood samples, mostly urine and respiratory samples. Finally, some clusters involved isolates from blood samples from given patients and non-sterile sites from others. Clusters involved unrelated patients.

Conclusions: Clusters were more frequently found in isolates sourcing from non-sterile samples from unrelated patients. The presence of endemic genotypes in the hospital environment may explain why apparently unrelated patients may become colonized by identical genotypes. In-depth characterization of clusters is needed.

	Number			Number of clusters		
	Isolates	Genotypes	Clusters	Blood/ Blood	Non-blood/ Non-blood	Blood/ Non-blood
<i>C. albicans</i>	253	208	15	0	10	5
<i>C. parapsilosis</i>	67	53	3	0	0	3
<i>C. tropicalis</i>	41	36	3	0	3	0
Overall	361	297	21	0	13	8