

O0863 **Molecular investigation reveals widespread invasive *Candida* genotypes in three European countries**

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Background: We previously reported *Candida* spp. clusters eventually found in patients admitted to different hospitals even in those located in different cities and countries. We here analysed the genotypes found in a large collection of candidaemia isolates from patients admitted to 15 hospitals located in Spain, Italy and Denmark to gain more insight into the presence of widespread genotypes.

Materials/methods: From January 2007 to September 2017, a total of 1477 isolates/patients from 5 hospitals in Madrid and Valencia (*C. albicans* n=522; *C. parapsilosis* n=369), 2 hospitals in Rome (*C. albicans* n=296; *C. parapsilosis* n=145) and 8 hospitals in Copenhagen (*C. albicans* n=132; *C. parapsilosis* n=13) were genotyped by means of species-specific microsatellite markers. The probability of identity (probability of finding identical genotypes by chance) was calculated. A cluster was defined as a group of ≥ 2 patients infected by an identical genotype; widespread genotypes were clusters involving patients from different countries.

Results: The probability of identity for *C. albicans* and *C. parapsilosis* was 2.2×10^9 and 1.6×10^6 respectively. A total of 1099 genotypes were detected, 955 (87%) were singleton and 144 (13%) were clusters. The proportion of clusters was not statistically different between species (*C. albicans*, 12.0%; *C. parapsilosis*, 15.5%). Many clusters were country-specific but a considerable number (35%; 50/144) were widespread genotypes involving around 17% of patients. Whereas some widespread genotypes (*C. albicans* =29; *C. parapsilosis* =13) were found in two countries, the remaining genotypes were found in the three countries (*C. albicans* =6; *C. parapsilosis* =2). The table shows the number of clusters found in single countries, in two countries, and in three countries. Most of *C. albicans* (n=22) and *C. parapsilosis* (n=10) widespread genotypes involved isolates from Spain and Italy, probably due to the large number of isolates from both countries.

	<i>C. albicans</i> n° of clusters (% isolates in clusters)			<i>C. parapsilosis</i> n° of clusters (% isolates in clusters)		
	Spain	Rome	Copenhagen	Spain	Rome	Copenhagen
Spain	31 (15%)			30 (32%)		
Rome	22 (10%)	19 (14%)		10 (12%)	9 (16%)	
Copenhagen	3 (1.2%)	4 (2.5%)	5 (4%)	1 (0.5%)	2 (3%)	0 (0%)
All countries		6 (5.3%)			2 (4.3%)	

Conclusions: Around 4.5% of genotypes were widespread and involved up to 17% of the candidaemia isolates studied. Mostly of the widespread genotypes (64%) were predominantly distributed between Spain and Italy.