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**Genotyping reveals the frequency of clusters of *Candida albicans*, *Candida parapsilosis*, and *Candida tropicalis* causing candidaemia in hospitals located in Madrid and Valencia, Spain**

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**Background:** The presence of *Candida* spp clusters (identical genotypes infecting different patients) might suggest either patient-to-patient transmission or widespread genotypes. We have searched for the presence of clusters in isolates of three relevant *Candida* species causing candidemia in patients admitted to 4 hospitals located in Spain.

**Material/methods:** We studied 287 *C. albicans*, *C. parapsilosis* and *C. tropicalis* isolates causing candidemia in patients admitted to four hospitals located at Spain [Madrid, n=3 (M1, M2, and M3) and Valencia, n=1 (V1)] from Jan-2014 to Dec-2015. Isolates were genotyped by means of species-specific microsatellite markers. Singleton genotypes were found only once whereas clusters were defined as isolates showing identical genotypes (the same alleles for all loci); widespread genotypes were those clusters involving isolates from different hospitals.

**Results:** A total of 240 genotypes were detected and overall, 10.4% (n=25) of them were clusters, a proportion that varied among species (7.3% *C. albicans*, 15% *C. parapsilosis* and 0% *C. tropicalis*) ( $P<0.05$ ).

	No. of isolates/single genotypes/clusters				
	Spain				Overall
	M1	M2	M3	V1	
<i>C. albicans</i>	51/47/2	30/28/1	8/6/1	44/39/2	133/113/9
<i>C. parapsilosis</i>	31/27/2	31/15/6	31/21/4	49/31/5	142/90/16
<i>C. tropicalis</i>	4/4/0	2/2/0	2/2/0	4/4/0	12/12/0
<b>Overall</b>	86/78/4	63/55/7	41/29/5	97/74/7	

Overall, 32% of the isolates/patients were involved in clusters, a proportion that was also different among species (15% *C. albicans*, 40% *C. parapsilosis*, and 0% *C. tropicalis*) ( $P<0.001$ ). Clusters of *C. albicans*, and *C. parapsilosis* involved 2-3 and 2-8 patients each, respectively. Some clusters (n=17) were found in single hospitals but the remaining 8 were widespread genotypes found in patients admitted to hospitals located at the same city (*C. albicans* =1; *C. parapsilosis* =2), or located at different cities (*C. albicans* =1; *C. parapsilosis* =4).

**Conclusions:** Around 10% of the *C. albicans* and *C. parapsilosis* isolates causing candidemia in the hospitals studied were clusters with *C. parapsilosis* as the species showing the highest proportion of clusters. Eight clusters (representing 3.3% of the genotypes) were geographically widespread and they probably do not indicate patient-to-patient transmission. An in-depth characterization of the clusters is being currently conducted